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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 13:07:09 ; Search time 3070.75 Seconds
(without alignments)
16232.024 Million cell updates/sec

Title: US-10-679-999-7
Perfect score: 1150
Sequence: 1 CATATGGAACCCAAATCTTG.....TCCGGGTTGTTAATGGATCC 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 5430052

Minimum DB seq length: 0
Maximum DB seq length: 1150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1150	100.0	1150	6	BD056517	BD056517 OB fusion
2	1134	98.6	1150	6	BD056519	BD056519 OB fusion
3	1117.8	97.2	1135	6	BD056521	BD056521 OB fusion
4	1105	96.1	1135	6	BD056523	BD056523 OB fusion
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7	694.8	60.4	990	6	AX047023	AX047023 Sequence
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11	694.4	60.4	762	6	AX556168	AX556168 Sequence
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ALIGNMENTS

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LOCUS BD056517 1150 bp DNA linear PAT 27-AUG-2002
DEFINITION OB fusion protein compositions and methods.
ACCESSION BD056517
VERSION BD056517.1 GI:22602123
KEYWORDS JP 2001512417-A/5.
SOURCE Aequorea victoria
ORGANISM Aequorea victoria
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
REFERENCE 1 (bases 1 to 1150)
AUTHORS Mann,M.B. and Hecht,R.I.
TITLE OB fusion protein compositions and methods
JOURNAL Patent: JP 2001512417-A 5 21-AUG-2001;

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            AMGEN INC
COMMENT     PN   JP 2001512417-A/5
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
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            CC   Strandedness: Double;
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Db       1141 TAATGGATCC 1150


RESULT 2
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LOCUS       BD056519                1150 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056519
VERSION     BD056519.1  GI:22602125
KEYWORDS    JP 2001512417-A/7.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1150)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 7 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/7
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
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            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
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            CC   Strandedness: Double;
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LOCUS       BD056521                1135 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056521
VERSION     BD056521.1  GI:22602127
KEYWORDS    JP 2001512417-A/9.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1135)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 9 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/9
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            PR   20-DEC-1996 US    08/770973
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Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
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Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
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Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
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Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741
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Qy        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801
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Db        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786

Qy        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861
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Db        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846

Qy        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921
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Db        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906

Qy        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981
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Db        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966

Qy        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041
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Db        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026

Qy       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101
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Db       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086

Qy       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
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Db       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
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RESULT 4
BD056523

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LOCUS       BD056523               1135 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056523
VERSION     BD056523.1  GI:22602129
KEYWORDS    JP 2001512417-A/11.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1135)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 11 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/11
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   /note= 'Met = ATG'
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .1135
                        /organism="Aequorea victoria"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:6100"
ORIGIN
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Query Match 96.1%; Score 1105; DB 6; Length 1135;
Best Local Similarity 98.7%; Pred. No. 1.2e-222;
Matches 1114; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy         22 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 81
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Db          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126

Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
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Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
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Db        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246

Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
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Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
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Db        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366

Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

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Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
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Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726

Qy        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786

Qy        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846

Qy        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906

Qy        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966

Qy        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026

Qy       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101
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Db       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086

Qy       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
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Db       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135


RESULT 5
AR173437
LOCUS       AR173437               1080 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 14 from patent US 6306395.
ACCESSION   AR173437
VERSION     AR173437.1  GI:17913757
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1080)
  AUTHORS   Nakamura,N. and Nagata,S.
  TITLE     Fas antigen derivatives
  JOURNAL   Patent: US 6306395-A 14 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .1080
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           60.5%;  Score 695.2;  DB 6;  Length 1080;
  Best Local Similarity   99.6%;  Pred. No. 3.1e-136;
  Matches  697;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 TATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT 62
              ||  || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 TAACGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT 440

Qy         63 CCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 CCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC 500

Qy        123 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA 560

Qy        183 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 242
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Db        561 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 620

Qy        243 GCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCT 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 GCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCT 680

Qy        303 GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA 740

Qy        363 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC 800

Qy        423 CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC 482
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Db        801 CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC 860

Qy        483 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAC 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAC 920

Qy        543 GCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAA 602
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Db        921 GCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAA 980

Qy        603 GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA 662
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Db        981 GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA 1040

Qy        663 CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||||||||
Db       1041 CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1080


RESULT 6
BD270544
LOCUS       BD270544               990 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Cytokine receptor mouse ZCYTOR10.
ACCESSION   BD270544
VERSION     BD270544.1  GI:33080312
KEYWORDS    JP 2002543786-A/23.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Presnell,S.R., Foster,D.C., Hammond,A.K. and Lok,S.
  TITLE     Cytokine receptor mouse ZCYTOR10
  JOURNAL   Patent: JP 2002543786-A 23 24-DEC-2002;
            ZYMOGENETICS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002543786-A/23
            PD   24-DEC-2002
            PF   11-MAY-2000 JP 2000616347
            PR   11-MAY-1999 US    09/309861
            PI   SCOTT R PRESNELL,DONALD C FOSTER,ANGELA K HAMMOND,SI LOK PC
            C12N15/09,C07K14/715,C07K16/28,C07K19/00,C12N1/15,C12N1/19, PC
            C12N1/21,
            PC   C12N5/10,C12P21/02,C12Q1/02,G01N33/53,G01N33/566//C12P21/08,
            PC   C12N15/00,
            PC   C12N5/00
            CC   Cytokine receptor mouse ZCYTOR10
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(990).
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           60.4%;  Score 694.8;  DB 6;  Length 990;
  Best Local Similarity   99.7%;  Pred. No. 3.8e-136;
  Matches  696;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
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Db        293 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 352

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
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Db        353 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 412

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
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Db        413 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 472

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
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Db        473 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 532

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Db        533 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 592

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 652

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 712

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
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Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
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Db        773 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 832

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
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Db        833 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 892

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 952

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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RESULT 7
AX047023
LOCUS       AX047023                990 bp    DNA     linear   PAT 15-DEC-2000
DEFINITION  Sequence 28 from Patent WO0068381.
ACCESSION   AX047023
VERSION     AX047023.1  GI:11876447
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Presnell,S.R., Foster,D.C., Hammond,A.K. and Lok,S.
  TITLE     Cytokine receptor mouse zcytor10
  JOURNAL   Patent: WO 0068381-A 28 16-NOV-2000;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
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     CDS             <1. .>990
                     /note="unnamed protein product"
                     /codon_start=1
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                     /db_xref="GI:11876448"
                     /db_xref="REMTREMBL:CAC18943"
                     /translation="ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG
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                     CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                     YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                     ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
                     TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK"
ORIGIN

  Query Match             60.4%;  Score 694.8;  DB 6;  Length 990;
  Best Local Similarity   99.7%;  Pred. No. 3.8e-136;
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  Matches  696;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 352

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 412

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 472

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
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Db        473 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 532

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
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Db        593 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 652

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
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Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
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Db        713 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 772

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
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Db        773 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 832

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
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Db        833 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 892

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
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Db        893 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 952

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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Db        953 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 990
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RESULT 8
AX365185
LOCUS       AX365185                990 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 37 from Patent WO0200721.
ACCESSION   AX365185
VERSION     AX365185.1  GI:18696941
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sprecher,C.A., Presnell,S.R., Gao,Z., Whitmore,T.E., Kuijper,J.L.
            and Maurer,M.F.
  TITLE     Cytokine receptor zcytor17
  JOURNAL   Patent: WO 0200721-A 37 03-JAN-2002;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
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                     TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK"
ORIGIN

  Query Match             60.4%;  Score 694.8;  DB 6;  Length 990;
  Best Local Similarity   99.7%;  Pred. No. 3.8e-136;
  Matches  696;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
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Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
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Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
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Db        413 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 472

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
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Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
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Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
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Db        713 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 772

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
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Db        773 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 832

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
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Db        833 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 892

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 952

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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Db        953 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 990


RESULT 9
AX478510
LOCUS       AX478510                990 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 14 from Patent WO0244209.
ACCESSION   AX478510
VERSION     AX478510.1  GI:22217282
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Presnell,S.R., Xu,W., Novak,J.E., Whitmore,T.E. and Grant,F.J.
  TITLE     Cytokine receptor zcytor19
  JOURNAL   Patent: WO 0244209-A 14 06-JUN-2002;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
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                     ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
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ORIGIN

  Query Match             60.4%;  Score 694.8;  DB 6;  Length 990;
  Best Local Similarity   99.7%;  Pred. No. 3.8e-136;
  Matches  696;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
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Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
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Db        413 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 472

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
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Db        473 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 532

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Db        533 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 592

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
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Db        653 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 712

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
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Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
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Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
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Db        953 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 990


RESULT 10
HSA294730
LOCUS       HSA294730               990 bp    mRNA    linear   PRI 09-FEB-2001
DEFINITION  Homo sapiens partial mRNA for immunoglobulin heavy chain constant
            region gamma 1 (IGHG1 gene).
ACCESSION   AJ294730
VERSION     AJ294730.1  GI:12054071
KEYWORDS    constant region; gamma 1; IGHG1 gene; immunoglobulin heavy chain.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   McLean,G.R., Nakouzi,A., Casadevall,A. and Green,N.S.
  TITLE     Human and murine immunoglobulin expression vector cassettes
  JOURNAL   Mol. Immunol. 37 (14), 837-845 (2000)
  MEDLINE   21157679
   PUBMED   11257305
REFERENCE   2  (bases 1 to 990)
  AUTHORS   McLean,G.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-SEP-2000) McLean G.R., Cell Biology, Albert Einstein
            College of Medicine, 1300 Morris Park Avenue, Bronx, New York
            10461, USA
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ORIGIN

  Query Match             60.4%;  Score 694.8;  DB 9;  Length 990;
  Best Local Similarity   99.7%;  Pred. No. 3.8e-136;
  Matches  696;  Conservative    0;  Mismatches    2;  Indents    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
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Db        293 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 352

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
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Db        413 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 472

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
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Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
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Db        593 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 652

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
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Db        653 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 712

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
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Db        713 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 772

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
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Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
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Db        833 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 892

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
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Db        893 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 952

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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Db        953 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 990


RESULT 11
AX556168
LOCUS       AX556168                762 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 17 from Patent WO0238766.
ACCESSION   AX556168
VERSION     AX556168.1  GI:25899545
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gross,J.A., Xu,W., Henne,R.M. and Grant,F.J.
  TITLE     Human tumor necrosis factor receptor
  JOURNAL   Patent: WO 0238766-A 17 16-MAY-2002;
            ZymoGenetics, Inc. (US)
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ORIGIN

Query Match 60.4%; Score 694.4; DB 6; Length 762;
Best Local Similarity 99.9%; Pred. No. 4.7e-136;
Matches 695; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db         64 GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 123

Qy         67 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 126
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Db        124 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 183

Qy        127 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 186
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Db        184 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 243

Qy        187 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 246
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Db        244 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 303

Qy        247 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 306
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Db        304 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 363

Qy        307 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 366
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Db        364 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 423

Qy        367 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 426
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Db        424 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 483

Qy        427 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 486
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Db        484 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 543

Qy        487 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 546
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Db        544 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 603

Qy        547 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 606
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Db        604 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 663

Qy        607 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 666
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RESULT 12
AR137115
LOCUS AR137115 1019 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 1 from patent US 6197294.
ACCESSION AR137115
VERSION AR137115.1 GI:14478624
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1019)
AUTHORS Tao,W., Wong,S., Hickey,W.F., Hammang,J.P. and Baetge,E.Edward.
TITLE Cell surface molecule-induced macrophage activation
JOURNAL Patent: US 6197294-A 1 06-MAR-2001;
FEATURES Location/Qualifiers
source 1. .1019
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/mol_type="unassigned DNA"

ORIGIN

Query Match 60.4%; Score 694.4; DB 6; Length 1019;
Best Local Similarity 99.9%; Pred. No. 4.6e-136;
Matches 695; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         67 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 126
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Db        433 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 492

Qy        187 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 246
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Qy        247 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 306
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Qy        307 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 366
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Qy        367 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 426
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Qy        547 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 606
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Qy        607 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 666
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RESULT 13
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LOCUS BD271954 1019 bp DNA linear PAT 17-JUL-2003
DEFINITION Cell surface molecule-induced macrophage activation.
ACCESSION BD271954
VERSION BD271954.1 GI:33081722
KEYWORDS JP 2002528078-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1019)
AUTHORS Tao,W., Wong,S., Hickey,W.F., Hammang,J.P. and Baetge,E.E.
TITLE Cell surface molecule-induced macrophage activation
JOURNAL Patent: JP 2002528078-A 1 03-SEP-2002;
NEUROTECH SA
COMMENT OS Homo sapiens (human)
PN JP 2002528078-A/1

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            PI   BAETGE
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  Query Match             60.4%;  Score 694.4;  DB 6;  Length 1019;
  Best Local Similarity   99.9%;  Pred. No. 4.6e-136;
  Matches  695;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 66
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Qy         67 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 126
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Db        373 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 432

Qy        127 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 186
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Qy        187 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 246
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Qy        247 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 306
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Qy        307 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 366
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Qy        487 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 546
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Db        793 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 852

Qy        547 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 606
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DEFINITION  Sequence 1 from patent US 6506891.
ACCESSION   AR275187
VERSION     AR275187.1  GI:29708174
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1019)
  AUTHORS   Tao,W., Wong,S., Hickey,W.F., Hammang,J.P. and Baetge,E.E.
  TITLE     Cell surface molecule-induced macrophage activation
  JOURNAL   Patent: US 6506891-A 1 14-JAN-2003;
FEATURES                Location/Qualifiers
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ORIGIN

  Query Match             60.4%;  Score 694.4;  DB 6;  Length 1019;
  Best Local Similarity   99.9%;  Pred. No. 4.6e-136;
  Matches  695;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 66
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        973 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1008


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LOCUS       AX350584                993 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 19 from Patent WO0183529.
ACCESSION   AX350584
VERSION     AX350584.1  GI:18616164
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Larrick,J.W. and Wycoff,K.L.
  TITLE     Novel immunoadhesin for the prevention of rhinovirus infection
  JOURNAL   Patent: WO 0183529-A 19 08-NOV-2001;
            Planet Biotechnology, Inc. (US)
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  Matches  695;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

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Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 5810876

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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24	691.2	60.1	699	2	AAT80158	Aat80158 Human IgG
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26	691.2	60.1	804	6	AAD43943	Aad43943 Human tPA
27	690.6	60.1	711	2	AAX87655	Aax87655 DNA encod
28	690.4	60.0	711	6	ABK89852	Abk89852 Synthetic
29	690.4	60.0	711	9	ADD25445	Add25445 Binding d
30	690.2	60.0	1001	9	ACF79681	Acf79681 Coding se
31	690	60.0	990	2	AAZ32778	Aaz32778 Human hea
32	690	60.0	990	7	ABV74602	Abv74602 Human hea
33	689.8	60.0	768	2	AAT10780	Aat10780 Coding se
34	689.6	60.0	703	7	AAD48236	Aad48236 Human imm
35	689.6	60.0	703	9	ADD32015	Add32015 Heterolog
36	689.6	60.0	762	7	AAD53759	Aad53759 Human mod
37	689.6	60.0	762	7	AAD53755	Aad53755 Human mod
38	688.2	59.8	768	2	AAQ96101	Aaq96101 IgG1 hing
39	687	59.7	1149	9	ADD25754	Add25754 Binding d
40	686.8	59.7	693	2	AAQ87592	Aaq87592 Human IgG
41	686.8	59.7	693	2	AAT71691	Aat71691 Human IgG
42	686.8	59.7	693	2	AAV62104	Aav62104 Human IgG
43	686.8	59.7	693	3	AAZ49172	Aaz49172 Human IgG
44	686.8	59.7	702	6	ABL52834	Abl52834 Human IgG
45	686.6	59.7	1129	2	AAT45262	Aat45262 Heregulin

ALIGNMENTS

```
RESULT 1
AAV32900
ID   AAV32900 standard; cDNA; 1150 BP.
XX
AC   AAV32900;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Recombinant human MetFc-OB cDNA.
XX
KW   Recombinant human MetFc-OB cDNA; chimeric; immunoglobulin; diabetes;
KW   high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
KW   ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             4. .1143
FT                   /*tag= a
FT                   /product= "Recombinant human Fc-OB"
FT   mat_peptide     7. .1140
FT                   /*tag= b
FT   misc_feature    700. .1140
FT                   /*tag= c
FT                   /note= "Encodes for the OB part of the fusion protein"
XX
PN   WO9828427-A1.
XX
PD   02-JUL-1998.
XX
PF   11-DEC-1997;   97WO-US023183.
XX
PR   20-DEC-1996;   96US-00770973.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Mann MB,  Hecht RI;
XX
DR   WPI; 1998-377658/32.
DR   P-PSDB; AAW49073.
XX
PT   New fusion proteins of OB and Fc - used for treating e.g. excess weight,
PT   diabetes, arterial sclerosis, arterial plaque, high blood lipid level,
PT   gall stones or stroke.
XX
```

```
PS   Disclosure; Fig 3A-3C; 107pp; English.
XX
CC   The present sequence represents a recombinant human MetFc-OB cDNA which
CC   encodes a recombinant human Fc-OB fusion protein. The invention provides
CC   Fc-OB fusion proteins whereby the Fc region of an immunoglobulin or its
CC   analogue is linked, either directly or indirectly using a linker, to the
CC   N-terminus of an OB protein or its analogue. The Fc-OB fusion proteins
CC   are claimed to demonstrate increased stability and clearance rate and
CC   decreased degradation as compared to OB protein or a fusion of Fc to the
CC   C-terminus of the OB protein. These Fc-OB fusion proteins are also
CC   claimed to be useful for treating excess weight in an individual or
CC   animal or for treating co-morbidities associated with excess fat such as
CC   diabetes, high blood lipid level, arterial sclerosis and stroke
XX
SQ   Sequence 1150 BP; 278 A; 367 C; 286 G; 219 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1150;  DB 2;  Length 1150;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-251;
  Matches 1150;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA 60
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Db          1 CATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA 60

Qy         61 CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120

Qy        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180

Qy        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240

Qy        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300

Qy        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360

Qy        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420

Qy        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480

Qy        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540

Qy        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600
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Db        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600

Qy        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660

Qy        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720

Qy        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780

Qy        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840

Qy        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900

Qy        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960

Qy        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020

Qy       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080

Qy       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140

Qy       1141 TAATGGATCC 1150
              ||||||||||
Db       1141 TAATGGATCC 1150


RESULT 2
AAV69685
ID   AAV69685 standard; DNA; 1150 BP.
XX
AC   AAV69685;
XX
DT   05-FEB-1999  (first entry)
XX
DE   Recombinant human metFc-OB protein encoding DNA.
XX
KW   Recombinant; metFc-OB protein; Fc region; immunoglobulin; Ig; OB;
KW   obesity; human; adiposity; blood lipid; diabetes type II; insulin;
KW   hypoglycaemic; antihypertensive; diuretic; appetite suppressant;
KW   suspension; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             4. .1143
FT                   /*tag= a
FT                   /product= "metFc-OB protein"
XX
PN   WO9846257-A1.
XX
PD   22-OCT-1998.
XX
PF   16-APR-1998;   98WO-US007828.
XX
PR   17-APR-1997;   97US-00843971.
PR   14-APR-1998;   98US-00059467.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Brems DN,  French DL,  Speed MA;
XX
DR   WPI; 1998-594525/50.
DR   P-PSDB; AAW83962.
XX
PT   Concentrated suspension of fusion of obesity protein with Fc
PT   immunoglobulin fragment - stable at physiological pH, used for e.g.
PT   reduction of weight and blood lipid levels, and for treatment of type II
PT   diabetes.
XX
PS   Disclosure; Fig 5A-C; 47pp; English.
XX
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CC   This DNA encodes a recombinant metFc-OB protein which consists of an Fc
CC   region of human immunoglobulin (Ig) fused to a human OB (obesity)
CC   protein. The invention provides a human OB protein suspension that
CC   contains at least 0.5 mg/ml of the human OB protein derivatised by
CC   attachment of the Fc region of an Ig to the N-terminus of OB, and has a
CC   pH 6-8. The suspensions are used to reduce weight, adiposity and blood
CC   lipid levels, to treat or prevent diabetes type II, and to increase lean
CC   mass and insulin sensitivity. They may be used in conjunction with
CC   insulin, hypoglycaemics, antihypertensives, diuretics, appetite
CC   suppressants etc. These suspensions are stable and active at
CC   physiological pH and are ready-for-use formulations that do not require
CC   freezing or freeze drying. As they are very concentrated, only small
CC   volumes are required and they provide a sustained-release effect, with
CC   increased potency and reduced frequency of injection
XX
SQ   Sequence 1150 BP; 278 A; 367 C; 286 G; 219 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 1150;  DB 2;  Length 1150;
  Best Local Similarity  100.0%;  Pred. No. 4.5e-251;
  Matches 1150;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA 60

Qy         61 CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120

Qy        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180

Qy        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240

Qy        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300
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Db        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300

Qy        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360

Qy        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420

Qy        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480

Qy        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540
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Db        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540

Qy        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600

Qy        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660

Qy        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720

Qy        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780

Qy        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840

Qy        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900

Qy        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960
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Db        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960

Qy        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020

Qy       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080
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Db       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080

Qy       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140

Qy       1141 TAATGGATCC 1150
              ||||||||||
Db       1141 TAATGGATCC 1150


RESULT 3
AAV32901
ID   AAV32901 standard; cDNA; 1150 BP.
XX
AC   AAV32901;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Recombinant human MetFc-OB variant 1 cDNA.
XX
KW   Recombinant human MetFc-OB variant 1 cDNA; chimeric; immunoglobulin;
KW   high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
KW   diabetes; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             4. .1143
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FT                   /product= "Recombinant human Fc-OB variant 1"
FT   mat_peptide     7. .1140
FT                   /*tag=  b
FT   mutation        19. .21
FT                   /*tag=  c
FT                   /note= "Changed from TGT in wild-type (AAV32900) to GCT
FT                   in mutant"
FT   misc_feature    700. .1140
FT                   /*tag=  d
FT                   /note= "Encodes for the OB part of the fusion protein"
XX
PN   WO9828427-A1.
XX
PD   02-JUL-1998.
XX
PF   11-DEC-1997;   97WO-US023183.
XX
PR   20-DEC-1996;   96US-00770973.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Mann MB,  Hecht RI;
XX
DR   WPI; 1998-377658/32.
```

```
DR   P-PSDB; AAW49074.
XX
PT   New fusion proteins of OB and Fc - used for treating e.g. excess weight,
PT   diabetes, arterial sclerosis, arterial plaque, high blood lipid level,
PT   gall stones or stroke.
XX
PS   Disclosure; Fig 4A-4C; 107pp; English.
XX
CC   The present sequence represents a recombinant human MetFc-OB variant 1
CC   cDNA which encodes a recombinant human Fc-OB fusion variant 1 protein
CC   having a C6A substitution when compared with the wild-type Fc-OB protein
CC   sequence shown in AAW49073. The invention provides Fc-OB fusion proteins
CC   whereby the Fc region of an immunoglobulin or its analogue is linked,
CC   either directly or indirectly using a linker, to the N-terminus of an OB
CC   protein or its analogue. The Fc-OB fusion proteins are claimed to
CC   demonstrate increased stability and clearance rate and decreased
CC   degradation as compared to OB protein or a fusion of Fc to the C-terminus
CC   of the OB protein. These Fc-OB fusion proteins are also claimed to be
CC   useful for treating excess weight in an individual or animal or for
CC   treating co-morbidities associated with excess fat such as diabetes, high
CC   blood lipid level, arterial sclerosis and stroke
XX
SQ   Sequence 1150 BP; 277 A; 365 C; 285 G; 223 T; 0 U; 0 Other;

  Query Match             98.6%;  Score 1134;  DB 2;  Length 1150;
  Best Local Similarity   99.1%;  Pred. No. 1.9e-247;
  Matches 1140;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 CATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA 60
              ||||||||||| ||||||  ||||||||||||||||||| ||||| || ||||| || |||
Db          1 CATATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAA 60

Qy         61 CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120
              |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTCCTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120

Qy        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180
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Db        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180

Qy        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240
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Db        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240

Qy        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300

Qy        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360

Qy        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420

Qy        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480

Qy        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540

Qy        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600

Qy        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660

Qy        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720

Qy        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780

Qy        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840

Qy        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900

Qy        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960

Qy        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020

Qy       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080

Qy       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140

Qy       1141 TAATGGATCC 1150
              ||||||||||
Db       1141 TAATGGATCC 1150


RESULT 4
AAV32902
ID   AAV32902 standard; cDNA; 1135 BP.
XX
AC   AAV32902;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Recombinant human MetFc-OB variant 2 cDNA.
XX
KW   Recombinant human MetFc-OB variant 2 cDNA; chimeric; immunoglobulin;
KW   high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
KW   diabetes; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
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FT                   /product= "Recombinant human Fc-OB variant 2"
FT   mat_peptide     7. .1125
FT                   /*tag=  b
FT   misc_feature    685. .1125
FT                   /*tag=  c
FT                   /note= "Encodes for the OB part of the fusion protein"
XX
PN   WO9828427-A1.
XX
PD   02-JUL-1998.
XX
PF   11-DEC-1997;   97WO-US023183.
XX
PR   20-DEC-1996;   96US-00770973.
XX
PA   (AMGE-) AMGEN INC.
XX
```

```
PI   Mann MB,  Hecht RI;
XX
DR   WPI; 1998-377658/32.
DR   P-PSDB; AAW49075.
XX
PT   New fusion proteins of OB and Fc - used for treating e.g. excess weight,
PT   diabetes, arterial sclerosis, arterial plaque, high blood lipid level,
PT   gall stones or stroke.
XX
PS   Disclosure; Fig 5A-5C; 107pp; English.
XX
CC   The present sequence represents a recombinant human MetFc-OB variant 2
CC   cDNA which encodes a recombinant human Fc-OB fusion variant 2 protein
CC   having a 5 residue deletion of residues 2-6 of the wild-type Fc-OB
CC   protein sequence shown in AAW49073. The invention provides Fc-OB fusion
CC   proteins whereby the Fc region of an immunoglobulin or its analogue is
CC   linked, either directly or indirectly using a linker, to the N-terminus
CC   of an OB protein or its analogue. The Fc-OB fusion proteins are claimed
CC   to demonstrate increased stability and clearance rate and decreased
CC   degradation as compared to OB protein or a fusion of Fc to the C-terminus
CC   of the OB protein. These Fc-OB fusion proteins are also claimed to be
CC   useful for treating excess weight in an individual or animal or for
CC   treating co-morbidities associated with excess fat such as diabetes, high
CC   blood lipid level, arterial sclerosis and stroke
XX
SQ   Sequence 1135 BP; 271 A; 361 C; 283 G; 220 T; 0 U; 0 Other;

  Query Match            97.2%;  Score 1117.8;  DB 2;  Length 1135;
  Best Local Similarity  99.4%;  Pred. No. 9.1e-244;
  Matches 1122;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGGACCGTCAGTC 81
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Db          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
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Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126

Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
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Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
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Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
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Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366

Qy        382 GGGCAGCCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGCAGCCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
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Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726

Qy        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786

Qy        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861
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Db        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846

Qy        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921
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Db        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906

Qy        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981
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Db        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966

Qy        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041
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Db        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026

Qy       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101
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Db       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086

Qy       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
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Db       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135


RESULT 5
AAV69686
ID   AAV69686 standard; DNA; 1135 BP.
XX
AC   AAV69686;
XX
DT   05-FEB-1999  (first entry)
XX
DE   Recombinant human metFc-OB protein variant encoding DNA.
XX
KW   Recombinant; metFc-OB protein; Fc region; immunoglobulin; Ig; OB;
KW   obesity; human; adiposity; blood lipid; diabetes type II; insulin;
KW   hypoglycaemic; antihypertensive; diuretic; appetite suppressant;
KW   suspension; variant; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             4. .1128
FT                   /*tag= a
FT                   /product= "metFc-OB protein variant"
XX
PN   WO9846257-A1.
XX
PD   22-OCT-1998.
XX
PF   16-APR-1998;   98WO-US007828.
XX
PR   17-APR-1997;   97US-00843971.
PR   14-APR-1998;   98US-00059467.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Brems DN,  French DL,  Speed MA;
XX
DR   WPI; 1998-594525/50.
DR   P-PSDB; AAW83963.
XX
```

PT Concentrated suspension of fusion of obesity protein with Fc
PT immunoglobulin fragment - stable at physiological pH, used for e.g.
PT reduction of weight and blood lipid levels, and for treatment of type II
PT diabetes.
XX
PS Disclosure; Fig 6A-C; 47pp; English.
XX
CC This DNA encodes a recombinant metFc-OB protein variant which consists of
CC an Fc region of human immunoglobulin (Ig) fused to a human OB (obesity)
CC protein. The invention provides a human OB protein suspension that
CC contains at least 0.5 mg/ml of the human OB protein derivatised by
CC attachment of the Fc region of an Ig to the N-terminus of OB, and has a
CC pH 6-8. The suspensions are used to reduce weight, adiposity and blood
CC lipid levels, to treat or prevent diabetes type II, and to increase lean
CC mass and insulin sensitivity. They may be used in conjunction with
CC insulin, hypoglycaemics, antihypertensives, diuretics, appetite
CC suppressants etc. These suspensions are stable and active at
CC physiological pH and are ready-for-use formulations that do not require
CC freezing or freeze drying. As they are very concentrated, only small
CC volumes are required and they provide a sustained-release effect, with
CC increased potency and reduced frequency of injection
XX
SQ Sequence 1135 BP; 271 A; 361 C; 283 G; 220 T; 0 U; 0 Other;

Query Match 97.2%; Score 1117.8; DB 2; Length 1135;
Best Local Similarity 99.4%; Pred. No. 9.1e-244;
Matches 1122; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy         22 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGGACCGTCAGTC 81
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Db          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126

Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
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Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
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Db        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246

Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
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Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366

Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
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Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
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Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726

Qy        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786

Qy        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846

Qy        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906

Qy        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966

Qy        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041
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Db        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026

Qy       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101
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Db       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086

Qy       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
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Db       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
```

RESULT 6
AAV32903
ID AAV32903 standard; cDNA; 1135 BP.
XX
AC AAV32903;
XX
DT 18-NOV-1998 (first entry)
XX
DE Recombinant human MetFc-OB variant 3 cDNA.
XX
KW Recombinant human MetFc-OB variant 3 cDNA; chimeric; immunoglobulin;
KW high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
KW diabetes; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX

FH	Key	Location/Qualifiers
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FT		/product= "Recombinant human Fc-OB variant 3"
FT	mat_peptide	7. .1125
FT		/*tag= b
FT	misc_feature	685. .1125
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FT		/note= "Encodes for the OB part of the fusion protein"

XX
PN WO9828427-A1.
XX
PD 02-JUL-1998.
XX
PF 11-DEC-1997; 97WO-US023183.
XX
PR 20-DEC-1996; 96US-00770973.
XX
PA (AMGE-) AMGEN INC.
XX
PI Mann MB, Hecht RI;
XX
DR WPI; 1998-377658/32.
DR P-PSDB; AAW49076.

```
XX
PT   New fusion proteins of OB and Fc - used for treating e.g. excess weight,
PT   diabetes, arterial sclerosis, arterial plaque, high blood lipid level,
PT   gall stones or stroke.
XX
PS   Disclosure; Fig 6A-6C; 107pp; English.
XX
CC   The present sequence represents a recombinant human MetFc-OB variant 3
CC   cDNA which encodes a recombinant human Fc-OB fusion variant 3 protein
CC   having the L16E, E99A, K101A and K103A substitutions when compared with
CC   the template protein shown in AAW49075. The invention provides Fc-OB
CC   fusion proteins whereby the Fc region of an immunoglobulin or its
CC   analogue is linked, either directly or indirectly using a linker, to the
CC   N-terminus of an OB protein or its analogue. The Fc-OB fusion proteins
CC   are claimed to demonstrate increased stability and clearance rate and
CC   decreased degradation as compared to OB protein or a fusion of Fc to the
CC   C-terminus of the OB protein. These Fc-OB fusion proteins are also
CC   claimed to be useful for treating excess weight in an individual or
CC   animal or for treating co-morbidities associated with excess fat such as
CC   diabetes, high blood lipid level, arterial sclerosis and stroke
XX
SQ   Sequence 1135 BP; 270 A; 365 C; 283 G; 217 T; 0 U; 0 Other;

  Query Match             96.1%;  Score 1105;  DB 2;  Length 1135;
  Best Local Similarity   98.7%;  Pred. No. 7.2e-241;
  Matches 1114;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 81
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Db          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
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Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
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Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
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Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
              |||||||||||||||||||||||||||||||||||||||||||||| |   |||
Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
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Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726

Qy        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786

Qy        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846

Qy        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906

Qy        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966

Qy        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026

Qy       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086

Qy       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135


RESULT 7
ADD25646
ID   ADD25646 standard; DNA; 714 BP.
XX
AC   ADD25646;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Binding domain-immunoglobulin fusion protein-associated DNA #107.
XX
KW   ds; Binding domain; immunoglobulin; fusion protein; cytostatic;
KW   antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW   neuroprotective; hinge region; immunoglobulin heavy chain;
KW   CH2 constant region; CH3 constant region; IgG1;
KW   antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW   malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW   rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW   type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS   Unidentified.
XX
PN   US2003118592-A1.
XX
PD   26-JUN-2003.
XX
PF   25-JUL-2002; 2002US-00207655.
XX
PR   17-JAN-2001; 2001US-0367358P.
PR   17-JAN-2002; 2002US-00053530.
PR   03-JUN-2002; 2002US-0385691P.
XX
PA   (GENE-) GENECRAFT INC.
XX
PI   Ledbetter JA,  Hayden-Ledbetter MS,  Thompson PA;
XX
DR   WPI; 2003-801317/75.
XX
PT   New binding domain-immunoglobulin fusion protein, useful for treating a
PT   subject having or suspected of having a malignant condition or a B-cell
PT   disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
PS   Disclosure; SEQ ID NO 207; 157pp; English.
```

```
XX
CC   Unidentified
XX
SQ   Sequence 714 BP; 180 A; 231 C; 186 G; 117 T; 0 U; 0 Other;

  Query Match           60.5%;  Score 695.2;  DB 9;  Length 714;
  Best Local Similarity  98.9%;  Pred. No. 5.6e-148;
  Matches  700;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          2 ATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC 61
              ||  ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 ATCAGGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC 64

Qy         62 TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCT 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCT 124

Qy        122 CCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 CCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA 184

Qy        182 AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG 244

Qy        242 AGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 AGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGC 304

Qy        302 TGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGA 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 TGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGA 364

Qy        362 AAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCAT 421
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 AAACAATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCAT 424

Qy        422 CCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATC 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 CCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATC 484

Qy        482 CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCA 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCA 544

Qy        542 CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACA 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACA 604

Qy        602 AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACA 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACA 664

Qy        662 ACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGA 709
              ||||||||||||||||||||||||||||||||||||||||||  | | |
Db        665 ACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGATCTA 712


RESULT 8
AAA54473
ID   AAA54473 standard; DNA; 990 BP.
XX
AC   AAA54473;
XX
DT   11-APR-2001  (first entry)
XX
DE   Zcytor 10::IgG gamma fusion construct.
XX
KW   zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand;
KW   binding; detection; modulation; recombinant cell; haematopoietic cell;
KW   lymphoid cell; myeloid cell; lymph; immune system; blood; bone;
KW   inflammatory response; inflammation; spleen; human; ds.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag= a
FT                   /product= "zcytor10::IgG gamma fusion protein"
XX
PN   WO200068381-A1.
XX
PD   16-NOV-2000.
XX
PF   11-MAY-2000; 2000WO-US012924.
XX
PR   11-MAY-1999;   99US-00309861.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Presnell SR,  Foster DC,  Hammond AK,  Lok S;
XX
DR   WPI; 2001-016096/02.
DR   P-PSDB; AAB04071.
XX
PT   New cytokine receptor mouse zcytor 10, useful for detecting ligands that
PT   stimulate proliferation or development of hematopoietic, lymphoid and
PT   myeloid cells.
XX
PS   Example 17; Page 118-120; 134pp; English.
XX
CC   Isolating a nucleotide which encodes the zcytor 10 cytokine receptor
CC   enables the production of recombinant cells expressing the receptor.
CC   Those cells can then be used to detect the presence of a modulator of
CC   zcytor10 protein by culturing the cells in the presence of a test ligand
CC   and comparing levels of activity of mouse zcytor10 in the presence and
CC   absence of the test sample. Similarly, detection of zcytor10 receptor
CC   ligand within a test sample can be achieved. The method comprising
CC   contacting a test sample containing an amino acid sequence from Cys15 or
CC   Gly25 to Pro230 of the zcytor 10 cytokine receptor and detecting the
CC   binding of the polypeptide to a ligand in the sample. Specified peptide
CC   fragments of the zcytor 10 cytokine receptor and the methods described
CC   are used to identify ligands that stimulate the proliferation and/or
CC   development of haematopoietic, lymphoid and myeloid cells. Peptide
CC   fragments of the cytokine receptor are useful for treating lymphoid,
CC   immune, inflammatory, splenic, blood or bone disorders and for generating
CC   antibodies directed against the receptor. A vector expressing a secreted
CC   human zcytor 10 heterodimer is constructed. In this construct the
CC   extracellular cytokine binding domain of zcytor 10 is fused to the heavy
CC   chain of IgG gamma and the extracellular portion of the the heteromeric
CC   cytokine receptor subunit (an interleukin receptor subunit) is fused to
CC   human kappa light chain (See GENESEQ record AAA54474). The two sequences
CC   are fused together using two primers (AAA54475, AAA54476)
XX
SQ   Sequence 990 BP; 234 A; 337 C; 259 G; 160 T; 0 U; 0 Other;

  Query Match           60.4%;  Score 694.8;  DB 4;  Length 990;
  Best Local Similarity  99.7%;  Pred. No. 7.4e-148;
  Matches  696;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 352

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 412

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 472

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 532
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Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 592

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 652

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 712

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 772

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 832

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        833 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 892

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 952

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||||
Db        953 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 990
```

RESULT 9
ABQ73076
ID ABQ73076 standard; cDNA; 990 BP.
XX
AC ABQ73076;
XX
DT 25-SEP-2002 (first entry)
XX
DE Human IgG gamma 1 heavy chain encoding cDNA SEQ ID NO:14.
XX
KW Human; zcytor19; cytokine receptor; immunosuppressive; cytostatic;
KW antirheumatic; antiarthritic; neuroprotective; antiinflammatory;
KW antidiabetic; nephrotropic; dermatological; anti-HIV; haemostatic;
KW vaccine; immune system; T-cell specific leukaemia; lymphoma; lupus;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; HIV;
KW diabetes mellitus; inflammatory bowel disease; Crohn's disease; asthma;
KW immunologic renal disease; glomerulonephritis; vasculitis; polyarteritis;
KW mesangioproliferative disease; chronic lymphocytic leukaemia; bronchitis;
KW secondary glomerulonephritis; scleroderma; amyloidosis; multiple myeloma;
KW haemolytic uraemic syndrome; renal neoplasm; urological neoplasm;
KW emphysema; chronic airway disease; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .990
FT /*tag= a
FT /partial
FT /product= "IgG gamma 1 heavy chain"
FT /note= "no stat or stop codons given"
XX
PN WO200244209-A2.
XX
PD 06-JUN-2002.
XX
PF 28-NOV-2001; 2001WO-US044808.
XX
PR 28-NOV-2000; 2000US-0253561P.
PR 07-FEB-2001; 2001US-0267211P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Xu W, Novak JE, Whitmore TE, Grant FJ;
XX
DR WPI; 2002-527700/56.
DR P-PSDB; ABB81641.
XX
PT Novel Zyctor19 polypeptides and polynucleotides useful for stimulating
PT immune responses in animals for producing antibodies, and for treating
PT autoimmune diseases, leukemia and asthma.
XX
PS Example 7; Page 169-171; 200pp; English.
XX
CC The present invention describes an isolated human zcytor19 protein (I),
CC and truncated zcytor19 proteins. (I) has immunosuppressive, cytostatic,
CC antirheumatic, antiarthritic, neuroprotective, antiinflammatory,
CC antidiabetic, nephrotropic, dermatological, anti-HIV and haemostatic
CC activities, and can be used in vaccines. (I) or an antibody binding (I)
CC can be used for suppressing the immune system for reducing rejection of
CC tissue or organ transplants and grafts and for treating T-cell specific
CC leukaemias or lymphomas and autoimmune diseases including rheumatoid
CC arthritis, multiple sclerosis, diabetes mellitus, inflammatory bowel
CC disease and Crohn's disease. The antibodies can also be used for treating
CC immunologic renal diseases, glomerulonephritis, mesangioproliferative
CC disease, chronic lymphocytic leukaemia, secondary glomerulonephritis or
CC vasculitis associated with lupus, polyarteritis, scleroderma, HIV-related
CC diseases, amyloidosis and haemolytic uraemic syndrome. (I) and the
CC antibodies can also be used for renal or urological neoplasms and
CC multiple myelomas, asthma, bronchitis, emphysema and other chronic airway
CC diseases. Human zcytor19 is located to chromosome 1, more specifically to
CC chromosome 1p36.11. The present sequence encodes a human IgG gamma 1
CC heavy chain protein, which is used in an example from the present
CC invention
XX
SQ Sequence 990 BP; 234 A; 337 C; 259 G; 160 T; 0 U; 0 Other;

Query Match 60.4%; Score 694.8; DB 6; Length 990;
Best Local Similarity 99.7%; Pred. No. 7.4e-148;
Matches 696; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 352

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 412

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 472

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 532

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 592

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 652

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 712

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 772
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```
Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 832

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        833 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 892

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 952

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||||
Db        953 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 990
```

RESULT 10
ABA93797
ID ABA93797 standard; cDNA; 990 BP.
XX
AC ABA93797;
XX
DT 01-MAY-2002 (first entry)
XX
DE Human immunoglobulin G gamma 1 cDNA sequence SEQ ID NO:37.
XX
KW Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
KW antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;
KW muscular; lymphoid; immune; inflammatory; spleenic; blood; bone;
KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
KW inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
XX
OS Homo sapiens.
XX
PN WO200200721-A2.
XX
PD 03-JAN-2002.
XX
PF 26-JUN-2001; 2001WO-US020484.
XX
PR 26-JUN-2000; 2000US-0214282P.
PR 29-JUN-2000; 2000US-0214955P.
PR 08-FEB-2001; 2001US-0267963P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL;
PI Maurer MF;
XX
DR WPI; 2002-090519/12.
DR P-PSDB; ABB05736.
XX
PT Isolated polynucleotide encoding a cytokine receptor zyctor17 which is
PT useful for treating and diagnosing lymphoid, immune, inflammatory,
PT spleenic, blood or bone disorders.
XX
PS Example 17; Page 185-186; 235pp; English.
XX
CC The present invention describes a cytokine receptor designated zcytor17.
CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
CC antirheumatic, antiarthritic and muscular activities. The zcytor17
CC proteins are useful for treating and diagnosing lymphoid, immune,
CC inflammatory, spleenic, blood or bone disorders. Agonists or anti-
CC zcytor17 antibodies are useful in stimulating cell-mediated immunity and
CC for stimulating lymphocyte proliferation, such as in the treatment of
CC infections involving immunosuppression, including certain viral
CC infections. They are also useful for inducting cytotoxicity and for
CC treating leukopenias. Antagonist of zcytor17 polypeptides are useful for
CC treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 990 BP; 234 A; 337 C; 259 G; 160 T; 0 U; 0 Other;

Query Match 60.4%; Score 694.8; DB 6; Length 990;
Best Local Similarity 99.7%; Pred. No. 7.4e-148;
Matches 696; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 352

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 412

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 472

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 532

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 592

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 652

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 712

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 772

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 832

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        833 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 892

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 952

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||||
Db        953 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 990
```

RESULT 11
ABN89435
ID ABN89435 standard; cDNA; 762 BP.
XX
AC ABN89435;
XX
DT 02-SEP-2002 (first entry)
XX
DE Human immunoglobulin gamma1 constant region nucleotide SEQ ID NO:17.
XX
KW Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;

```
KW   autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
KW   multiple sclerosis; insulin dependent diabetes mellitus; asthma;
KW   rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
KW   glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
KW   pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
KW   light chain neuropathy; hypertension; large vessel disease;
KW   graft-versus host disease; graft rejection; Crohn's disease; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             7. .762
FT                   /*tag=  a
FT                   /product= "immunoglobulin gamma1 constant region"
XX
PN   WO200238766-A2.
XX
PD   16-MAY-2002.
XX
PF   05-NOV-2001; 2001WO-US047018.
XX
PR   07-NOV-2000; 2000US-0246449P.
PR   20-DEC-2000; 2000US-0257131P.
PR   28-JUN-2001; 2001US-0301715P.
PR   29-AUG-2001; 2001US-0315565P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Gross JA,  Xu W,  Henne RM,  Grant FJ;
XX
DR   WPI; 2002-508212/54.
DR   P-PSDB; ABB81490.
XX
PT   Novel isolated human tumor necrosis factor receptor polypeptide, termed
PT   Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage
PT   renal failure or renal disease and lymphoma.
XX
PS   Example 4; Page 141-142; 154pp; English.
XX
CC   The present invention describes a human tumour necrosis factor receptor
CC   designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
CC   dermatological, antiinflammatory, neuroprotective, antidiabetic,
CC   antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
CC   activities, and can be used in gene therapy. (I) can be used for
CC   inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
CC   (e.g. ZTNF4), for treating disorders and diseases associated with B
CC   lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
CC   inhibiting the proliferation of tumour cells. (I) is useful for treating
CC   autoimmune disorders such as systemic lupus erythematosus, myasthenia
CC   gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
CC   rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
CC   or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
CC   leukaemia, nephritis, and pyelonephritis, and for treating renal
CC   neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
CC   amyloidosis, hypertension, large vessel diseases, graft-versus host
CC   disease, graft rejection and Crohn's disease. (I) is useful for
CC   modulating the immune system, for regulating B cell responses and
CC   development, for modulating development of other cells, antibody
CC   production and cytokine production, and for modulating T and B cell
CC   communication. Human Ztnfr12 is located to chromosome 22q13.2. The
CC   present sequence encodes human immunoglobulin gamma1 constant region,
CC   which is used in an example from the present invention
XX
SQ   Sequence 762 BP; 182 A; 249 C; 202 G; 129 T; 0 U; 0 Other;

  Query Match             60.4%;  Score 694.4;  DB 6;  Length 762;
  Best Local Similarity   99.9%;  Pred. No. 8.6e-148;
  Matches  695;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 66
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 123

Qy         67 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 183

Qy        127 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 243

Qy        187 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 303

Qy        247 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 363

Qy        307 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 423

Qy        367 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 483

Qy        427 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 543

Qy        487 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 603

Qy        547 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 663

Qy        607 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 723

Qy        667 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||||||||||||||||||||||||||||||||
Db        724 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 759


RESULT 12
AAD53735
ID   AAD53735 standard; DNA; 762 BP.
XX
AC   AAD53735;
XX
DT   28-MAY-2003  (first entry)
XX
DE   Human wild-type immunoglobulin gamma1 region encoding DNA.
XX
KW   Transmembrane activator; calcium modulator; nephrotropic; antibacterial;
KW   TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
KW   anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
KW   glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
KW   dermatological; neuroprotective; cyclophilin ligand-interactor; human;
KW   autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
KW   diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             7. .762
FT                   /*tag=  a
FT                   /product= "Human wild-type immunoglobulin gamma1 region"
XX
PN   WO200294852-A2.
XX
```

PD 28-NOV-2002.
XX
PF 20-MAY-2002; 2002WO-US015910.
XX
PR 24-MAY-2001; 2001US-0293343P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Rixon MW, Gross JA;
XX
DR WPI; 2003-148455/14.
DR P-PSDB; AAE35214.
XX
PT Transmembrane activator and calcium modulator and cyclophilin ligand-
PT interactor (TACI)-immunoglobulin fusion protein, for treating cancer or
PT diabetes, comprises a TACI receptor group and an immunoglobulin group.
XX
PS Example 1; Col 90-92; 71pp; English.
XX
CC The invention relates to fusion proteins comprising transmembrane
CC activator and calcium modulator and cyclophilin ligand-interactor (TACI)
CC receptor group that binds tumour necrosis factor-like protein (ZTNF)2 or
CC ZTNF4; and an immunoglobulin group comprising a constant region of an
CC immunoglobulin. The invention is used to manufacture a medicament for
CC inhibiting the proliferation of tumour cells in a mammalian subject. The
CC composition comprising the fusion protein may also be used in treating
CC autoimmune diseases (e.g. systemic lupus erythematosus, multiple
CC sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal
CC diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft
CC rejection, anaemia and septic shock. The fusion proteins are also used in
CC gene therapy. The present sequence is human wild-type immunoglobulin
CC gammal region encoding DNA. This sequence is used in the exemplification
CC of the invention
XX
SQ Sequence 762 BP; 182 A; 249 C; 202 G; 129 T; 0 U; 0 Other;

Query Match 60.4%; Score 694.4; DB 7; Length 762;
Best Local Similarity 99.9%; Pred. No. 8.6e-148;
Matches 695; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          7 GAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 66
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 123

Qy         67 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 183

Qy        127 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 243

Qy        187 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 303

Qy        247 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 363

Qy        307 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 423

Qy        367 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 483

Qy        427 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 543

Qy        487 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 603

Qy        547 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 663

Qy        607 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 723

Qy        667 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||||||||||||||||||||||||||||||||
Db        724 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 759
```

RESULT 13
AAA53126
ID AAA53126 standard; cDNA; 1019 BP.
XX
AC AAA53126;
XX
DT 15-SEP-2003 (revised)
DT 15-SEP-2000 (first entry)
XX
DE Human TR-Fc-delta-CH nucleotide sequence SEQ ID NO:1.
XX
KW Human; transferrin receptor; immunoglobulin G; IgG; chimeric;
KW hTR-Fc-delta-CH; hTR-Fc-delta-H; immune response; immunosuppressant;
KW cell surface molecule induced macrophage activation; antidiabetic;
KW antiarthritic; dermatological; antiinflammatory; autoimmune disorder;
KW diabetes; multiple sclerosis; rheumatoid arthritis;
KW systemic lupus erythematosus; ss.
XX
OS Homo sapiens.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 16. .1011
FT /*tag= a
FT /product= "hTR-Fc-delta-CH"
XX
PN WO200024897-A1.
XX
PD 04-MAY-2000.
XX
PF 21-OCT-1999; 99WO-US024630.
XX
PR 26-OCT-1998; 98US-00178869.
XX
PA (CYTO-) CYTOTHERAPEUTICS INC.
XX
PI Tao W, Wong S, Hickey WF, Hammang JP, Baetge EE;
XX
DR WPI; 2000-350739/30.
DR P-PSDB; AAY91106.
XX
PT Transformed cell containing a recombinant polynucleotide encoding an
PT immunostimulatory cell surface polypeptide which induces removal of the
PT cell when expressed, useful for treating various autoimmune diseases.
XX
PS Example 1; Page 45-48; 64pp; English.
XX
CC The present invention describes a transformed cell (C1) containing a
CC recombinant polynucleotide (N1) comprising a promoter linked to a
CC sequence encoding an immunostimulatory cell surface polypeptide (P1),
CC where expression of P1 induces the removal of C1 from a host. C1
CC expressing P1 induces macrophage activation, resulting in the rejection
CC of the cell by a host. C1 expressing P1 is useful for treating various
CC autoimmune disorders such as diabetes, multiple sclerosis, rheumatoid
CC arthritis, systemic lupus erythematosus. The present sequence encodes a
CC human transferrin receptor and immunoglobulin G (IgG) heavy chain
CC fragment chimeric protein, which is used in an example from the present

```
CC   invention. (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ   Sequence 1019 BP; 270 A; 287 C; 265 G; 197 T; 0 U; 0 Other;

  Query Match             60.4%;  Score 694.4;  DB 3;  Length 1019;
  Best Local Similarity   99.9%;  Pred. No. 9.1e-148;
  Matches  695;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 66
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 372

Qy         67 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 432

Qy        127 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 492

Qy        187 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 552

Qy        247 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 612

Qy        307 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 672

Qy        367 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 732

Qy        427 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        733 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 792

Qy        487 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        793 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 852

Qy        547 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        853 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 912

Qy        607 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        913 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 972

Qy        667 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||||||||||||||||||||||||||||||||
Db        973 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1008


RESULT 14
AAN90779
ID   AAN90779 standard; DNA; 1136 BP.
XX
AC   AAN90779;
XX
DT   25-MAR-2003  (revised)
DT   31-OCT-2002  (revised)
DT   14-MAY-1990  (first entry)
XX
DE   Sequence of the linkered immunoglobulin gamma chain fragment.
XX
KW   Immunoglobulin gamma chain; IgG1 heavy chain constant region.
XX
OS   Homo sapiens.
XX

FH   Key             Location/Qualifiers
FT   CDS             8. .1123
FT                   /*tag=  a
XX
PN   EP314317-A.
XX
PD   03-MAY-1989.
XX
PF   03-OCT-1988;    88EP-00309194.
XX
PR   02-OCT-1987;    87US-00104329.
PR   28-SEP-1988;    88US-00250785.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Capon DJ,  Gregrory TJ;
XX
DR   WPI; 1989-131855/18.
DR   P-PSDB; AAP91918.
XX
PT   Compsns. contg. adheson variants - useful in therapy and diagnostics,
PT   e.g. CD4 variants which are therapeutically useful for treating human
PT   immuno-deficiency virus.
XX
PS   Fig 4a-4b; Page ?; 36pp; English.
XX
CC   The polypeptide it codes for may be fused to the first 180 N-terminal
CC   residues of CD4 at the C-terminus. The fusion protein may be used for
CC   antiviral of immunomodulatory therapy particularly in treatment of HIV
CC   infection. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on
CC   25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI
CC   field.) (Updated on 25-MAR-2003 to correct DR field.)
XX
SQ   Sequence 1136 BP; 256 A; 385 C; 303 G; 192 T; 0 U; 0 Other;

  Query Match             60.3%;  Score 693.6;  DB 1;  Length 1136;
  Best Local Similarity   99.4%;  Pred. No. 1.4e-147;
  Matches  696;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 482

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 542

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 602

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 662

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Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
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RESULT 15
ADD25745
ID ADD25745 standard; DNA; 924 BP.
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AC ADD25745;
XX
DT 15-JAN-2004 (first entry)
XX
DE Binding domain-immunoglobulin fusion protein-associated DNA #165.
XX
KW ds; Binding domain; immunoglobulin; fusion protein; cytostatic;
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW neuroprotective; hinge region; immunoglobulin heavy chain;
KW CH2 constant region; CH3 constant region; IgG1;
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
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XX
PN US2003118592-A1.
XX
PD 26-JUN-2003.
XX
PF 25-JUL-2002; 2002US-00207655.
XX
PR 17-JAN-2001; 2001US-0367358P.
PR 17-JAN-2002; 2002US-00053530.
PR 03-JUN-2002; 2002US-0385691P.
XX
PA (GENE-) GENECRAFT INC.
XX
PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX
DR WPI; 2003-801317/75.
XX
PT New binding domain-immunoglobulin fusion protein, useful for treating a
PT subject having or suspected of having a malignant condition or a B-cell
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
PS Disclosure; SEQ ID NO 306; 157pp; English.
XX
CC Unidentified
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SQ Sequence 924 BP; 239 A; 290 C; 235 G; 160 T; 0 U; 0 Other;

  Query Match   60.3%; Score 693.4; DB 9; Length 924;
  Best Local Similarity 99.9%; Pred. No. 1.5e-147;
  Matches 694; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Qy        548 CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA 607
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Search completed: May 7, 2004, 06:57:07
Job time : 349 secs

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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 13:07:09 ; Search time 63.5 Seconds
(without alignments)
10050.292 Million cell updates/sec

Title: US-10-679-999-7
Perfect score: 1150
Sequence: 1 CATATGGAACCCAAATCTTG.....TCCGGGTTGTTAATGGATCC 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1246516

Minimum DB seq length: 0
Maximum DB seq length: 1150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	695.2	60.5	1080	4	US-09-180-100-14	Sequence 14, Appl
2	694.4	60.4	1019	3	US-09-178-869-1	Sequence 1, Appli
3	694.4	60.4	1019	4	US-09-761-413-1	Sequence 1, Appli
4	691.6	60.1	1135	1	US-08-236-311-8	Sequence 8, Appli
5	691.6	60.1	1135	3	US-08-457-918-8	Sequence 8, Appli
6	691.2	60.1	699	2	US-08-595-043A-49	Sequence 49, Appl
7	690	60.0	990	4	US-09-301-593-21	Sequence 21, Appl
8	689.8	60.0	768	2	US-08-284-391B-32	Sequence 32, Appl
9	689.8	60.0	768	3	US-09-218-950-32	Sequence 32, Appl
10	686.8	59.7	693	1	US-08-322-805-3	Sequence 3, Appli
11	686.8	59.7	693	2	US-08-429-499-3	Sequence 3, Appli
12	686.8	59.7	693	3	US-09-152-733-3	Sequence 3, Appli
13	685	59.6	705	4	US-09-023-655-1223	Sequence 1223, Ap
14	684.2	59.5	745	1	US-07-943-843-7	Sequence 7, Appli
15	684.2	59.5	745	1	US-08-236-918A-14	Sequence 14, Appl
16	684.2	59.5	745	1	US-08-347-003-7	Sequence 7, Appli
17	684.2	59.5	745	4	US-09-150-864A-14	Sequence 14, Appl
18	683.8	59.5	705	1	US-07-797-556-3	Sequence 3, Appli
19	683.8	59.5	705	1	US-08-308-881-3	Sequence 3, Appli
20	683.8	59.5	705	2	US-09-058-263-3	Sequence 3, Appli
21	683.8	59.5	705	2	US-09-059-099-3	Sequence 3, Appli
22	683.8	59.5	705	3	US-09-058-264-3	Sequence 3, Appli
23	683.8	59.5	705	4	US-09-455-962-3	Sequence 3, Appli
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26	683.6	59.4	740	1	US-08-360-923A-3	Sequence 3, Appli
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43	681	59.2	773	4	US-09-428-082B-1065	Sequence 1065, Ap
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45	680.6	59.2	761	4	US-09-428-082B-1057	Sequence 1057, Ap

ALIGNMENTS

RESULT 1
US-09-180-100-14
; Sequence 14, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 6306395io
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-180-100-14

Query Match 60.5%; Score 695.2; DB 4; Length 1080;
Best Local Similarity 99.6%; Pred. No. 2.2e-170;
Matches 697; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          3 TATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT 62
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Qy        663 CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702

Db       1041 CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1080


RESULT 2
US-09-178-869-1
; Sequence 1, Application US/09178869B
; Patent No. 6197294
; GENERAL INFORMATION:
;  APPLICANT: Tao, Weng
;  APPLICANT: Wong, Shou
;  APPLICANT: Hickey, William F
;  APPLICANT: Hammang, Joseph P.
;  APPLICANT: Baetge, E. Edward
;  TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
;  FILE REFERENCE: 17810-043
;  CURRENT APPLICATION NUMBER: US/09/178,869B
;  CURRENT FILING DATE: 1998-10-26
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1019
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: ()..)
;   OTHER INFORMATION: Description of Sequence: Recombinant
;   OTHER INFORMATION: Polynucleotide
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (16)..(1008)
US-09-178-869-1

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  Best Local Similarity  99.9%;  Pred. No. 3.5e-170;
  Matches  695;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 66

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Qy         67 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 126

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Qy        127 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 186

Db        433 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 492

Qy        187 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 246

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Qy        667 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702

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RESULT 3
US-09-761-413-1
; Sequence 1, Application US/09761413
; Patent No. 6506891
; GENERAL INFORMATION:
;  APPLICANT: Tao, Weng
;  APPLICANT:  Wong, Shou
;  APPLICANT:  Hickey, William F
;  APPLICANT:  Hammang, Joseph P.
;  APPLICANT:  Baetge, E. Edward
;  TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
;  FILE REFERENCE: 17810-043
;  CURRENT APPLICATION NUMBER: US/09/761,413
;  CURRENT FILING DATE:  2001-01-16
;  PRIOR APPLICATION NUMBER: US/09/178,869
;  PRIOR FILING DATE: 1998-10-26
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1019
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: ()..)
;   OTHER INFORMATION: Description of Sequence: Recombinant
;   OTHER INFORMATION: Polynucleotide
;   NAME/KEY: CDS
;   LOCATION: (16)..(1008)
US-09-761-413-1

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  Best Local Similarity  99.9%;  Pred. No. 3.5e-170;
  Matches  695;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 732

Qy        427 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        733 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 792

Qy        487 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        793 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 852

Qy        547 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        853 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 912

Qy        607 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        913 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 972

Qy        667 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||
Db        973 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1008
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```
RESULT 4
US-08-236-311-8
; Sequence 8, Application US/08236311
; Patent No. 5565335
;  GENERAL INFORMATION:
;    APPLICANT:  Capon, Daniel J.
;    APPLICANT:  Gregory, Timothy J.
;    TITLE OF INVENTION:  Adheson Variants
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/236,311
;      FILING DATE:  02-MAY-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/936190
;      FILING DATE:  26-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/842777
;      FILING DATE:  18-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/250785
;      FILING DATE:  28-SEP-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/104329
;      FILING DATE:  02-OCT-1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  444P1C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1135 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-236-311-8

  Query Match             60.1%;  Score 691.6;  DB 1;  Length 1135;
  Best Local Similarity   99.4%;  Pred. No. 1.9e-169;
  Matches  694;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 482

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 542

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 602

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 TCAAGTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 662

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        663 AGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 722

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 782

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 842

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 902

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 962

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1022

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1023 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1082
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Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||||||||||||||||||||||||||||||||||
Db       1083 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1120


RESULT 5
US-08-457-918-8
; Sequence 8, Application US/08457918
; Patent No. 6117655
;  GENERAL INFORMATION:
;    APPLICANT:  Capon, Daniel J.
;    APPLICANT:  Gregory, Timothy J.
;    TITLE OF INVENTION:  Adheson Variants
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/457,918
;      FILING DATE:  1-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/236311
;      FILING DATE:  02-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/936190
;      FILING DATE:  26-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/842777
;      FILING DATE:  18-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/250785
;      FILING DATE:  28-SEP-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/104329
;      FILING DATE:  02-OCT-1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kubinec, Jeffrey S.
;      REGISTRATION NUMBER:  36,575
;      REFERENCE/DOCKET NUMBER:  P0444P1C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-8228
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1135 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-457-918-8

  Query Match             60.1%;  Score 691.6;  DB 3;  Length 1135;
  Best Local Similarity   99.4%;  Pred. No. 1.9e-169;
  Matches  694;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 482

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 542

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 602

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 TCAAGTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 662

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        663 AGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 722

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 782

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 842

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 902

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 962

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1022

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1023 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1082

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||||
Db       1083 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1120


RESULT 6
US-08-595-043A-49
; Sequence 49, Application US/08595043A
; Patent No. 5935824
;  GENERAL INFORMATION:
;    APPLICANT:  SGARLATO, GREGORY D.
;    TITLE OF INVENTION:  PROTEIN EXPRESSION SYSTEM
;    NUMBER OF SEQUENCES:  90
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MEDLEN & CARROLL
;      STREET:  220 MONTGOMERY STREET, SUITE 2200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/595,043A
;      FILING DATE:  31-JAN-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARROLL, PETER G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  SGAR-00371
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  49:
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```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  699 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..699
US-08-595-043A-49

  Query Match           60.1%;  Score 691.2;  DB 2;  Length 699;
  Best Local Similarity  99.6%;  Pred. No. 2.1e-169;
  Matches  693;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 GAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 66
              || |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db          1 GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCAGAACTCCTG 60

Qy         67 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 120

Qy        127 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 180

Qy        187 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 240

Qy        247 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 306
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        241 TACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 300

Qy        307 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 360

Qy        367 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 420

Qy        427 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 480

Qy        487 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 540

Qy        547 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 600

Qy        607 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 660

Qy        667 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||||||||||||||||||||||||||||||||
Db        661 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 696


RESULT 7
US-09-301-593-21
; Sequence 21, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
;  APPLICANT: Park, John E.
;  APPLICANT: Garin-Chesa, Pilar
;  APPLICANT: Bamberger, Uwe
;  APPLICANT: Leger, Olivier
;  APPLICANT: Saldanha, Jose W.
;  APPLICANT: Rettig, Wolfgang J.
;  TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
;  FILE REFERENCE: 0652.1890001
;  CURRENT APPLICATION NUMBER: US/09/301,593A
;  CURRENT FILING DATE: 1999-04-29
;  EARLIER APPLICATION NUMBER: EP 98107925.4
;  EARLIER FILING DATE: 1998-04-30
;  EARLIER APPLICATION NUMBER: US 60/086,049
;  EARLIER FILING DATE: 1998-05-18
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
;   LENGTH: 990
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-301-593-21

  Query Match           60.0%;  Score 690;  DB 4;  Length 990;
  Best Local Similarity  99.3%;  Pred. No. 4.8e-169;
  Matches  693;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 352

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 412

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 472

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 532

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        533 AGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 592

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 652

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 712

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              |||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 GGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 772

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 832

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        833 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 892

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 952

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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Db        953 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 990


RESULT 8
US-08-284-391B-32
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; Sequence 32, Application US/08284391B
; Patent No. 5851828
;  GENERAL INFORMATION:
;    APPLICANT:  Seed, Brian
;    APPLICANT:  Banapour, Babak
;    APPLICANT:  Romeo, Charles
;    APPLICANT:  Kolanus, Waldemar
;    TITLE OF INVENTION:  TARGETED CYTOLYSIS OF HIV-INFECTED
;    TITLE OF INVENTION:  CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Clark & Elbing LLP
;      STREET:  176 Federal Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/284,391B
;      FILING DATE:  02-AUG-1994
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/195,395
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  07/847,566
;      FILING DATE:  06-MAR-1992
;      APPLICATION NUMBER:  07/665,961
;      FILING DATE:  07-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elbing, Karen L
;      REGISTRATION NUMBER:  35,238
;      REFERENCE/DOCKET NUMBER:  00786/247001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-428-0200
;      TELEFAX:  617-428-7045
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  768 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-284-391B-32

  Query Match           60.0%;  Score 689.8;  DB 2;  Length 768;
  Best Local Similarity  98.3%;  Pred. No. 4.9e-169;
  Matches  697;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          7 GAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 66
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 67

Qy         67 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 126
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 127

Qy        127 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 186
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 187

Qy        187 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 246
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 247

Qy        247 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 306
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        248 TACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 307

Qy        307 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 367

Qy        367 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 427

Qy        427 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 487

Qy        487 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 547

Qy        547 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 607

Qy        607 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 667

Qy        667 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGA 715
              |||||||||||||||||||||||||||||||||||  || |  | |||
Db        668 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGGCTGCAACTGGACGAGA 716


RESULT 9
US-09-218-950-32
; Sequence 32, Application US/09218950
; Patent No. 6284240
;  GENERAL INFORMATION:
;    APPLICANT:  Seed, Brian
;    APPLICANT:  Banapour, Babak
;    APPLICANT:  Romeo, Charles
;    APPLICANT:  Kolanus, Waldemar
;    TITLE OF INVENTION:  TARGETED CYTOLYSIS OF HIV-INFECTED
;    TITLE OF INVENTION:  CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Clark & Elbing LLP
;      STREET:  176 Federal Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/218,950
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/284,391
;      FILING DATE:  02-AUG-1994
;      APPLICATION NUMBER:  08/195,395
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  07/847,566
;      FILING DATE:  06-MAR-1992
;      APPLICATION NUMBER:  07/665,961
;      FILING DATE:  07-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elbing, Karen L
;      REGISTRATION NUMBER:  35,238
;      REFERENCE/DOCKET NUMBER:  00786/247001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-428-0200
;
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;       TELEFAX:  617-428-7045
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  32:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  768 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-09-218-950-32

  Query Match             60.0%;  Score 689.8;  DB 3;  Length 768;
  Best Local Similarity   98.3%;  Pred. No. 4.9e-169;
  Matches  697;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          7 GAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 66
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 67

Qy         67 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 126
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 127

Qy        127 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 186
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 187

Qy        187 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 246
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 247

Qy        247 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 306
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        248 TACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 307

Qy        307 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 366
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 367

Qy        367 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 426
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Db        368 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 427

Qy        427 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 486
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 487

Qy        487 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 546
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 547

Qy        547 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 606
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 607

Qy        607 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 666
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Db        608 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 667

Qy        667 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGA 715
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Db        668 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGGCTGCAACTGGACGAGA 716


RESULT 10
US-08-322-805-3
; Sequence 3, Application US/08322805
; Patent No. 5620889
;  GENERAL INFORMATION:
;    APPLICANT:  Lynch, David
;    APPLICANT:  Alderson, Mark
;    TITLE OF INVENTION:  Fas antagonists and uses thereof
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/322,805
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/136,817
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Launer, Charlene A
;      REGISTRATION NUMBER:  33,035
;      REFERENCE/DOCKET NUMBER:  2815
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-389-4387
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  693 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-322-805-3

  Query Match             59.7%;  Score 686.8;  DB 1;  Length 693;
  Best Local Similarity   99.7%;  Pred. No. 2.8e-168;
  Matches  688;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         13 AAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGGA 72
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGGA 60

Qy         73 CCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCT 132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCT 120

Qy        133 GAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG 180

Qy        193 TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC 240

Qy        253 AGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAG 312
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAG 300

Qy        313 GAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCC 372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCC 360

Qy        373 AAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAG 432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAG 420

Qy        433 CTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC 480

Qy        493 GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTG 552
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Db        481 GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTG 540

Qy        553 CTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGG 612
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGG 600

Qy        613 CAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACG 672
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACG 660

Qy        673 CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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Db        661 CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 690


RESULT 11
US-08-429-499-3
; Sequence 3, Application US/08429499
; Patent No. 5830469
;  GENERAL INFORMATION:
;    APPLICANT:  Lynch, David
;    APPLICANT:  Alderson, Mark
;    TITLE OF INVENTION:  Fas antagonists and uses thereof
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/429,499
;      FILING DATE:  26-APR-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/136,817
;      FILING DATE:  14-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Launer, Charlene A
;      REGISTRATION NUMBER:  33,035
;      REFERENCE/DOCKET NUMBER:  2815
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-389-4387
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  693 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-429-499-3

  Query Match             59.7%;  Score 686.8;  DB 2;  Length 693;
  Best Local Similarity   99.7%;  Pred. No. 2.8e-168;
  Matches  688;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         13 AAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGA 72
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGA 60

Qy         73 CCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCT 132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCT 120

Qy        133 GAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG 180

Qy        193 TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC 240

Qy        253 AGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAG 312
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Db        241 AGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAG 300

Qy        313 GAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCC 372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCC 360

Qy        373 AAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAG 432
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Db        361 AAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAG 420

Qy        433 CTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC 480

Qy        493 GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTG 552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTG 540

Qy        553 CTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGG 612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGG 600

Qy        613 CAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACG 672
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Db        601 CAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACG 660

Qy        673 CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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Db        661 CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 690


RESULT 12
US-09-152-733-3
; Sequence 3, Application US/09152733
; Patent No. 6015559
;  GENERAL INFORMATION:
;    APPLICANT:  Lynch, David
;    APPLICANT:  Alderson, Mark
;    TITLE OF INVENTION:  Fas antagonists and uses thereof
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/152,733
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/136,817
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Launer, Charlene A
;      REGISTRATION NUMBER:  33,035
;      REFERENCE/DOCKET NUMBER:  2815
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;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-389-4387
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  693 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-09-152-733-3

  Query Match             59.7%;  Score 686.8;  DB 3;  Length 693;
  Best Local Similarity   99.7%;  Pred. No. 2.8e-168;
  Matches  688;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         13 AAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGA 72
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGA 60

Qy         73 CCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCT 132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCT 120

Qy        133 GAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG 180

Qy        193 TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC 240

Qy        253 AGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAG 312
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAG 300

Qy        313 GAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCC 372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCC 360

Qy        373 AAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAG 432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAG 420

Qy        433 CTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC 480

Qy        493 GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTG 552
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Db        481 GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTG 540

Qy        553 CTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGG 612
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Db        541 CTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGG 600

Qy        613 CAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACG 672
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Db        601 CAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACG 660

Qy        673 CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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Db        661 CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 690


RESULT 13
US-09-023-655-1223
; Sequence 1223, Application US/09023655
; Patent No. 6607879
;  GENERAL INFORMATION:
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  Susan G. Stuart
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1508
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,655
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0001 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1223:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  705 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g243865
US-09-023-655-1223

  Query Match             59.6%;  Score 685;  DB 4;  Length 705;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-168;
  Matches  685;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         18 TTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTC 77
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Qy         78 AGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGT 137
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Db         61 AGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGT 120

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Db        121 CACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGT 180

Qy        198 GGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAC 257
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Qy        258 GTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTA 317
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Db        241 GTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTA 300

Qy        318 CAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGC 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGC 360

Qy        378 CAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGAC 437
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Db        361 CAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGAC 420
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Qy        438 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT 480

Qy        498 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA 557
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA 540

Qy        558 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 617
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Db        541 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 600

Qy        618 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 677
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Qy        678 GAGCCTCTCCCTGTCTCCGGGTAAA 702
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RESULT 14
US-07-943-843-7
; Sequence 7, Application US/07943843
; Patent No. 5284755
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Beckmann, M. P.
; TITLE OF INVENTION: Leukemia Inhibitory Factor Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/943,843
; FILING DATE: 19920911
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2606-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; TELEFAX: 206-587-0606
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; IMMEDIATE SOURCE:
; CLONE: hIgG1Fc
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..739
US-07-943-843-7

Query Match 59.5%; Score 684.2; DB 1; Length 745;
Best Local Similarity 98.2%; Pred. No. 1.4e-167;
Matches 692; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
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Db         99 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 158

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Db        159 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 218

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 278

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Db        279 AGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 338

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
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Db        339 ATGGCAAGGACTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATGCAGAAAA 398

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
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Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
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RESULT 15
US-08-236-918A-14
; Sequence 14, Application US/08236918A
; Patent No. 5674704
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple 7.5.3
; SOFTWARE: Microsoft Word, Version #6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,918A

; FILING DATE: 06-May-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,843
; FILING DATE: 07-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2801-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: hIgG1Fc
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..739
US-08-236-918A-14

Query Match 59.5%; Score 684.2; DB 1; Length 745;
Best Local Similarity 98.2%; Pred. No. 1.4e-167;
Matches 692; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
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Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
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Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
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Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
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Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGA 709
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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Gapop 10.0 , Gapext 1.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1134	98.6	1150	13	US-10-679-999-10	Sequence 10, Appl
3	1117.8	97.2	1135	13	US-10-679-999-13	Sequence 13, Appl
4	1105	96.1	1135	13	US-10-679-999-16	Sequence 16, Appl
5	695.4	60.5	1012	13	US-10-272-899A-7	Sequence 7, Appli
6	695.4	60.5	1094	13	US-10-272-899A-71	Sequence 71, Appl
7	695.2	60.5	714	15	US-10-207-655-207	Sequence 207, App
8	695.2	60.5	1080	9	US-09-949-713-14	Sequence 14, Appl
9	694.8	60.4	990	10	US-09-995-898A-14	Sequence 14, Appl
10	694.8	60.4	990	10	US-09-892-949-37	Sequence 37, Appl
11	694.8	60.4	990	13	US-10-420-034A-14	Sequence 14, Appl
12	694.8	60.4	993	13	US-10-383-902A-4	Sequence 4, Appli
c 13	694.8	60.4	993	13	US-10-383-902A-5	Sequence 5, Appli
14	694.8	60.4	1104	16	US-10-452-646-10	Sequence 10, Appl
15	694.4	60.4	762	15	US-10-008-063-17	Sequence 17, Appl
16	694.4	60.4	762	15	US-10-152-363A-5	Sequence 5, Appli
17	694.4	60.4	1019	15	US-10-341-836-1	Sequence 1, Appli
18	693.4	60.3	924	15	US-10-207-655-306	Sequence 306, App
19	693.4	60.3	1066	17	US-10-408-901-1	Sequence 1, Appli
20	693.2	60.3	993	14	US-10-047-542-19	Sequence 19, Appl
21	693.2	60.3	993	15	US-10-320-231A-80	Sequence 80, Appl
22	692.8	60.2	776	9	US-09-934-060A-31	Sequence 31, Appl
23	692.8	60.2	1077	15	US-10-233-150-4	Sequence 4, Appli
24	692.8	60.2	1134	15	US-10-363-427-15	Sequence 15, Appl
25	691.6	60.1	993	14	US-10-060-714-26	Sequence 26, Appl
26	691.6	60.1	1135	15	US-10-097-044A-8	Sequence 8, Appli
27	691.2	60.1	762	15	US-10-152-363A-38	Sequence 38, Appl
28	691.2	60.1	804	9	US-09-996-357-11	Sequence 11, Appl
29	690.6	60.1	1012	13	US-10-272-899A-9	Sequence 9, Appli
30	690.6	60.1	1094	13	US-10-272-899A-69	Sequence 69, Appl
31	690.4	60.0	711	15	US-10-207-655-6	Sequence 6, Appli
32	690.4	60.0	711	15	US-10-053-530-6	Sequence 6, Appli
33	690.2	60.0	991	16	US-10-418-836-6	Sequence 6, Appli
34	690.2	60.0	1001	13	US-10-323-904-2	Sequence 2, Appli
35	690	60.0	990	15	US-10-121-464-19	Sequence 19, Appl
36	690	60.0	990	15	US-10-159-006-21	Sequence 21, Appl
37	690	60.0	993	16	US-10-366-709-51	Sequence 51, Appl
38	689.8	60.0	768	10	US-09-939-537-32	Sequence 32, Appl
39	689.6	60.0	703	13	US-10-433-108-33	Sequence 33, Appl
40	689.6	60.0	762	15	US-10-152-363A-28	Sequence 28, Appl
41	689.6	60.0	762	15	US-10-152-363A-36	Sequence 36, Appl
42	688.4	59.9	987	16	US-10-370-749-36	Sequence 36, Appl
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45	685	59.6	705	17	US-10-641-643-1223	Sequence 1223, Ap

ALIGNMENTS

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RESULT 1
US-10-679-999-7
; Sequence 7, Application US/10679999
; Publication No. US20040067520A1
;  GENERAL INFORMATION:
;       APPLICANT: Mann, Michael B.
;                  Hecht, Randy I.
;       TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                           METHODS
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Amgen Inc.
;            STREET: 1840 DeHavilland Drive
;            CITY: Thousand Oaks
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 91320-1789
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/679,999
;            FILING DATE: 06-Oct-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/568,528
;            FILING DATE: 09-May-2000
;            APPLICATION NUMBER: 09/267,517
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Knight, Matthew W.
;            REGISTRATION NUMBER: 36,846
;            REFERENCE/DOCKET NUMBER: A-416
;  INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
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;             LENGTH: 1150 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;         FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION:  4
;             OTHER INFORMATION:  /note= "Met = ATG"
;         SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-679-999-7

  Query Match             100.0%;  Score 1150;  DB 13;  Length 1150;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-312;
  Matches 1150;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 CATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA 60

Qy         61 CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120

Qy        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180
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Db        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180

Qy        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240

Qy        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300

Qy        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360

Qy        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420

Qy        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480

Qy        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540
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Db        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540

Qy        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600
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Db        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600

Qy        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660
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Db        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660

Qy        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720
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Db        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720

Qy        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780
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Db        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780

Qy        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840
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Db        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840

Qy        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900

Qy        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960
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Db        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960

Qy        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020
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Db        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020

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Db       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080

Qy       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140
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Db       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140

Qy       1141 TAATGGATCC 1150
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Db       1141 TAATGGATCC 1150


RESULT 2
US-10-679-999-10
; Sequence 10, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;         APPLICANT: Mann, Michael B.
;                    Hecht, Randy I.
;         TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                             METHODS
;         NUMBER OF SEQUENCES: 18
;         CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;         COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;         ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 10:
;         SEQUENCE CHARACTERISTICS:
;             LENGTH: 1150 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;         FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION:  4
;             OTHER INFORMATION:  /note= "Met = ATG"
;         SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-679-999-10
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  Best Local Similarity  99.1%;  Pred. No. 8.3e-308;
  Matches 1140;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

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Db          1 CATATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAA 60

Qy         61 CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120
              |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTCCTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120

Qy        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180
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Db        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180

Qy        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240
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Db        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360

Qy        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420
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Db        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420

Qy        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480
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Db        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480

Qy        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540
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Db        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540

Qy        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600
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Db        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600

Qy        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660
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Db        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660

Qy        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720
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Db        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720

Qy        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780
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Db        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780

Qy        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840
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Qy        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900
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Db        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900

Qy        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960
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Qy       1141 TAATGGATCC 1150
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RESULT 3
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; Sequence 13, Application US/10679999
; Publication No. US20040067520A1
;  GENERAL INFORMATION:
;       APPLICANT: Mann, Michael B.
;                  Hecht, Randy I.
;       TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                           METHODS
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Amgen Inc.
;            STREET: 1840 DeHavilland Drive
;            CITY: Thousand Oaks
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 91320-1789
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/679,999
;            FILING DATE: 06-Oct-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/568,528
;            FILING DATE: 09-May-2000
;            APPLICATION NUMBER: 09/267,517
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Knight, Matthew W.
;            REGISTRATION NUMBER: 36,846
;            REFERENCE/DOCKET NUMBER: A-416
;  INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1135 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  misc_feature
;            LOCATION:  4
;            OTHER INFORMATION:  /note= "Met = ATG"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-679-999-13
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  Best Local Similarity  99.4%;  Pred. No. 2.9e-303;
  Matches 1122;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

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Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

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Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
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Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
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Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726

Qy        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786

Qy        802 CAGAAAGTTACAGGCCTGGACTTCATCCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861
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Db        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906

Qy        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966

Qy        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026

Qy       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086

Qy       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135

RESULT 4
US-10-679-999-16
; Sequence 16, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 16:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1135 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION:  4
;             OTHER INFORMATION:  /note= "Met = ATG"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-679-999-16

  Query Match             96.1%;  Score 1105;  DB 13;  Length 1135;
  Best Local Similarity   98.7%;  Pred. No. 1.1e-299;
  Matches 1114;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 81
              |||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126

Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246

Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
              |||||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
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Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726

Qy        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786

Qy        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846

Qy        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906

Qy        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966

Qy        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026

Qy       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086

Qy       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135


RESULT 5
US-10-272-899A-7
; Sequence 7, Application US/10272899A
; Publication No. US20040033561A1
; GENERAL INFORMATION:
;  APPLICANT: O'Keefe, Theresa L.
;  APPLICANT:  Healy, Judith Jacques
;  APPLICANT:  Newman, Walter
;  APPLICANT:  Ponath, Paul
;  APPLICANT:  Bruce Keyt
;  TITLE OF INVENTION: IMMUNOGLOBULIN DNA CASSETTE MOLECULES,
;  TITLE OF INVENTION:  MONOBODY CONSTRUCTS, METHODS OF PRODUCTION, AND METHODS OF
;  TITLE OF INVENTION:  USE THEREFOR
;  FILE REFERENCE: MPI01-244P2RM
;  CURRENT APPLICATION NUMBER: US/10/272,899A
;  CURRENT FILING DATE:  2002-10-17
;  PRIOR APPLICATION NUMBER: 60/350,166
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: 60/392,364
;  PRIOR FILING DATE: 2002-06-26
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 1012
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: human IgG1-WT DNA
US-10-272-899A-7

  Query Match             60.5%;  Score 695.4;  DB 13;  Length 1012;
  Best Local Similarity   99.1%;  Pred. No. 8.7e-185;
  Matches  699;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 362

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 422

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 482

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 542

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 602

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 662

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        663 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 722

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 782

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 842

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 902

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 962

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGA 709
              ||||||||||||||||||||||||||||||||||||||  | | |
Db        963 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAATCTA 1007


RESULT 6
US-10-272-899A-71
; Sequence 71, Application US/10272899A
; Publication No. US20040033561A1
; GENERAL INFORMATION:
;  APPLICANT: O'Keefe, Theresa L.
;  APPLICANT:  Healy, Judith Jacques
;  APPLICANT:  Newman, Walter
;  APPLICANT:  Ponath, Paul
;  APPLICANT:  Bruce Keyt
```

```
;  TITLE OF INVENTION: IMMUNOGLOBULIN DNA CASSETTE MOLECULES,
;  TITLE OF INVENTION:  MONOBODY CONSTRUCTS, METHODS OF PRODUCTION, AND METHODS OF
;  TITLE OF INVENTION:  USE THEREFOR
;  FILE REFERENCE: MPI01-244P2RM
;  CURRENT APPLICATION NUMBER: US/10/272,899A
;  CURRENT FILING DATE:  2002-10-17
;  PRIOR APPLICATION NUMBER: 60/350,166
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: 60/392,364
;  PRIOR FILING DATE: 2002-06-26
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71
;   LENGTH: 1094
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: immunoglobulin cassette sequence Leader-HuWT_55
US-10-272-899A-71

  Query Match             60.5%;  Score 695.4;  DB 13;  Length 1094;
  Best Local Similarity   99.1%;  Pred. No. 8.8e-185;
  Matches  699;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 444

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 504

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 564

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 624

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 684

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 744

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 804

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 864

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 924

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 984

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1044

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGA 709
              |||||||||||||||||||||||||||||||||||  | | |
Db       1045 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAATCTA 1089
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```
RESULT 7
US-10-207-655-207
; Sequence 207, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey A.
;  APPLICANT:  Hayden-Ledbetter, Martha S.
;  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
;  FILE REFERENCE: 390069.401C1
;  CURRENT APPLICATION NUMBER: US/10/207,655
;  CURRENT FILING DATE:  2002-07-25
;  NUMBER OF SEQ ID NOS: 426
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 207
;   LENGTH: 714
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fusion polynucleotide
US-10-207-655-207

  Query Match             60.5%;  Score 695.2;  DB 15;  Length 714;
  Best Local Similarity   98.9%;  Pred. No. 9.1e-185;
  Matches  700;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          2 ATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC 61
              || ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 ATCAGGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC 64

Qy         62 TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCT 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCT 124

Qy        122 CCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 CCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA 184

Qy        182 AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG 244

Qy        242 AGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 AGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGC 304

Qy        302 TGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGA 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 TGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGA 364

Qy        362 AAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCAT 421
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 AAACAATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCAT 424

Qy        422 CCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATC 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 CCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATC 484

Qy        482 CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCA 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCA 544

Qy        542 CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACA 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACA 604

Qy        602 AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACA 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACA 664

Qy        662 ACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGA 709
              |||||||||||||||||||||||||||||||||||  | | |
Db        665 ACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGATCTA 712
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RESULT 8
US-09-949-713-14
; Sequence 14, Application US/09949713
; Patent No. US20020044944A1
; GENERAL INFORMATION:
;  APPLICANT: NAKAMURA, No. US20020044944A1io
;  APPLICANT:  NAGATA, Shigekazu
;  TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
;  FILE REFERENCE: 1110-207P
;  CURRENT APPLICATION NUMBER: US/09/949,713
;  CURRENT FILING DATE:  2001-09-12
;  PRIOR APPLICATION NUMBER: US/09/180,100
;  PRIOR FILING DATE: 1998-11-02
;  PRIOR APPLICATION NUMBER: PCT/JP97/01502
;  PRIOR FILING DATE: 1997-05-01
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 1080
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-949-713-14

  Query Match             60.5%;  Score 695.2;  DB 9;  Length 1080;
  Best Local Similarity   99.6%;  Pred. No. 1e-184;
  Matches  697;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 TATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT 62
              ||  || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 TAACGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT 440

Qy         63 CCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 CCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC 500

Qy        123 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA 560

Qy        183 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 620

Qy        243 GCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCT 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 GCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCT 680

Qy        303 GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA 740

Qy        363 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC 800

Qy        423 CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC 860

Qy        483 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAC 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAC 920

Qy        543 GCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAA 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 GCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAA 980

Qy        603 GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA 662
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        981 GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA 1040

Qy        663 CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||||||||||||||||||||||||||||||||||||
Db       1041 CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1080


RESULT 9
US-09-995-898A-14
; Sequence 14, Application US/09995898A
; Publication No. US20030027253A1
; GENERAL INFORMATION:
;  APPLICANT: Presnell, Scott R.
;  APPLICANT:  Xu, Wenfeng
;  APPLICANT:  No. US20030027253A1ak, Julia E.
;  APPLICANT:  Whitmore, Theodore E.
;  APPLICANT:  Grant, Francis J.
;  TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
;  FILE REFERENCE: 00-108
;  CURRENT APPLICATION NUMBER: US/09/995,898A
;  CURRENT FILING DATE:  2001-11-28
;  PRIOR APPLICATION NUMBER: US 60/253,561
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: US 60/267,211
;  PRIOR FILING DATE: 2001-02-07
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
;   LENGTH: 990
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(990)
US-09-995-898A-14

  Query Match             60.4%;  Score 694.8;  DB 10;  Length 990;
  Best Local Similarity   99.7%;  Pred. No. 1.3e-184;
  Matches  696;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 352

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 412

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 472

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 532

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 592

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 652

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 712

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 772

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 832
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Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        833 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 892

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 952

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||||
Db        953 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 990


RESULT 10
US-09-892-949-37
; Sequence 37, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
;  APPLICANT: Sprecher, Cindy A.
;  APPLICANT:  Presnell, Scott R.
;  APPLICANT:  Gao, Zeren
;  APPLICANT:  Whitmore, Theodore E.
;  APPLICANT:  Kuijper, Joseph L.
;  APPLICANT:  Maurer, Mark F.
;  TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
;  FILE REFERENCE: 00-42
;  CURRENT APPLICATION NUMBER: US/09/892,949
;  CURRENT FILING DATE:  2001-06-26
;  PRIOR APPLICATION NUMBER: US 60/214,282
;  PRIOR FILING DATE: 2000-06-26
;  PRIOR APPLICATION NUMBER: US 60/214,955
;  PRIOR FILING DATE: 2000-06-29
;  PRIOR APPLICATION NUMBER: US 60/267,963
;  PRIOR FILING DATE: 2001-08-02
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 37
;   LENGTH: 990
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(990)
US-09-892-949-37

  Query Match             60.4%;  Score 694.8;  DB 10;  Length 990;
  Best Local Similarity   99.7%;  Pred. No. 1.3e-184;
  Matches  696;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 352

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 412

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 472

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 532

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 592

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 652

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 712

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 772

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 832

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        833 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 892

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 952

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||||
Db        953 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 990


RESULT 11
US-10-420-034A-14
; Sequence 14, Application US/10420034A
; Publication No. US20040029228A1
; GENERAL INFORMATION:
;  APPLICANT: Presnell, Scott R.
;  APPLICANT:  Xu, Wenfeng
;  APPLICANT:  No. US20040029228A1ak, Julia E.
;  APPLICANT:  Whitmore, Theodore E.
;  APPLICANT:  Grant, Francis J.
;  APPLICANT:  Kindsvogel, Wayne R.
;  APPLICANT:  Klucher, Kevin M.
;  TITLE OF INVENTION: CYTOKINE RECEPTOR
;  FILE REFERENCE: 02-10
;  CURRENT APPLICATION NUMBER: US/10/420,034A
;  CURRENT FILING DATE:  2003-04-18
;  PRIOR APPLICATION NUMBER: 60/373,813
;  PRIOR FILING DATE: 2002-04-19
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 990
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(990)
US-10-420-034A-14

  Query Match             60.4%;  Score 694.8;  DB 13;  Length 990;
  Best Local Similarity   99.7%;  Pred. No. 1.3e-184;
  Matches  696;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 352

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 412

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 472

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 532
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Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 592

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 652

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 712

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 772

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 832

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        833 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 892

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 952

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||||||||||||||||||||||||||||||||||
Db        953 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 990
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RESULT 12
US-10-383-902A-4
; Sequence 4, Application US/10383902A
; Publication No. US20030224408A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Mullberg, Jurgen
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: LIGAND SCREENING AND DISCOVERY
; FILE REFERENCE: 10280-042001
; CURRENT APPLICATION NUMBER: US/10/383,902A
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/362,403
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 993
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(990)
; FEATURE:
; OTHER INFORMATION: synthetically generated plasmid sequence
US-10-383-902A-4

Query Match 60.4%; Score 694.8; DB 13; Length 993;
Best Local Similarity 99.7%; Pred. No. 1.3e-184;
Matches 696; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 352

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 412

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 472

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 532

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 592

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 652

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 712

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 772

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 832

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        833 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 892

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 952

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||||||||||||||||||||||||||||||||||
Db        953 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 990
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RESULT 13
US-10-383-902A-5/c
; Sequence 5, Application US/10383902A
; Publication No. US20030224408A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Mullberg, Jurgen
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: LIGAND SCREENING AND DISCOVERY
; FILE REFERENCE: 10280-042001
; CURRENT APPLICATION NUMBER: US/10/383,902A
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/362,403
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 993
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated plasmid sequence
US-10-383-902A-5

Query Match 60.4%; Score 694.8; DB 13; Length 993;
Best Local Similarity 99.7%; Pred. No. 1.3e-184;
Matches 696; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
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Db        701 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 642
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Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        641 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 582

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
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Db        581 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 522

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
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Db        521 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 462

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
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Db        401 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 342

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
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Db        341 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 282

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
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Db        281 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 222

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
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Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
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Db        161 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 102

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
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Db        101 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 42

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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Db         41 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 4


RESULT 14
US-10-452-646-10
; Sequence 10, Application US/10452646
; Publication No. US20040018593A1
; GENERAL INFORMATION:
;  APPLICANT: Carton, Jill M.
;  APPLICANT:  Staquet, Kimberly C.
;  APPLICANT:  Scallon, Bernard J.
;  APPLICANT:  Jill, Giles-Komar
;  TITLE OF INVENTION: ANTI-RELP FUSION ANTIBODIES, COMPOSITIONS, METHODS AND USES
;  FILE REFERENCE: CEN0296 NP
;  CURRENT APPLICATION NUMBER: US/10/452,646
;  CURRENT FILING DATE:  2003-06-02
;  PRIOR APPLICATION NUMBER: US 60/385,305
;  PRIOR FILING DATE: 2002-06-03
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
;   LENGTH: 1104
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-452-646-10

  Query Match           60.4%;  Score 694.8;  DB 16;  Length 1104;
  Best Local Similarity   99.7%;  Pred. No. 1.3e-184;
  Matches  696;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 GAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 66
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Db        406 GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 465

Qy         67 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 525

Qy        127 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 585

Qy        187 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 645

Qy        247 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 306
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        646 TACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 705

Qy        307 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 765

Qy        367 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 825

Qy        427 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 885

Qy        487 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 546
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Db        886 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 945

Qy        547 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 606
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Db        946 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 1005

Qy        607 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 666
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Db       1006 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 1065

Qy        667 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGT 704
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Db       1066 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGT 1103


RESULT 15
US-10-008-063-17
; Sequence 17, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
;  APPLICANT: Gross, Jane A.
;  APPLICANT:  Xu, Wenfeng
;  APPLICANT:  Henne, Randal M.
;  APPLICANT:  Grant, Francis, J.
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
;  FILE REFERENCE: 00-103
;  CURRENT APPLICATION NUMBER: US/10/008,063
;  CURRENT FILING DATE:  2001-11-05
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 762
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (7)...(759)
US-10-008-063-17

  Query Match           60.4%;  Score 694.4;  DB 15;  Length 762;
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Best Local Similarity 99.9%; Pred. No. 1.5e-184;
Matches 695; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          7 GAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 66
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 123

Qy         67 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 183

Qy        127 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 243

Qy        187 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 303

Qy        247 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 363

Qy        307 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 423

Qy        367 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 483

Qy        427 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 543

Qy        487 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 603

Qy        547 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 663

Qy        607 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 666
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Db        664 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 723

Qy        667 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||
Db        724 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 759
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Search completed: May 9, 2004, 11:51:54
Job time : 375.25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 13:07:09 ; Search time 2222.5 Seconds
(without alignments)
15451.747 Million cell updates/sec

Title: US-10-679-999-7
Perfect score: 1150
Sequence: 1 CATATGGAACCCAAATCTTG.....TCCGGGTTGTTAATGGATCC 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 54314686

Minimum DB seq length: 0
Maximum DB seq length: 1150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
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22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	694.8	60.4	871	12	BG753979	BG753979 602709506
2	694.8	60.4	983	13	BQ708975	BQ708975 AGENCOURT
3	694	60.3	843	12	BM007897	BM007897 603617582
4	693.8	60.3	941	13	BQ712021	BQ712021 AGENCOURT
5	693.2	60.3	925	13	BQ709152	BQ709152 AGENCOURT
6	692.4	60.2	973	13	BQ706204	BQ706204 AGENCOURT
7	692.2	60.2	858	13	BX346946	BX346946 BX346946
8	691.6	60.1	919	13	BQ709339	BQ709339 AGENCOURT
9	691	60.1	897	13	BQ709144	BQ709144 AGENCOURT
10	690	60.0	947	13	BQ709771	BQ709771 AGENCOURT
11	689.8	60.0	881	13	BQ711291	BQ711291 AGENCOURT
c 12	687.8	59.8	1013	13	BX360518	BX360518 BX360518
13	687.4	59.8	757	12	BG674795	BG674795 602620925
14	687.4	59.8	914	13	BQ712363	BQ712363 AGENCOURT
15	685.6	59.6	856	13	BQ709859	BQ709859 AGENCOURT
16	682.8	59.4	892	12	BG397723	BG397723 602438784
17	682.8	59.4	897	12	BM008412	BM008412 603617406
18	682.8	59.4	902	13	BU146962	BU146962 AGENCOURT
c 19	681.6	59.3	1015	13	BX367600	BX367600 BX367600
c 20	681.2	59.2	1147	13	BX360330	BX360330 BX360330
c 21	680.8	59.2	860	13	BX437583	BX437583 BX437583
c 22	680.4	59.2	985	13	BX457369	BX457369 BX457369
c 23	680.4	59.2	1034	13	BX337959	BX337959 BX337959
24	679	59.0	940	13	BQ705928	BQ705928 AGENCOURT
c 25	678.8	59.0	954	12	BG746184	BG746184 602723696
c 26	678.8	59.0	1142	13	BX414495	BX414495 BX414495
c 27	678.4	59.0	898	13	BX415442	BX415442 BX415442
28	677.4	58.9	958	13	BQ706140	BQ706140 AGENCOURT
29	677.4	58.9	961	13	BQ710233	BQ710233 AGENCOURT
c 30	676.8	58.9	885	13	BX437308	BX437308 BX437308
c 31	675.4	58.7	879	13	BX336029	BX336029 BX336029
c 32	674.4	58.6	1149	13	BX381020	BX381020 BX381020
33	674	58.6	926	12	BG755166	BG755166 602711488
34	672.8	58.5	1014	12	BM914505	BM914505 AGENCOURT
c 35	671.4	58.4	1093	13	BX428863	BX428863 BX428863
36	671	58.3	941	13	BQ711680	BQ711680 AGENCOURT
c 37	668.8	58.2	1009	13	BX456658	BX456658 BX456658
38	668.6	58.1	925	13	BQ709853	BQ709853 AGENCOURT
c 39	668.4	58.1	883	13	BX454398	BX454398 BX454398
c 40	667.6	58.1	951	12	BG746233	BG746233 602723760
c 41	667.4	58.0	877	13	BX324928	BX324928 BX324928
c 42	667.4	58.0	921	13	BX359858	BX359858 BX359858
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44	666.4	57.9	873	13	BQ708562	BQ708562 AGENCOURT
c 45	665.6	57.9	980	13	BX325701	BX325701 BX325701

ALIGNMENTS

RESULT 1
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LOCUS BG753979 871 bp mRNA linear EST 15-MAY-2001
DEFINITION 602709506F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4846201 5', mRNA sequence.
ACCESSION BG753979
VERSION BG753979.1 GI:14064632
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 871)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1686 row: k column: 02
High quality sequence stop: 848.

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FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4846201"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             60.4%;  Score 694.8;  DB 12;  Length 871;
  Best Local Similarity   99.7%;  Pred. No. 1.9e-132;
  Matches  696;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 79

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 139

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 199

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
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Db        200 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 259

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Db        260 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 319

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
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Db        320 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 379

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
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Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
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Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
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Db        500 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 559

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
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Db        560 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 619

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
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Db        620 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 679

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||||
Db        680 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 717
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RESULT 2
BQ708975
LOCUS       BQ708975                983 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8353514 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279683
            5', mRNA sequence.
ACCESSION   BQ708975
VERSION     BQ708975.1  GI:21847874
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 983)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2469  row: k  column: 12
            High quality sequence stop: 604.
FEATURES             Location/Qualifiers
     source          1. .983
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6279683"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             60.4%;  Score 694.8;  DB 13;  Length 983;
  Best Local Similarity   99.7%;  Pred. No. 2e-132;
  Matches  696;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 66

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 126

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 186

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 246

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 306

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 366
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Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 426

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 486

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 546

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 606

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 666

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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Db        667 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 704
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RESULT 3
BM007897

LOCUS	BM007897 843 bp mRNA linear EST 30-OCT-2001
DEFINITION	603617582F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450469 5', mRNA sequence.
ACCESSION	BM007897
VERSION	BM007897.1 GI:16522238
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 843)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Mark Watson cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM1939 row: d column: 22 High quality sequence stop: 833.

FEATURES	Location/Qualifiers
source	1. .843 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5450469" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH_MGC_113" /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 60.3%; Score 694; DB 12; Length 843;
Best Local Similarity 99.3%; Pred. No. 2.8e-132;
Matches 697; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 150

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 210

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 270

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 330

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 390

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 450

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 510

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 570

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 630

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 690

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 750

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTAC 706
              | ||||||||||||||||||||||||||||||||||||  ||
Db        751 ATTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAC 792
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RESULT 4
BQ712021

LOCUS	BQ712021 941 bp mRNA linear EST 16-JUL-2002
DEFINITION	AGENCOURT_8418162 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281403 5', mRNA sequence.
ACCESSION	BQ712021
VERSION	BQ712021.1 GI:21850920
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 941)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Mark Watson cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2474 row: c column: 04
High quality sequence stop: 638.

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FEATURES             Location/Qualifiers
     source          1. .941
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6281403"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             60.3%;  Score 693.8;  DB 13;  Length 941;
  Best Local Similarity   99.6%;  Pred. No. 3.2e-132;
  Matches  695;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 92

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 152

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 212

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 272

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 332

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 392

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 452

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 512

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
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Db        513 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 572

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 632

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        633 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGANGCTCTGCACAACC 692

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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Db        693 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 730
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RESULT 5
BQ709152
LOCUS       BQ709152                925 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8485151 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301245
            5', mRNA sequence.
ACCESSION   BQ709152
VERSION     BQ709152.1  GI:21848051
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 925)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2516  row: m  column: 22
            High quality sequence stop: 739.
FEATURES             Location/Qualifiers
     source          1. .925
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6301245"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             60.3%;  Score 693.2;  DB 13;  Length 925;
  Best Local Similarity   99.6%;  Pred. No. 4.3e-132;
  Matches  695;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 90

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 150

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 210

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 270

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 330

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        331 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 390

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 450

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 510

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 570

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 630

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 690

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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Db        691 ACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 728


RESULT 6
BQ706204
LOCUS       BQ706204                 973 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8352308 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277592
            5', mRNA sequence.
ACCESSION   BQ706204
VERSION     BQ706204.1  GI:21845103
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 973)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2464  row: d  column: 09
            High quality sequence stop: 640.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             60.2%;  Score 692.4;  DB 13;  Length 973;
  Best Local Similarity   96.3%;  Pred. No. 6.3e-132;
  Matches  708;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
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Db         91 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 150

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
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Db        151 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 210

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
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Db        211 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 270

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
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Db        271 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 330

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Db        331 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 390

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
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Db        391 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 450

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
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Db        451 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 510

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
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Db        511 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 570

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
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Db        571 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 630

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
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Db        631 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 690

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||| |||||||||||||||||||||||||||||| ||||||||||||
Db        691 GCAGGTGGCAGCAGGNGAACGTCTTCTCATGCTCCGTGATGCATGAAGCTCTGCACAACC 750

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGG 724
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Db        751 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGCGACGGGCGGGAAAGC 810

Qy        725 ACGACACCAAAACCT 739
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Db        811 CCCCCTCCCCAGGCT 825


RESULT 7
BX346946
LOCUS       BX346946                 858 bp    mRNA    linear   EST 05-MAY-2003
DEFINITION  BX346946 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI039YP09 5-PRIME, mRNA sequence.
ACCESSION   BX346946
VERSION     BX346946.1  GI:30377150
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 858)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
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            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 7198.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0AT021ZE05_T01957_1&cluster=7198.r.
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0AT021ZE05_T01957_1.
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                      /note="1st strand cDNA was primed with a NotI-oligo(dT)
                      primer. Five prime end enriched, double-strand cDNA was
                      digested with Not I and cloned into the Not I and EcoR V
                      sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             60.2%;  Score 692.2;  DB 13;  Length 858;
  Best Local Similarity   99.4%;  Pred. No. 6.6e-132;
  Matches  694;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
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Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
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Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
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Db        168 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 227

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
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Db        228 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 287

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Db        348 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 407

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
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Db        408 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 467

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
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Db        528 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 587

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
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Db        588 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 647

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
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Db        648 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTNCGTGATGCATGAGGCTCTGCACAACC 707

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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Db        708 ACTACACGCAGAAGAGCCTCTCCCTGTCTTCGGGTAAA 745


RESULT 8
BQ709339
LOCUS       BQ709339                 919 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_7976429 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214450
            5', mRNA sequence.
ACCESSION   BQ709339
VERSION     BQ709339.1  GI:21848238
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 919)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2381  row: m  column: 11
            High quality sequence stop: 576.
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                      /clone_lib="NIH_MGC_113"
                      /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                      EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                      into EcoRI/XhoI sites using the following 5' adaptor:
                      GGCACGAG(G). Library constructed by Ling Hong in the
                      laboratory of Gerald M. Rubin (University of California,
                      Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                      Superscript II RT (Life Technologies). Note: this is a
                      NIH_MGC Library."
ORIGIN

  Query Match             60.1%;  Score 691.6;  DB 13;  Length 919;
  Best Local Similarity   99.4%;  Pred. No. 9.1e-132;
  Matches  694;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
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Db        100 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 159

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
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Db        160 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 219

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
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Db        220 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 279

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
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Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
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Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
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Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
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Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
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Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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RESULT 9
BQ709144
LOCUS       BQ709144                 897 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8474994 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301566
            5', mRNA sequence.
ACCESSION   BQ709144
VERSION     BQ709144.1  GI:21848043
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 897)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2517  row: k  column: 07
            High quality sequence stop: 628.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
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ORIGIN

  Query Match           60.1%;  Score 691;  DB 13;  Length 897;
  Best Local Similarity  99.3%;  Pred. No. 1.2e-131;
  Matches  694;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
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Db         33 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 92

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
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Db         93 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 152

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
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Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
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Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
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Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
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RESULT 10
BQ709771
LOCUS       BQ709771                 947 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8353965 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278583
            5', mRNA sequence.
ACCESSION   BQ709771
VERSION     BQ709771.1  GI:21848670
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 947)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
```

```
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2466  row: m  column: 16
            High quality sequence start: 3
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FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match            60.0%;  Score 690;  DB 13;  Length 947;
  Best Local Similarity  99.3%;  Pred. No. 2e-131;
  Matches  693;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 239

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
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Db        240 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 299

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 359

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 419

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Db        420 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 479

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 539

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 599

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 659

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
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Db        660 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 719

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 779

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        780 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACCACC 839

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||||||||||||||||||||  ||||||||
Db        840 ACTACACGCAGAAGAGCCTCTCCCTGTCCTCGGGTAAA 877


RESULT 11
BQ711291
LOCUS       BQ711291                881 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8347186 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279096
            5', mRNA sequence.
ACCESSION   BQ711291
VERSION     BQ711291.1  GI:21850190
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 881)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2468  row: c  column: 01
            High quality sequence stop: 721.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6279096"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match            60.0%;  Score 689.8;  DB 13;  Length 881;
  Best Local Similarity  99.7%;  Pred. No. 2.1e-131;
  Matches  691;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 179

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
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Db        180 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 239

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 299

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 359
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Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 419

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 479

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 539

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 599

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
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Db        600 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 659

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
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Db        660 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 719

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 779

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG 697
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Db        780 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG 812
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RESULT 12
BX360518/c
LOCUS       BX360518                1013 bp    mRNA    linear   EST 05-MAY-2003
DEFINITION  BX360518 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI071YG21 3-PRIME, mRNA sequence.
ACCESSION   BX360518
VERSION     BX360518.1  GI:30372442
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1013)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 7198.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI071AD11NP1&cluster=7198.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI071AD11NP1.
FEATURES             Location/Qualifiers
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                     /clone="CS0DI071YG21"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
```

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ORIGIN

  Query Match           59.8%;  Score 687.8;  DB 13;  Length 1013;
  Best Local Similarity  98.4%;  Pred. No. 5.7e-131;
  Matches  687;  Conservative    6;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        785 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 726

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        725 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 666

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        665 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 606

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 546

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Db        545 AGTACAACANGMCGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 486

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||:|:||||||||||||||||
Db        485 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTMCMAGCCCCCATCGAGAAAA 426

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 366

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        365 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTTTATCCCA 306

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 246

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              |||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 CTCCCKTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 186

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 126

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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Db        125 ACTACACGCAGAAGAGCCTCTCCCYBTCTCCGGGTAAA 88
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RESULT 13
BG674795
LOCUS       BG674795                757 bp    mRNA    linear   EST 01-MAY-2001
DEFINITION  602620925F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4746150 5',
            mRNA sequence.
ACCESSION   BG674795
VERSION     BG674795.1  GI:13906191
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 757)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
```

```
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
            Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10594  row: b  column: 07
            High quality sequence stop: 755.
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4746150"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Skn3"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match           59.8%;  Score 687.4;  DB 12;  Length 757;
  Best Local Similarity   99.0%;  Pred. No. 6.1e-131;
  Matches  691;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 79

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
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Db         80 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 139

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
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Db        200 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 259

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Db        260 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 319

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 379

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 439

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              |||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 GGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 499

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
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Db        500 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 559

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
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Db        560 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGA 619

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
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Db        620 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAANC 679

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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RESULT 14
BQ712363
LOCUS       BQ712363                914 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8475100 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301405
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ACCESSION   BQ712363
VERSION     BQ712363.1  GI:21851262
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 914)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2517  row: d  column: 14
            High quality sequence stop: 585.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match           59.8%;  Score 687.4;  DB 13;  Length 914;
  Best Local Similarity   99.0%;  Pred. No. 6.6e-131;
  Matches  691;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         52 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 111

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
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Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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RESULT 15
BQ709859
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DEFINITION  AGENCOURT_8349888 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6280560
            5', mRNA sequence.
ACCESSION   BQ709859
VERSION     BQ709859.1  GI:21848758
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 856)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2471  row: p  column: 01
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FEATURES             Location/Qualifiers
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                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
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ORIGIN
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  Query Match           59.6%;  Score 685.6;  DB 13;  Length 856;
  Best Local Similarity  98.7%;  Pred. No. 1.5e-130;
  Matches  691;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
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Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
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Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Db        367 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 426

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
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Db        427 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 486

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Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
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Job time : 2227.5 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 13:07:09 ; Search time 3070.75 Seconds
(without alignments)
16232.024 Million cell updates/sec

Title: US-10-679-999-8
Perfect score: 1150
Sequence: 1 GTATACCTTGGGTTTAGAAC.....AGGCCCAACAATTACCTAGG 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 5430052

Minimum DB seq length: 0
Maximum DB seq length: 1150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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2: gb_htg:*
3: gb_in:*
4: gb_om:*
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8: gb_pl:*
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12: gb_sy:*
13: gb_un:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1		1150	100.0	1150	6	BD056518	BD056518 OB fusion
2		1134	98.6	1150	6	BD056520	BD056520 OB fusion
3		1117.8	97.2	1135	6	BD056522	BD056522 OB fusion
4		1105	96.1	1135	6	BD056524	BD056524 OB fusion
5		676.2	58.8	1142	6	I27618	I27618 Sequence 9
6		674.4	58.6	861	6	BD263010	BD263010 Dimeric t
7		673	58.5	684	6	BD263000	BD263000 Dimeric t
8		440.8	38.3	454	6	BD004077	BD004077 Methods o
9		440.8	38.3	454	6	BD056516	BD056516 OB fusion
10		378.4	32.9	491	6	BD004075	BD004075 Methods o
11		378.4	32.9	491	6	BD056514	BD056514 OB fusion
12		50.8	4.4	908	8	AB029092	AB029092 Cucumis s
13		50.8	4.4	1110	8	AB029147	AB029147 Cucumis s
14		43	3.7	468	6	I27620	I27620 Sequence 12
15		43	3.7	746	6	A51599	A51599 Sequence 9
16	c	40.4	3.5	1057	6	E02180	E02180 DNA sequenc
17	c	40.4	3.5	1057	6	E02181	E02181 DNA sequenc
18	c	40	3.5	533	6	AR365256	AR365256 Sequence
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20		39.6	3.4	200	6	AX039201	AX039201 Sequence
21		39.6	3.4	200	6	AX039301	AX039301 Sequence
22		39.6	3.4	200	6	AX039447	AX039447 Sequence
23		39.6	3.4	200	6	AX039510	AX039510 Sequence
24		39.4	3.4	1011	6	AX616829	AX616829 Sequence
25	c	39	3.4	1046	3	AY058495	AY058495 Drosophil
26	c	38.6	3.4	462	10	AY300753	AY300753 Mesocrice
27	c	38.6	3.4	564	10	AY300754	AY300754 Mesocrice
28		38	3.3	789	6	AX756672	AX756672 Sequence
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35	c	37.8	3.3	451	10	MUSIR3E2	M10668 Mouse DNA w
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37	c	37.4	3.3	688	6	A86256	A86256 Sequence 91
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41	c	36.8	3.2	675	1	USO539323	AJ539323 Unculture
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43	c	36.4	3.2	744	6	BD180141	BD180141 Highly th
44	c	36.4	3.2	1029	4	TGU65923	U65923 Tupaia glis
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ALIGNMENTS

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LOCUS BD056518 1150 bp DNA linear PAT 27-AUG-2002
DEFINITION OB fusion protein compositions and methods.
ACCESSION BD056518
VERSION BD056518.1 GI:22602124
KEYWORDS JP 2001512417-A/6.
SOURCE Aequorea victoria
ORGANISM Aequorea victoria
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
REFERENCE 1 (bases 1 to 1150)
AUTHORS Mann,M.B. and Hecht,R.I.
TITLE OB fusion protein compositions and methods
JOURNAL Patent: JP 2001512417-A 6 21-AUG-2001;

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            AMGEN INC
COMMENT     PN   JP 2001512417-A/6
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
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ORIGIN

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Qy        901 AGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGAC 960
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Qy       1141 ATTACCTAGG 1150
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RESULT 2
BD056520
LOCUS       BD056520               1150 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056520
VERSION     BD056520.1  GI:22602126
KEYWORDS    JP 2001512417-A/8.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1150)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 8 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/8
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
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ORIGIN

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Qy          1 GTATACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTT 60
              |||||||||||| |||||  ||||||||||||||||| ||||| || ||||| || |||
Db          1 GTATACCTTGGTTTTAGACGACTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTT 60
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Qy        61 GAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAG 120
             |||||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 GAGGACCCCCCAGGAAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAG 120

Qy       121 AGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 AGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAG 180

Qy       181 TTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 TTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTC 240

Qy       241 CTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACC 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACC 300

Qy       301 GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 360

Qy       361 TTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGT 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 TTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGT 420

Qy       421 AGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATA 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 AGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATA 480

Qy       481 GGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG 540

Qy       541 TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTG 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTG 600

Qy       601 TTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTG 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 TTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTG 660

Qy       661 TTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAA 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 TTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAA 720

Qy       721 GTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTG 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 GTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTG 780

Qy       781 TGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTG 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 TGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTG 840

Qy       841 GGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGG 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 GGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGG 900

Qy       901 AGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGAC 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 AGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGAC 960

Qy       961 GACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 GACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA 1020

Qy      1021 GACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGAC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 GACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGAC 1080

Qy      1081 AGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACA 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 AGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACA 1140

Qy      1141 ATTACCTAGG 1150
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Db      1141 ATTACCTAGG 1150
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RESULT 3
BD056522
LOCUS       BD056522                1135 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056522
VERSION     BD056522.1  GI:22602128
KEYWORDS    JP 2001512417-A/10.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1135)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 10 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/10
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .1135
                        /organism="Aequorea victoria"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:6100"
ORIGIN

  Query Match             97.2%;  Score 1117.8;  DB 6;  Length 1135;
  Best Local Similarity   99.4%;  Pred. No. 9.5e-259;
  Matches 1122;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         22 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 81
              |||||||||||||||| ||||| || ||||| || ||||||||||||| || ||||||
Db          7 CTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGAAGTCAG 66

Qy         82 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126

Qy        142 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186

Qy        202 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246

Qy        262 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 306

Qy        322 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366

Qy        382 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426

Qy        442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
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Qy        502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561
Db        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546

Qy        562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621
Db        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606

Qy        622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681
Db        607 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 666

Qy        682 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 741
Db        667 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 726

Qy        742 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 801
Db        727 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 786

Qy        802 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 861
Db        787 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 846

Qy        862 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 921
Db        847 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 906

Qy        922 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 981
Db        907 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 966

Qy        982 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1041
Db        967 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1026

Qy       1042 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1101
Db       1027 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1086

Qy       1102 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
Db       1087 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
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RESULT 4
BD056524
LOCUS       BD056524               1135 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056524
VERSION     BD056524.1  GI:22602130
KEYWORDS    JP 2001512417-A/12.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1135)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 12 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/12
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .1135
                     /organism="Aequorea victoria"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:6100"
ORIGIN

  Query Match             96.1%;  Score 1105;  DB 6;  Length 1135;
  Best Local Similarity   98.7%;  Pred. No. 1.2e-255;
  Matches 1114;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         22 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 81
Db          7 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAG 66

Qy         82 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 141
Db         67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126

Qy        142 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 201
Db        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186

Qy        202 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 261
Db        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246

Qy        262 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 321
Db        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGT 306

Qy        322 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 381
Db        307 ACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366

Qy        382 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 441
Db        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426

Qy        442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501
Db        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486

Qy        502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561
Db        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546

Qy        562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621
Db        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606

Qy        622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681
Db        607 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 666

Qy        682 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 741
Db        667 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 726

Qy        742 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 801
Db        727 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 786

Qy        802 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 861
Db        787 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 846

Qy        862 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 921
Db        847 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 906

Qy        922 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 981
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Db        907 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 966

Qy        982 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1026

Qy       1042 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1086

Qy       1102 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135


RESULT 5
I27618
LOCUS       I27618                1142 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 9 from patent US 5565335.
ACCESSION   I27618
VERSION     I27618.1  GI:1818394
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1142)
  AUTHORS   Capon,D.J. and Gregory,T.J.
  TITLE     Adhesion variants
  JOURNAL   Patent: US 5565335-A 9 15-OCT-1996;
FEATURES             Location/Qualifiers
     source          1. .1142
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           58.8%;  Score 676.2;  DB 6;  Length 1142;
  Best Local Similarity   98.6%;  Pred. No. 2.9e-152;
  Matches  695;  Conservative    0;  Mismatches    3;  Indels    7;  Gaps    1;

Qy          5 ACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 64
              | ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 AACTCGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 482

Qy         65 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 542

Qy        125 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 602

Qy        185 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 662

Qy        245 TCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 304
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Db        663 TCATGTTGTCGTGCATGGCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 722

Qy        305 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 364
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Db        723 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 782

Qy        365 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 842

Qy        425 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 902

Qy        485 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 962

Qy        545 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 1022

Qy        605 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGAC 657
              |||||||||||||||||||||||||||||||||||||       |||||||||||||||||
Db       1023 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGAC 1082

Qy        658 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 702
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1083 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 1127


RESULT 6
BD263010
LOCUS       BD263010                861 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and
            having thrombopoietic activity.
ACCESSION   BD263010
VERSION     BD263010.1  GI:33072778
KEYWORDS    JP 2002536960-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 861)
  AUTHORS   Liu,C.F., Feige,U. and Cheetham,J.
  TITLE     Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and
            having thrombopoietic activity
  JOURNAL   Patent: JP 2002536960-A 12 05-NOV-2002;
            AMGEN INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002536960-A/12
            PD   05-NOV-2002
            PF   22-OCT-1999 JP 2000578340
            PR   23-OCT-1998 US    60/105348
            PI   CHUAN FA LIU,ULRICH FEIGE,JANET CHEETHAM
            PC   C12N15/09,A61K38/00,A61P7/00,C07K14/52,C07K19/00,C12N1/15, PC
             C12N1/19,
            PC   C12N1/21,C12N5/10,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC
            Description of Artificial Sequence: oligonucleotide FH   Key
                 Location/Qualifiers
            FT   source          1. .861
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .861
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match           58.6%;  Score 674.4;  DB 6;  Length 861;
  Best Local Similarity   97.7%;  Pred. No. 7.9e-152;
  Matches  684;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          4 TACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAG 63
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Db         24 TTCCTCCTTATTGTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAG 83

Qy         64 GACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGG 123
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Db         84 GACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGG 143

Qy        124 GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC 183
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Db        144 GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC 203

Qy        184 AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC 243
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Db        204 AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC 263

Qy        244 GTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGAC 303
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Db        264 GTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGAC 323

Qy        304 TTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 TTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT 383

Qy        364 TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG 443

Qy        424 GCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGG 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 GCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGG 503

Qy        484 TCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGC 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 TCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGC 563

Qy        544 GGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTC 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 GGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTC 623

Qy        604 TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG 683

Qy        664 GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTC 703
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Db        684 GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTC 723
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RESULT 7
BD263000

LOCUS	BD263000 684 bp DNA linear PAT 17-JUL-2003
DEFINITION	Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and having thrombopoietic activity.
ACCESSION	BD263000
VERSION	BD263000.1 GI:33072768
KEYWORDS	JP 2002536960-A/2.
SOURCE	synthetic construct
ORGANISM	synthetic construct artificial sequences.
REFERENCE	1 (bases 1 to 684)
AUTHORS	Liu,C.F., Feige,U. and Cheetham,J.
TITLE	Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and having thrombopoietic activity
JOURNAL	Patent: JP 2002536960-A 2 05-NOV-2002; AMGEN INC
COMMENT	OS Artificial Sequence PN JP 2002536960-A/2 PD 05-NOV-2002 PF 22-OCT-1999 JP 2000578340 PR 23-OCT-1998 US 60/105348 PI CHUAN FA LIU,ULRICH FEIGE,JANET CHEETHAM PC C12N15/09,A61K38/00,A61P7/00,C07K14/52,C07K19/00,C12N1/15, PC C12N1/19, PC C12N1/21,C12N5/10,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC Description of Artificial Sequence: oligonucleotide FH Key Location/Qualifiers FT source 1. .684 FT /organism='Artificial Sequence'.
FEATURES	Location/Qualifiers
source	1. .684 /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"
ORIGIN	

Query Match 58.5%; Score 673; DB 6; Length 684;
Best Local Similarity 99.3%; Pred. No. 1.7e-151;
Matches 676; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy         22 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 81
              |||||||||||||||| ||||| || ||||| || ||||||||||||||||||||||||||
Db          4 CTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGTCAG 63

Qy         82 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 141
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Db         64 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 123

Qy        142 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 201
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Db        124 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 183

Qy        202 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 243

Qy        262 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 303

Qy        322 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 363

Qy        382 CCCGTCGGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 CCCGTCGGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 423

Qy        442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 483

Qy        502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 543

Qy        562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621
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Db        544 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 603

Qy        622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681
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Db        604 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 663

Qy        682 GAGAGGGACAGAGGCCCATTT 702
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Db        664 GAGAGGGACAGAGGCCCATTT 684
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RESULT 8
BD004077

LOCUS	BD004077 454 bp DNA linear PAT 31-JAN-2002
DEFINITION	Methods of increasing sensitivity of an individual to OB protein by up-regulating OB protein receptor.
ACCESSION	BD004077
VERSION	BD004077.1 GI:18632038
KEYWORDS	JP 2001501177-A/4.
SOURCE	unidentified
ORGANISM	unidentified unclassified.
REFERENCE	1 (bases 1 to 454)
AUTHORS	Pelleymounter,M.A.
TITLE	Methods of increasing sensitivity of an individual to OB protein by up-regulating OB protein receptor
JOURNAL	Patent: JP 2001501177-A 4 30-JAN-2001; AMGEN INC
COMMENT	OS Unidentified PN JP 2001501177-A/4 PD 30-JAN-2001 PF 26-AUG-1997 JP 1998511882 PR 30-AUG-1996 US 08/705981 PI MARY ANN PELLEYMOUNTER PC A61K38/00,A61K31/425,A61P1/16,A61P3/04,A61P3/06,A61P3/10, PC

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            A61P9/10,
            PC   A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .454
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
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                      /db_xref="taxon:32644"
ORIGIN

  Query Match            38.3%;  Score 440.8;  DB 6;  Length 454;
  Best Local Similarity  98.5%;  Pred. No. 1.7e-95;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              ||||||||||||||||||||||||||||||||||||||||||    ||||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
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Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
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Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
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Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 9
BD056516
LOCUS       BD056516                454 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056516
VERSION     BD056516.1  GI:22602122
KEYWORDS    JP 2001512417-A/4.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 454)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 4 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/4
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .454
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ORIGIN

  Query Match            38.3%;  Score 440.8;  DB 6;  Length 454;
  Best Local Similarity  98.5%;  Pred. No. 1.7e-95;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
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Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              ||||||||||||||||||||||||||||||||||||||||||    ||||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
              |||||||||||||||||||||||||||||||||||| | ||||||||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
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Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
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Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
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Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 10
BD004075
LOCUS       BD004075                491 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Methods of increasing sensitivity of an individual to OB protein by
            up-regulating OB protein receptor.
ACCESSION   BD004075
VERSION     BD004075.1  GI:18632036
KEYWORDS    JP 2001501177-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 491)
  AUTHORS   Pelleymounter,M.A.
  TITLE     Methods of increasing sensitivity of an individual to OB protein by
            up-regulating OB protein receptor
  JOURNAL   Patent: JP 2001501177-A 2 30-JAN-2001;
            AMGEN INC
COMMENT     OS   Unidentified
            PN   JP 2001501177-A/2
            PD   30-JAN-2001
            PF   26-AUG-1997 JP 1998511882
            PR   30-AUG-1996 US    08/705981
            PI   MARY ANN PELLEYMOUNTER
            PC   A61K38/00,A61K31/425,A61P1/16,A61P3/04,A61P3/06,A61P3/10, PC
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            PC   A61K37/02
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            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .491
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ORIGIN

  Query Match            32.9%;  Score 378.4;  DB 6;  Length 491;
  Best Local Similarity  89.8%;  Pred. No. 1.9e-80;
  Matches  406;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
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Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
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Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
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Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||  ||||||
Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
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Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

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Db        400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
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Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491


RESULT 11
BD056514
LOCUS       BD056514                491 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056514
VERSION     BD056514.1  GI:22602120
KEYWORDS    JP 2001512417-A/2.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 491)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 2 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/2
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
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            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .491
                     /organism="Aequorea victoria"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:6100"
ORIGIN

  Query Match            32.9%;  Score 378.4;  DB 6;  Length 491;
  Best Local Similarity  89.8%;  Pred. No. 1.9e-80;
  Matches  406;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              |||||||||||||||||||||||||||||||    | ||||||||   ||||| || ||
Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
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Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
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Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
                | | |||||||||| |||   | ||| || |||| |||||||||||||||||    ||
Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||  |||
Db        400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
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Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491


RESULT 12
AB029092
LOCUS       AB029092                908 bp    mRNA    linear   PLN 15-APR-2003
DEFINITION  Cucumis sativus mRNA for arabinogalactan protein, complete cds.
ACCESSION   AB029092
VERSION     AB029092.2  GI:29893813
KEYWORDS    .
SOURCE      Cucumis sativus (cucumber)
  ORGANISM  Cucumis sativus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
REFERENCE   1
  AUTHORS   Park,M.H., Suzuki,Y., Chono,M., Knox,J.P. and Yamaguchi,I.
  TITLE     CsAGP1, a Gibberellin-Responsive Gene from Cucumber Hypocotyls,
            Encodes a Classical Arabinogalactan Protein and Is Involved in Stem
            Elongation
  JOURNAL   Plant Physiol. 131 (3), 1450-1459 (2003)
  MEDLINE   22531811
   PUBMED   12644694
REFERENCE   2  (bases 1 to 908)
  AUTHORS   Chono,M., Suzuki,Y. and Yamaguchi,I.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-JUN-1999) Makiko Chono, University of Tokyo, Applied
```

```
            Biological Chemistry; Yayoi 1-1-1, Bunkyo-ku, Tokyo 113-8657, Japan
            (E-mail:mchono@pgrl.ch.a.u-tokyo.ac.jp, Tel:+81-3-5841-5160,
            Fax:+81-3-5841-8025)
COMMENT     On Apr 16, 2003 this sequence version replaced gi:5443647.
FEATURES             Location/Qualifiers
     source          1. .908
                     /organism="Cucumis sativus"
                     /mol_type="mRNA"
                     /db_xref="taxon:3659"
                     /clone="203-1/5"
                     /note="obtained by differential display analysis"
     CDS             21. .752
                     /codon_start=1
                     /product="arabinogalactan protein"
                     /protein_id="BAC75541.1"
                     /db_xref="GI:29893814"
                     /translation="MGRQSVIALVLICAVVAGVGGQSPAAAPTTTPAATPPVAATYPP
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ORIGIN

  Query Match             4.4%;  Score 50.8;  DB 8;  Length 908;
  Best Local Similarity   46.0%;  Pred. No. 0.19;
  Matches  172;  Conservative    0;  Mismatches  202;  Indels    0;  Gaps    0;

Qy        133 CTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACC 192
              | ||||    | | || ||  ||||   || | || | |  |||| |       | | |
Db        283 CACCAGCCAGCACTCCTCCGACTGCTTCCGTTCCTGCCAGCTCTCCTCCGGCTGCTTCCG 342

Qy        193 ATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTG 252
              | |||||  | | || |||  |  ||| ||||  |  | |    || |||  ||  |||
Db        343 TTCCACCTAGCTCTCCACCAGCTGCTACCGTTCCGGCTAGCTCTCCGCCTGTTCCAGTTC 402

Qy        253 TCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTC 312
              ||   |    |||||||  ||| |  ||   |   | ||| | | | | |
Db        403 CGGTTAGTTCTCCACCAGTTTCAGTACCGGTGAGCTCTCCTCCAGTACCAACTCCAACGG 462

Qy        313 CTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGG 372
              |  || || ||| ||  |  | |   |  | | |  | | |   || ||||
Db        463 AATCTCCTCCCGCTCCCGAAAGTTCTCCTCCTGCCCCAGTCGCGTCGCCTCCTGTTGAGG 522

Qy        373 TTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTC 432
              || | |   |    |  ||    |   || |   |  | |    | |||  |||
Db        523 TTCCTGCCCCGGCACCTAGCAAGAAGAAGTCAAAGAAGCACAGAGCACCAGCTCCTTCTC 582

Qy        433 GACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAG 492
              |  | | |||||||||   | |          || | | | ||  || | |  | |
Db        583 CAGCGTTGCTTGGTCCACCTGCGCCTCCTTCTGAAGCTCCTGCAGGAAGCGAGGAAGGTC 642

Qy        493 CGGCACCTCACCCT 506
              | || ||   ||||
Db        643 CTGCGCCCAGCCCT 656


RESULT 13
AB029147
LOCUS       AB029147                1110 bp    mRNA    linear   PLN 23-JUN-1999
DEFINITION  Cucumis sativus mRNA expressed in cucumber hypocotyls, complete
            cds.
ACCESSION   AB029147
VERSION     AB029147.1  GI:5139694
KEYWORDS    .
SOURCE      Cucumis sativus (cucumber)
  ORGANISM  Cucumis sativus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
REFERENCE   1  (bases 1 to 1110)
  AUTHORS   Chono,M., Suzuki,Y. and Yamaguchi,I.
  TITLE     Molecular cloning of genes expressed in cucumber hypocotyls
  JOURNAL   Published Only in DataBase (1999)
REFERENCE   2  (bases 1 to 1110)
  AUTHORS   Chono,M., Suzuki,Y. and Yamaguchi,I.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-JUN-1999) Makiko Chono, University of Tokyo, Applied
            Biological Chemistry; Yayoi 1-1-1, Bunkyo-ku, Tokyo 113-8657, Japan
            (E-mail:mchono@pgrl.ch.a.u-tokyo.ac.jp, Tel:+81-3-5841-5160,
            Fax:+81-3-5841-8025)
FEATURES             Location/Qualifiers
     source          1. .1110
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                     /mol_type="mRNA"
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     CDS             21. .752
                     /note="expressed in cucumber hypocotyls"
                     /codon_start=1
                     /protein_id="BAA81686.1"
                     /db_xref="GI:5139695"
                     /translation="MGRQSVIALVLICAVVAGVGGQSPAAAPTTTPAATPPVAATYPP
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                     PPAASVPPSSPPAATVPASSPPVPVPVSSPPVSVPVSSPPVPTPTESPPAPESSPPAP
                     VASPPVEVPAPAPSKKKSKKHRAPAPSPALLGPPAPPSEAPAGSEEGPAPSPSLEDKS
                     GAEALMKVAGSLALGWAAVAVSIIF"
ORIGIN

  Query Match             4.4%;  Score 50.8;  DB 8;  Length 1110;
  Best Local Similarity   46.0%;  Pred. No. 0.19;
  Matches  172;  Conservative    0;  Mismatches  202;  Indels    0;  Gaps    0;

Qy        133 CTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACC 192
              | ||||    | | || ||  ||||   || | || | |  |||| |       | | |
Db        283 CACCAGCCAGCACTCCTCCGACTGCTTCCGTTCCTGCCAGCTCTCCTCCGGCTGCTTCCG 342

Qy        193 ATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTG 252
              | |||||  | | || |||  |  ||| ||||  |  | |    || |||  ||  |||
Db        343 TTCCACCTAGCTCTCCACCAGCTGCTACCGTTCCGGCTAGCTCTCCGCCTGTTCCAGTTC 402

Qy        253 TCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTC 312
              ||   |    |||||||  ||| |  ||   |   | ||| | | | | |
Db        403 CGGTTAGTTCTCCACCAGTTTCAGTACCGGTGAGCTCTCCTCCAGTACCAACTCCAACGG 462

Qy        313 CTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGG 372
              |  || || ||| ||  |  | |   |  | | |  | | |   || ||||
Db        463 AATCTCCTCCCGCTCCCGAAAGTTCTCCTCCTGCCCCAGTCGCGTCGCCTCCTGTTGAGG 522

Qy        373 TTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTC 432
              || | |   |    |  ||    |   || |   |  | |    | |||  |||
Db        523 TTCCTGCCCCGGCACCTAGCAAGAAGAAGTCAAAGAAGCACAGAGCACCAGCTCCTTCTC 582

Qy        433 GACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAG 492
              |  | | |||||||||   | |          || | | | ||  || | |  | |
Db        583 CAGCGTTGCTTGGTCCACCTGCGCCTCCTTCTGAAGCTCCTGCAGGAAGCGAGGAAGGTC 642

Qy        493 CGGCACCTCACCCT 506
              | || ||   ||||
Db        643 CTGCGCCCAGCCCT 656


RESULT 14
I27620
LOCUS       I27620                  468 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 12 from patent US 5565335.
ACCESSION   I27620
VERSION     I27620.1  GI:1818396
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 468)
  AUTHORS   Capon,D.J. and Gregory,T.J.
  TITLE     Adhesion variants
  JOURNAL   Patent: US 5565335-A 12 15-OCT-1996;
FEATURES             Location/Qualifiers
     source          1. .468
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                     /organism="unknown"
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ORIGIN

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  Best Local Similarity   49.5%;  Pred. No. 14;
  Matches  143;  Conservative    0;  Mismatches  140;  Indels    6;  Gaps    1;

Qy        394 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 453
              | ||||   || | || | | || |||||    ||  || |||           | |
Db        127 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 186

Qy        454 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 507
              |    |||||| | ||   |||||||||||| ||   |   ||  ||||      |||
Db        187 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 246

Qy        508 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 567
              | |       ||  |||  |||  | |  |||       |       |      |  ||| ||
Db        247 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 306

Qy        568 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 627
              |||  |  ||||  ||||  || ||  ||  |||       |   || |    || |||
Db        307 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 366

Qy        628 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 676
              | | | |||   || |  ||| |||  |||  |   | |  |||  |||
Db        367 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 415


RESULT 15
A51599
LOCUS       A51599                   746 bp    DNA     linear   PAT 10-MAR-1997
DEFINITION  Sequence 9 from Patent WO9616990.
ACCESSION   A51599
VERSION     A51599.1  GI:2304408
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 746)
  AUTHORS   Ellis,J.H. and Lewis,A.P.
  TITLE     HUMANIZED ANTIBODIES TO CD38
  JOURNAL   Patent: WO 9616990-A 9 06-JUN-1996;
            WELLCOME FOUND (GB)
COMMENT     Other publication AU 3933695 960619.
FEATURES             Location/Qualifiers
     source          1. .746
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             3.7%;  Score 43;  DB 6;  Length 746;
  Best Local Similarity   49.5%;  Pred. No. 14;
  Matches  143;  Conservative    0;  Mismatches  140;  Indels    6;  Gaps    1;

Qy        394 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 453
              | ||||   || | || | | || |||||    ||  || |||           | |
Db        429 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 488

Qy        454 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 507
              |    ||||||| | ||   |||||||||||| ||   |   ||  ||||      |||
Db        489 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 548

Qy        508 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 567
              | |       ||  |||  |||  | |  |||       |       |      |  ||| ||
Db        549 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 608

Qy        568 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 627
              |||  |  ||||  |||||  || ||  ||  |||       |   || |    || |||
Db        609 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 668

Qy        628 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 676
              | | | |||   || |  ||| |||  |||  |   | |  |||  |||
Db        669 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 717


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Job time : 3073.75 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 13:07:09 ; Search time 332.75 Seconds
(without alignments)
14681.977 Million cell updates/sec

Title: US-10-679-999-8
Perfect score: 1150
Sequence: 1 GTATACCTTGGGTTTAGAAC.....AGGCCCAACAATTACCTAGG 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 5810876

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
2: geneseqn1990s:*
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4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	53.6	4.7	138	7	AAL51057	Aal51057 Cyclic si
	2	42.4	3.7	52	2	AAQ29203	Aaq29203 3' heavy
	3	42.4	3.7	52	2	AAQ29205	Aaq29205 3' heavy
	4	40.6	3.5	268	2	AAT20112	Aat20112 Human gen
c	5	40.4	3.5	486	4	AAF75507	Aaf75507 Polygluta
c	6	40.4	3.5	1057	2	AAQ03405	Aaq03405 Streptomy
	7	40.2	3.5	926	6	ABZ11846	Abz11846 Human pol
c	8	40	3.5	543	2	AAQ23092	Aaq23092 Antigen t
	9	39.4	3.4	1011	6	ABS78695	Abs78695 S. aeroco
c	10	39	3.4	922	4	ABL09597	Abl09597 Drosophil
	11	38	3.3	789	7	AAD56497	Aad56497 Human VLC
	12	38	3.3	810	6	ABZ22164	Abz22164 Human elo
	13	38	3.3	813	6	AAD42270	Aad42270 Human ELG
	14	38	3.3	813	6	ABZ22162	Abz22162 Human elo
	15	38	3.3	815	6	ABN86918	Abn86918 Human NOV
	16	38	3.3	815	6	ABN86919	Abn86919 Human NOV
	17	38	3.3	818	7	ABZ24216	Abz24216 Human LCE
	18	38	3.3	1147	6	ABZ22165	Abz22165 Human elo
c	19	37.6	3.3	717	7	ADA07157	Ada07157 Ptilosarc
	20	37.2	3.2	536	9	ADB68842	Adb68842 Minority
	21	37.2	3.2	629	7	ACA24037	Aca24037 Prokaryot
c	22	36	3.1	705	6	ABK73567	Abk73567 Bacillus
	23	35.8	3.1	558	4	AAF61431	Aaf61431 Synthetic
	24	35.8	3.1	558	4	AAF61428	Aaf61428 Synthetic
c	25	35.6	3.1	1098	7	ADA70957	Ada70957 Rice gene
	26	35.4	3.1	1014	4	ABL15657	Abl15657 Drosophil
c	27	35.2	3.1	1005	7	ADA69785	Ada69785 Rice gene
c	28	35	3.0	1147	2	AAT97188	Aat97188 Immunoglo
	29	34.8	3.0	249	2	AAX54615	Aax54615 Endotheli
	30	34.8	3.0	249	3	AAA34062	Aaa34062 Human ade
	31	34.8	3.0	249	3	AAF20184	Aaf20184 Human low
	32	34.8	3.0	249	7	ABZ95878	Abz95878 Human nuc
c	33	34.8	3.0	799	2	AAV55831	Aav55831 Nucleotid
c	34	34.8	3.0	1144	3	AAC56023	Aac56023 Eucalyptu
c	35	34.6	3.0	41	2	AAX25644	Aax25644 EPO-fusio
c	36	34.6	3.0	422	3	AAC79295	Aac79295 Human lun
c	37	34.6	3.0	422	4	AAD23371	Aad23371 Human lun
c	38	34.6	3.0	422	9	ADD66645	Add66645 Human lun
c	39	34.6	3.0	422	9	ADE87899	Ade87899 Human lun
	40	34.6	3.0	950	6	ABK71707	Abk71707 Human dit
c	41	34.4	3.0	431	8	ACD25835	Acd25835 Maize EST
c	42	34.4	3.0	795	2	AAV55830	Aav55830 FLGA inse
	43	34.2	3.0	780	7	ACA37806	Aca37806 Prokaryot
c	44	34	3.0	621	3	AAF11323	Aaf11323 Aspergill
c	45	34	3.0	693	4	AAF87193	Aaf87193 Human ion

ALIGNMENTS

RESULT 1
AAL51057
ID AAL51057 standard; DNA; 138 BP.
XX
AC AAL51057;
XX
DT 20-FEB-2003 (first entry)
XX
DE Cyclic single-strand anti-tumour antibody-related coding sequence #6.
XX
KW Cyclic single-strand anti-tumour antibody; anti-tumour Fab; ds;
KW anti-human Cd3 Fab; anti-human CD28 Fab; immunotherapy; tumour;
KW ovarian cancer.
XX
OS Unidentified.
XX
PN WO200283738-A1.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-CN000252.
XX
PR 11-APR-2001; 2001CN-00110554.
XX
PA (GENE-) INST GENETICS CAS.
PA (BEIJ-) BEIJING ABT GENETIC ENG TECHNOLOGY CO LT.
XX
PI Huang H, Cheng J, Wang X, Song L, Zhang Z, Lin Q, Gu Y;
XX
DR WPI; 2003-075525/07.
DR P-PSDB; AAO16031.
XX
PT Cyclic single-strand tri-specific antibody made from antitumor Fab,
PT single-strand antibody and modified anti-human CD3 or CD28 Fab,
PT applicable in early-stage diagnosis, and prevention or treatment of
PT tumors e.g. ovarian cancer.
XX
PS Disclosure; Fig 4A; 49pp; Chinese.
XX
CC The invention comprises a cyclic single-strand anti-tumour antibody, the
CC antibody of the invention is obtained by combining anti-tumour Fab and
CC modified anti-human Cd3 or CD28 Fab. The antibody is useful in the
CC immunotherapy of tumours - particularly ovarian cancer, including the
CC sensitive early-stage diagnosis and post-operative eradication of
CC disease. The present DNA sequence encodes a peptide which was used in the
CC invention

```
XX
SQ   Sequence 138 BP; 35 A; 37 C; 39 G; 27 T; 0 U; 0 Other;

  Query Match             4.7%;  Score 53.6;  DB 7;  Length 138;
  Best Local Similarity   93.3%;  Pred. No. 4.6e-05;
  Matches   56;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        250 TTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCG 309
              ||||||||||||||| || || ||||||||||||||| |||||||||||||||||||||||
Db         61 TTGTCGTGCATGGCCCAACATTCGCAGGAGTGGCATGACGTGGTCCTGACCGACTTACCG 120


RESULT 2
AAQ29203
ID   AAQ29203 standard; DNA; 52 BP.
XX
AC   AAQ29203;
XX
DT   25-MAR-2003  (revised)
DT   26-FEB-1993  (first entry)
XX
DE   3' heavy chain CH1 overlapping primer for insert A.
XX
KW   Dicistronic expression vector; fusion PCR; antibody; cDNA library; ss.
XX
OS   Synthetic.
XX
PN   WO9215678-A1.
XX
PD   17-SEP-1992.
XX
PF   27-FEB-1992;   92WO-US001475.
XX
PR   01-MAR-1991;   91US-00663442.
XX
PA   (STRA-) STRATAGENE.
XX
PI   Sorge JA;
XX
DR   WPI; 1992-331724/40.
XX
PT   Prodn. of dicistronic DNA library used to make antibodies, etc. -
PT   includes forming 1st and 2nd PCR admixtures, subjecting them to PCR
PT   thermo-cycles, sepg. double stranded DNA, hybridising, etc.
XX
PS   Claim 14; Page 101; 143pp; English.
XX
CC   This PCR primer is used in fusion PCR, to amplify inserts between the
CC   heavy chain and lamB sequences, and also to fuse the light chain and lamB
CC   sequence, to allow expression of the heavy chain and lamB as a fusion
CC   protein and the light chain as a separate protein. Fusion PCR reaction is
CC   used to produce two fragments with cohesive termini, which when mixed
CC   hybridise to form an overlapping DNA duplex that is internally primed.
CC   Subsequent PCR extends the non-overlapping region to form a hybrid DNA
CC   mol. that is dicistronic contg. a first polypeptide coding sequence and a
CC   second polypeptide coding sequence linked by a dicstronic bridge. This
CC   method thus allows fusion prior to vector ligation, avoiding the
CC   cumbersome separate cloning of fragments. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 52 BP; 8 A; 9 C; 20 G; 15 T; 0 U; 0 Other;

  Query Match             3.7%;  Score 42.4;  DB 2;  Length 52;
  Best Local Similarity   88.5%;  Pred. No. 0.047;
  Matches   46;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          7 CTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGAC 58
              || |||||||||||||||||||||||||  | ||||||  ||||||||||
Db          1 CTCGGGTTTAGAACACTGTTTTGAGTGTGATCAGGTGGCCGGGGTCGTGGAC 52


RESULT 3
AAQ29205
ID   AAQ29205 standard; DNA; 52 BP.
XX
AC   AAQ29205;
XX
DT   25-MAR-2003  (revised)
DT   26-FEB-1993  (first entry)
XX
DE   3' heavy chain CH1 overlapping primer for insert B.
XX
KW   Dicistronic expression vector; fusion PCR; antibody; cDNA library; ss.
XX
OS   Synthetic.
XX
PN   WO9215678-A1.
XX
PD   17-SEP-1992.
XX
PF   27-FEB-1992;   92WO-US001475.
XX
PR   01-MAR-1991;   91US-00663442.
XX
PA   (STRA-) STRATAGENE.
XX
PI   Sorge JA;
XX
DR   WPI; 1992-331724/40.
XX
PT   Prodn. of dicistronic DNA library used to make antibodies, etc. -
PT   includes forming 1st and 2nd PCR admixtures, subjecting them to PCR
PT   thermo-cycles, sepg. double stranded DNA, hybridising, etc.
XX
PS   Claim 14; Page 101; 143pp; English.
XX
CC   This PCR primer is used in fusion PCR, to amplify inserts between the
CC   heavy chain and lamB sequences, and also to fuse the light chain and lamB
CC   sequence, to allow expression of the heavy chain and lamB as a fusion
CC   protein and the light chain as a separate protein. Fusion PCR reaction is
CC   used to produce two fragments with cohesive termini, which when mixed
CC   hybridise to form an overlapping DNA duplex that is internally primed.
CC   Subsequent PCR extends the non-overlapping region to form a hybrid DNA
CC   mol. that is dicistronic contg. a first polypeptide coding sequence and a
CC   second polypeptide coding sequence linked by a dicstronic bridge. This
CC   method thus allows fusion prior to vector ligation, avoiding the
CC   cumbersome separate cloning of fragments. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 52 BP; 8 A; 9 C; 20 G; 15 T; 0 U; 0 Other;

  Query Match             3.7%;  Score 42.4;  DB 2;  Length 52;
  Best Local Similarity   88.5%;  Pred. No. 0.047;
  Matches   46;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          7 CTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGAC 58
              || |||||||||||||||||||||||||  | ||||||  ||||||||||
Db          1 CTCGGGTTTAGAACACTGTTTTGAGTGTGATCAGGTGGCCGGGGTCGTGGAC 52


RESULT 4
AAT20112
ID   AAT20112 standard; cDNA to mRNA; 268 BP.
XX
AC   AAT20112;
XX
DT   29-JUL-1996  (first entry)
XX
DE   Human gene signature HUMGS01256.
XX
KW   Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW   human; cloning; mapping; non-biased library; diagnosis; detection;
KW   cell typing; abnormal cell function; ss.
XX
OS   Homo sapiens.
XX
```

PN WO9514772-A1.
XX
PD 01-JUN-1995.
XX
PF 11-NOV-1994; 94WO-JP001916.
XX
PR 12-NOV-1993; 93JP-00355504.
XX
PA (MATS/) MATSUBARA K.
PA (OKUB/) OKUBO K.
XX
PI Matsubara K, Okubo K;
XX
DR WPI; 1995-206931/27.
XX
PT Single-stranded DNA for identifying gene signatures - isolated from 3'-
PT directed human cDNA library that reflects relative abundance of corresp.
PT mRNA in specific human tissues.
XX
PS Claim 1; Page 563; 2245pp; Japanese.
XX
CC A single-stranded DNA (or its complementary strand or the corresp. double
CC -stranded DNA) which comprises one of the 7837 "GS" sequences given in
CC AAT19001-T26837 and which is able to hybridise to part of human genomic
CC DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were
CC obtained from 3'-directed cDNA libraries prepared from various human
CC tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using
CC poly(T) as the sole primer. Since the 3'- untranslated sequence is unique
CC to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise
CC with specific mRNAs. Each library is constructed so as to reflect
CC accurately the relative abundance of different mRNAs in the particular
CC tissue from which it was derived. The appearance frequency of a given GS
CC in a cDNA library can be determined (esp. using primers and probes
CC derived from the GS sequences) as a means of diagnosing abnormal cell
CC function or for recognising different cell types
XX
SQ Sequence 268 BP; 68 A; 54 C; 70 G; 62 T; 0 U; 14 Other;

Query Match 3.5%; Score 40.6; DB 2; Length 268;
Best Local Similarity 53.9%; Pred. No. 0.31;
Matches 82; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

```
Qy        937 CTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGAC 996
              ||||||| |||     | |   || | || | |   ||   |  |||||  |||
Db          4 CTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGACCAAGGAA 63

Qy        997 GGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCA 1056
              |     |||| || ||  |||| |    | | ||  | |  | | ||| ||| | |||
Db         64 GAGCTTTGAAGGCCTGAGGTCTGCGNAAGGTGGGAGGAGGCAGACGCCCTGCGTGGCCCA 123

Qy       1057 ATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1088
              |||| ||| || ||  |||| | ||  | |
Db        124 TGGTCGGGGCGTCCACGCCGAGGCCGGCAACA 155
```

RESULT 5
AAF75507/c
ID AAF75507 standard; DNA; 486 BP.
XX
AC AAF75507;
XX
DT 09-MAY-2001 (first entry)
XX
DE Polyglutamine tract coding sequence #2.
XX
KW Animal model; polyglutamine tract; neurodegenerative disorder; HDJ1;
KW heat shock protein 40; tetratricopeptide repeat protein 2; TPR2; stroke;
KW myeloid leukaemia factor 1; MLF; human; fruit fly; Alzheimer's disease;
KW Parkinson's disease; CJD; BSE; Huntington's disease; head trauma; cancer;
KW ds.
XX
OS Drosophila sp.
XX

PN WO200112238-A1.
XX
PD 22-FEB-2001.
XX
PF 14-AUG-2000; 2000WO-US022496.
XX
PR 12-AUG-1999; 99US-0148933P.
PR 12-AUG-1999; 99US-0148934P.
PR 18-JAN-2000; 2000US-0177047P.
PR 19-MAY-2000; 2000US-0205720P.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Benzer S, Kazemi-Esfarjani P;
XX
DR WPI; 2001-147537/15.
XX
PT Identifying genes or other compounds that modulate polyglutamine
PT toxicity, useful for treating Alzheimer's disease, Parkinson's disease
PT and Creutzfeldt-Jakob disease.
XX
PS Disclosure; Fig 1A; 275pp; English.
XX
CC The present invention describes a method of screening for genes which
CC modulate polyglutamine toxicity using animal models with polyglutamine
CC sequences that cause toxicity in the animal. The model is preferably
CC Drosophila, and toxic polyglutamine sequences include the human and
CC Drosophila heat shock protein 40/HDJ1, tetratricopeptide repeat protein 2
CC (TPR2) and myeloid leukaemia factor 1 (MLF) genes. The model is useful
CC for identifying treatments for neurodegenerative and proliferative
CC disorders, including Alzheimer's disease, Parkinson's disease,
CC Creutzfeldt-Jacob's disease (CJD), bovine spongiform encephalopathy
CC (BSE), Huntington's disease, Machado-Joseph disease, spinocerebellar
CC ataxias, dentatorubropallidoluysian atrophy, Kennedy's disease, stroke,
CC head trauma and cancer
XX
SQ Sequence 486 BP; 193 A; 164 C; 108 G; 21 T; 0 U; 0 Other;

Query Match 3.5%; Score 40.4; DB 4; Length 486;
Best Local Similarity 45.2%; Pred. No. 0.46;
Matches 149; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

```
Qy         97 TTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTG 156
              ||   | | |||| |  |     |  |   | |  || | ||    ||  |  |   ||
Db        375 TTGCTGCTGCTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTG 316

Qy        157 CACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTA 216
              |  | | |||| |||    | | | |   ||||    |||  |||| |   || |   |
Db        315 CTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGCTGCTGCTG 256

Qy        217 TTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAG 276
              || | ||| |  ||         | ||  |  |||||  ||   ||   |    || || |
Db        255 TTGCTGTTGTTGCTGTTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTGCTG 196

Qy        277 GAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTG 336
              |  |  |    || | |||       | | | |  ||||   | | | |  ||||
Db        195 CTGCTGTTGCTGTTGCTGCTGCTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTG 136

Qy        337 TTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTT 396
              | | |  |   | |  | |||  | | || |  | | | ||| |   |   |  ||
Db        135 CTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTG 76

Qy        397 GGTGTCCACATGTGGGACGGGGGTAGGGCC 426
                | |  || |||   |  |  |||||
Db         75 TTGCTGCTGCTGGGGGGTTGACGGTGGGCC 46
```

RESULT 6
AAQ03405/c
ID AAQ03405 standard; DNA; 1057 BP.
XX
AC AAQ03405;
XX

DT 25-MAR-2003 (revised)
DT 10-MAR-2003 (revised)
DT 19-AUG-1990 (first entry)
XX
DE Streptomyces gene encoding prepro xylanase.
XX
KW Secretory expression vector; actinomycetes; Streptomyces; xylanase gene;
KW endo-1,4-beta-D-xylanase; EC-3.2.1.8; endo-1,3-beta-D-xylanase;
KW EC-3.2.1.32.
XX
OS Streptomyces sp.
XX
FH Key Location/Qualifiers
FT CDS 416. .475
FT /*tag= a
XX
PN JP02002377-A.
XX
PD 08-JAN-1990.
XX
PF 08-JUN-1988; 88JP-00140990.
XX
PR 08-JUN-1988; 88JP-00140990.
XX
PA (BANY) BANYU PHARM CO LTD.
XX
DR WPI; 1990-053427/08.
DR P-PSDB; AAR03202.
XX
PT DNA fragment for manifestation secretory vector for actinomycetes - using
PT Streptomyces spp. as host.
XX
PS Page 876; Fig 3; 17pp; Japanese.
XX
CC Streptomyces or E. coli transformed with a secretory expression vector
CC contg. the sequence efficiently secrete the protein into the culture
CC medium. This sequence is identical to that of patent JO 2002-379-A.
CC (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003
CC to correct PR field.)
XX
SQ Sequence 1057 BP; 186 A; 390 C; 336 G; 145 T; 0 U; 0 Other;

Query Match 3.5%; Score 40.4; DB 2; Length 1057;
Best Local Similarity 44.8%; Pred. No. 0.64;
Matches 155; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

Qy 270 GTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCA 329
Db 784 GGCGTTGTACCGGGTCGTCTTGTAGATGTCGTAGGTGCCGCCGTCGCTGTGGACGGTGCC 725

Qy 330 GAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG 389
Db 724 CCGGTACTCGCCGGTGGGCCGGTAGCTGCCCCAGTTGTCGACGATGTAGTACTCGACGAG 665

Qy 390 GGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCA 449
Db 664 CGGGTTGGAGGTCCAGCCGTAGAGGCAGCCGTAGCCGTTGCCCGACGGGTTGAACCAGCC 605

Qy 450 GTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTC 509
Db 604 GGTGTACCGGACGGTCCGGCGCCCGCCGTTGGCCCAGCCCTTGCCGGCCACGAAGTTGCC 545

Qy 510 GTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAG 569
Db 544 GCAGTTGGTCCACCGGGTGCTGTAGCTGCCGCCGCCGTTGAGCGTCATGGAGACGGACCC 485

Qy 570 GAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 615
Db 484 GCCGCCGTCGGTCCAGAACGAGTAGTACATGCCGTCGTACCCGGTC 439

RESULT 7
ABZ11846

ID ABZ11846 standard; cDNA; 926 BP.
XX
AC ABZ11846;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human polynucleotide SEQ ID NO 728.
XX
KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200270539-A2.
XX
PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-US005095.
XX
PR 05-MAR-2001; 2001US-00799451.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX
DR WPI; 2002-759812/82.
DR P-PSDB; ABP69629.
XX
PT New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.
XX
PS Claim 1; SEQ ID NO 728; 1012pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising a
CC nucleotide sequence selected from any of 948 sequences (ABZ11119-
CC ABZ12066) or their mature protein coding portion, active domain coding
CC protein or complementary sequences. The polynucleotides are useful for
CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical
CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 926 BP; 159 A; 240 C; 307 G; 220 T; 0 U; 0 Other;

Query Match 3.5%; Score 40.2; DB 6; Length 926;
Best Local Similarity 47.8%; Pred. No. 0.69;
Matches 117; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

Qy 92 GGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACC 151
Db 510 GGGGGCTGTGGTTCCTGTGGGGGCTCCAAGGGGGGCTGTGGCTCCTGTGGGGGCTCCAAG 569

Qy 152 ACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCC 211
Db 570 GGGGGCTGTGGTTCTTGTGGGGGCTCCAAGGGGGGCTGTGGCTCCTGTGGGGGCTCCAAA 629

```
Qy        212 ACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGT 271
              |  |||||   |  ||   ||      |  ||| ||  |    |   | ||
Db        630 GGTGGCTGTGGTTCCTGTGGGGGCTCCAAGGGGGGCTGTGGTTCTTGTGGCTGCTCCCAG 689

Qy        272 CGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGA 331
              |||   |  | | | | || | ||| ||  |   | ||   || || |  | |||||
Db        690 TGCAATTGCTGTAAGCCCTGCTGCTGTCCCTCAGGCTGTGGATCCTGCTGCCAGTCCAGC 749

Qy        332 GGTTG 336
              | ||
Db        750 TGCTG 754
```

RESULT 8
AAQ23092/c
ID AAQ23092 standard; DNA; 543 BP.
XX
AC AAQ23092;
XX
DT 25-MAR-2003 (revised)
DT 17-AUG-1992 (first entry)
XX
DE Antigen tc-7a gene.
XX
KW Oocysts; MAb 12-07; sporozoite; ss.
XX
OS Eimeria tenella.
XX
PN WO9204460-A.
XX
PD 19-MAR-1992.
XX
PF 05-SEP-1991; 91WO-US006430.
XX
PR 12-SEP-1990; 90US-00581693.
XX
PA (GEMX) GENEX CORP.
XX
PI Jacobson JW, Strausberg RL, Wilson SD, Pope SH, Strausberg SL;
PI Ruff MD, Augustine PC, Danforth HD;
XX
DR WPI; 1992-114365/14.
DR P-PSDB; AAR22392.
XX
PT Vaccine against avian coccidiosis - comprising recombinant eimeria
PT antigen ac-18 or ac-6b gene, or microorganisms expressing them.
XX
PS Claim 5; Page 39 + Fig 5; 56pp; English.
XX
CC To identify antigens of E. tenella, expression libraries were prepd. in
CC lambda vector, lambda gt11, using cDNA prepd. from polyA mRNA isolated
CC from E. tenella oocysts. The cDNA expression library was screened with
CC monoclonal antibody (MAb) 12-07 which was raised against the sporozoite
CC stage of E. tenella. The library to be screened was plated on a host that
CC allows lysis and plaque formation. During induction of the antigens
CC encoded by the phage, the plaques were identified by screening the
CC filters with Mab 12-07. The cDNA inserts from the MAb 12-07 positive
CC phage were cloned into bacteriophage M13 and subjected to sequence
CC analysis. Following sequence analysis, E. tenella antigen tc-7a was
CC identified. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 543 BP; 229 A; 135 C; 161 G; 18 T; 0 U; 0 Other;

  Query Match   3.5%; Score 40; DB 2; Length 543;
  Best Local Similarity   47.3%; Pred. No. 0.62;
  Matches 121; Conservative   0; Mismatches 135; Indels   0; Gaps   0;

```
Qy        104 TCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGG 163
              |||    ||  |||  |  |      |   || | |      ||  || |  |||   | |
Db        450 TCCCCCAGGCTTACCTGCTGCTGATGCTGCTGCTGCTCTTGCTGCAGCTGCTGTTGTTGC 391

Qy        164 TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT 223
              |||| ||  ||  |||  | |  | ||| |||| || ||||   | | |
Db        390 TGCTGTTGCTGCTTGTGTTTTCGCTTTCTCTGCTTCTGCTGCTGCTCCTGCTGCTCCTTC 331

Qy        224 TCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGC 283
              | | |   ||  || |    |    |||  |  | ||   | || |  || | || ||
Db        330 GGTTTCTGTTCGTGCTTCCGCTGCCTTTGCTGCTCCTGCTGCTCCTGCTGCGGCTGTCGC 271

Qy        284 AGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGG 343
              | |  |||| |||    |  | | ||| ||  || |   | | |||  | || | | |
Db        270 TGCAGCTGGTGCTGCTGCAGCTCCTGTTGCTGCTGCTGCTGCTGCAGCTGGTGCTGCTGC 211

Qy        344 AGGGTCGGGGGTAGCT 359
              ||      |  | ||||
Db        210 AGCTGGTGCTGCAGCT 195
```

RESULT 9
ABS78695
ID ABS78695 standard; DNA; 1011 BP.
XX
AC ABS78695;
XX
DT 29-AUG-2003 (revised)
DT 16-DEC-2002 (first entry)
XX
DE S. aerocolonigenes DNA encoding UNBU.
XX
KW Enediyne; warhead structure; ds; cancer; cytostatic; PKSE; gene;
KW polyketide synthase; TEBC; UNBL; UNBV; UNBU; genetic engineering;
KW thioesterase unique to enediyne biosynthetic loci;
KW unique to enediyne biosynthetic loci.
XX
OS Lechevalieria aerocolonigenes.
XX
PN CA2387401-A1.
XX
PD 04-SEP-2002.
XX
PF 21-MAY-2002; 2002CA-02387401.
XX
PR 21-MAY-2001; 2001US-0291959P.
PR 03-DEC-2001; 2001US-0334604P.
XX
PA (ECOP-) ECOPIA BIOSCIENCES INC.
XX
PI Staffa A, Farnet CM, Zazopoulos E;
XX
DR WPI; 2002-692206/75.
DR P-PSDB; ABG97456.
XX
PT New enediyne polyketide synthase polypeptides involved in synthesis of
PT the warhead structure in enediyne compounds useful in design of new
PT enediyne compounds and identification of new enediyne biosynthetic loci.
XX
PS Claim 1; Page 247; 310pp; English.
XX
CC The invention relates to purified/isolated polypeptides involved in
CC synthesis of the warhead structure in enediyne compounds, or their
CC fragments or sequences 75% homologous to them. The polypeptides comprise
CC five families of proteins: PKSE (polyketide synthase), TEBC (thioesterase
CC unique to enediyne biosynthetic loci), UNBL, UNBV and UNBU (unique to
CC enediyne biosynthetic loci L, B and V). The proteins are isolated from 10
CC different micro-organisms. Also included are the nucleic acids encoding
CC the proteins, antibodies specifically binding the polypeptides, and a
CC computer system/computer readable medium comprising the sequences
CC referred to above. The polypeptides and polynucleotides are useful in
CC genetic engineering to design new enediyne compounds (which are potential
CC anti-cancer drugs) and identify new enediyne biosynthetic loci. They can
CC also be used to identify enediyne biosynthesis genes/gene fragments from
CC samples containing genomic DNA e.g. in biomass from an environmental
CC source (such as a mixed microbial culture/population of organisms), pure
CC cultures or genomic libraries obtained from a mixed population of
CC organisms or from pure culture. The present sequence encodes an enzyme of

```
CC   the enediyne warhead structure biosynthetic pathway. (Updated on 29-AUG-
CC   2003 to standardise OS field)
XX
SQ   Sequence 1011 BP; 138 A; 331 C; 348 G; 194 T; 0 U; 0 Other;

  Query Match             3.4%;  Score 39.4;  DB 6;  Length 1011;
  Best Local Similarity   48.4%;  Pred. No. 1.2;
  Matches  109;  Conservative    0;  Mismatches  116;  Indels    0;  Gaps    0;

Qy        111 GGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCT 170
              |||||     || | |   |    | |   |  | |  || ||||| | |||
Db        507 GGAGTGGACCAGCGGCGTCGTCGACGCGCTGATCCCCGTCCTCCTGCTCGCGGCCGGCAC 566

Qy        171 GGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTT 230
              |   |||  |    ||| |||| | | |  ||||   |||  |  |    |    | ||
Db        567 GATGCTCAACGCGAAGCTGACGAAGAAGATCCCGCTGATCCTGGGCTGGGTGGGTGGGTT 626

Qy        231 CGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGT 290
              ||  |   |   |||  ||  |||  | | |  ||| ||||   |   |   || | |
Db        627 CGTCCTGCAGGCCGTGCTGCGTTCGGCCTTCACCGACCTGTCGATCGTCAGTGCGGTCCT 686

Qy        291 GGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTT 335
              |    | ||||    | ||||| || |||||||   | | | | |
Db        687 GCCGATCACCGGAACAGCGTTCATCCTGTTCACCAACTACATGAT 731


RESULT 10
ABL09597/c
ID   ABL09597 standard; cDNA; 922 BP.
XX
AC   ABL09597;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 23273.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ss.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US009231.
XX
PR   23-MAR-2000; 2000US-0191637P.
PR   11-JUL-2000; 2000US-00614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   P-PSDB; ABB65494.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signaling and cell-cell
PT   interactions.
XX
PS   Claim 1; SEQ ID NO 23273; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC   ABB72072). The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 922 BP; 231 A; 257 C; 238 G; 196 T; 0 U; 0 Other;

  Query Match             3.4%;  Score 39;  DB 4;  Length 922;
  Best Local Similarity   48.4%;  Pred. No. 1.5;
  Matches  108;  Conservative    0;  Mismatches  115;  Indels    0;  Gaps    0;

Qy        254 CGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCC 313
              ||| |||||  ||  | |||   | |  || |  | ||  |   | | |   |  |||
Db        383 CGTCCATGGGGCAGAACTCGAGAGTGGCGCCGTCCTTGTGCTGTAACACCAGCCGATTCT 324

Qy        314 TCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT 373
              |   |  |||  |   | |   ||   |     |  ||| ||     |  ||| ||||||
Db        323 TGTGGAACACCATGTCGGGCAGGTGGGGCAGCTGCAGGGAGTGCTGGTAGTGGCAGAGGT 264

Qy        374 TTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCG 433
              | |    | | || | |  | ||    ||| ||  ||       || ||   || |||
Db        263 CGCAGCGGTCGGCCGAGTCCTTGGGACAGCACTTGGCGGTGCCCAGTTGGCAGCTGCTCT 204

Qy        434 ACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAA 476
              | || | |  | |   ||  ||| || || |||||    |||
Db        203 TCAGGATGTGCGACTTCTCATACTTGATGGCCCAGTCGTGGAA 161


RESULT 11
AAD56497
ID   AAD56497 standard; DNA; 789 BP.
XX
AC   AAD56497;
XX
DT   27-AUG-2003  (first entry)
XX
DE   Human VLCFABE MOOSE00004 DNA from ctg13284.
XX
KW   Human; very long chain fatty acid biosynthesis enzyme; VLFA; VLCFABE;
KW   non-insulin dependent diabetes mellitus; NIDDM; adrenoleukodystrophy;
KW   ALD; autosomal dominant macular dystrophy; adMD; Alzheimer's disease;
KW   coronary heart disease; stroke; myocardial infarction; gene therapy;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
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FT                   /product= "Human VLCFABE protein"
FT                   /note= "No start and stop codon"
FT                   /partial
XX
PN   WO2003040392-A2.
XX
PD   15-MAY-2003.
XX
PF   04-NOV-2002; 2002WO-IB004610.
XX
PR   06-NOV-2001; 2001US-0332864P.
XX
PA   (DECO-) DECODE GENETICS EHF.
XX
PI   Betts M,  Sigurdsson GT;
XX
DR   WPI; 2003-430674/40.
DR   P-PSDB; AAE37330.
XX
PT   New isolated nucleic acid molecule comprising a very long chain fatty
PT   acid biosynthesis enzyme nucleic acid, useful for treating a disease
PT   associated with the biosynthesis enzyme nucleic acid.
XX
PS   Claim 1; Page 86; 90pp; English.
XX
CC   The invention relates to very long chain fatty acid (VLFA) biosynthesis
CC   enzymes (VLCFABE) and polynucleotides encoding such proteins. Sequences
CC   of the invention are useful for treating VLCFABE diseases such as non-
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CC   insulin dependent diabetes mellitus (NIDDM), adrenoleukodystrophy (ALD),
CC   autosomal dominant macular dystrophy (adMD), Alzheimer's disease and
CC   coronary heart diseases such as stroke and myocardial infarction. They
CC   are also used in gene therapy. The present sequence is human VLCFABE DNA
XX
SQ   Sequence 789 BP; 204 A; 215 C; 172 G; 198 T; 0 U; 0 Other;

  Query Match             3.3%;  Score 38;  DB 7;  Length 789;
  Best Local Similarity   47.2%;  Pred. No. 2.7;
  Matches  116;  Conservative    0;  Mismatches  130;  Indels    0;  Gaps    0;

Qy         75 CAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACT 134
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Db        438 CAAGAACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCAT 497

Qy        135 CCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCAT 194
              |  ||  ||  || ||   ||| |  | |      ||   | ||     | | || ||||
Db        498 CATGTACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCAT 557

Qy        195 GCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTC 254
              || | |   |   ||| ||  | || | | | | | | || ||| || ||  |||  |  |
Db        558 GCTCATCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCAC 617

Qy        255 GTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCT 314
              || |||        |||   ||||  || ||   | | |      |   ||   || | |
Db        618 GTACATCTGGAGGCAGGATCAGGGATGCCACACCACGATGGAACACTTATTCTGGTCCTT 677

Qy        315 CATGTT 320
              ||| ||
Db        678 CATCTT 683


RESULT 12
ABZ22164
ID   ABZ22164 standard; cDNA; 810 BP.
XX
AC   ABZ22164;
XX
DT   12-MAR-2003  (first entry)
XX
DE   Human elongase HSELO1-like protein encoding cDNA SEQ ID NO:5.
XX
KW   Human; elongase; elongase HSELO1-like protein; enzyme; cytostatic;
KW   antidiabetic; antiasthmatic; anti-HIV; antiparkinsonian; nootropic;
KW   neuroprotective; tranquilliser; antimigraine; analgesic; neuroleptic;
KW   cerebroprotective; gene therapy; cancer; diabetes; CNS disorder; asthma;
KW   metabolic disease; central nervous system disorder; COPD; dementia;
KW   Parkinson's disease; multiple sclerosis; stroke; Alzheimer's disease;
KW   Huntington's disease; Creutzfeldt-Jakob disease; HIV; schizophrenia;
KW   psychosis; attention deficit disorder; headache pain; migraine; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag=  a
FT                   /partial
FT                   /product= "elongase HSELO1-like protein"
FT                   /note= "no stop codon given"
XX
PN   WO200262974-A2.
XX
PD   15-AUG-2002.
XX
PF   07-FEB-2002; 2002WO-EP001262.
XX
PR   08-FEB-2001; 2001US-0267135P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Zhu Z;
XX
DR   WPI; 2002-636596/68.
DR   P-PSDB; ABP56418.
XX
PT   New isolated human elongase HSELO1-like polynucleotide and encoded
PT   peptide, useful for treating, preventing and ameliorating diseases such
PT   as COPD, cancer, metabolic disease, diabetes, CNS disorders, or asthma.
XX
PS   Claim 1; Fig 5; 128pp; English.
XX
CC   The present sequence encodes a human elongase HSELO1-like protein (I).
CC   (I) has cytostatic, antidiabetic, antiasthmatic, anti-HIV, nootropic,
CC   antiparkinsonian, neuroprotective, tranquilliser, antimigraine,
CC   analgesic, neuroleptic and cerebroprotective activities, and can be used
CC   in gene therapy. (I) can be used in the treatment of a disease, such as
CC   cancer, diabetes, central nervous system (CNS) disorder, asthma,
CC   metabolic disease or COPD. The human elongase HSELO1-like protein is
CC   useful in preventing, treating or ameliorating the diseases cited above,
CC   including Parkinson's disease, dementia, multiple sclerosis, stroke, HIV,
CC   Alzheimer's disease, Huntington's disease, Creutzfeldt-Jakob disease,
CC   schizophrenia, psychosis, attention deficit disorders, pain associated
CC   with CNS disorders, with cancer, or headache pain, e.g. migraine. It can
CC   also be useful in identifying test compounds that may act as activators
CC   or inhibitors at the enzyme's active site, or in raising specific
CC   antibodies that can block and effectively reduce its activity
XX
SQ   Sequence 810 BP; 195 A; 231 C; 181 G; 203 T; 0 U; 0 Other;

  Query Match             3.3%;  Score 38;  DB 6;  Length 810;
  Best Local Similarity   47.2%;  Pred. No. 2.7;
  Matches  116;  Conservative    0;  Mismatches  130;  Indels    0;  Gaps    0;

Qy         75 CAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACT 134
              ||    | || | |   |  ||     ||||| |      | |||   | |     |   |
Db        480 CAAGAACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCAT 539

Qy        135 CCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCAT 194
              |  ||  ||  || ||   ||| |  | |      ||   | ||     | | || ||||
Db        540 CATGTACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCAT 599

Qy        195 GCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTC 254
              || | |   |   ||| ||  | || | | | | | | || ||| || ||  |||  |  |
Db        600 GCTCATCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCAC 659

Qy        255 GTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCT 314
              || |||        |||   ||||  || ||   | | |      |   ||   || | |
Db        660 GTACATCTGGAGGCAGGATCAGGGATGCCACACCACGATGGAACACTTATTCTGGTCCTT 719

Qy        315 CATGTT 320
              ||| ||
Db        720 CATCTT 725


RESULT 13
AAD42270
ID   AAD42270 standard; DNA; 813 BP.
XX
AC   AAD42270;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Human ELG6 gene.
XX
KW   Human; elongase; therapy; enzyme; polyunsaturated fatty acid; sinusitis;
KW   PUFA disorder; cardiovascular disorder; articular cartilage degradation;
KW   peripheral vascular disease; atherosclerosis; coronary artery disease;
KW   inflammatory disorder; pancreatitis; asthma; gastrointestinal disorder;
KW   osteoarthritis; rheumatoid arthritis; congenital liver disease; cancer;
KW   acne; Sjogren's syndrome; body weight disorder; cerebrovascular disease;
KW   acute respiratory distress syndrome; hypercholesterolaemia; alcoholism;
KW   postviral fatigue; psychiatric disorder; pre-menstrual syndrome; eczema;
KW   Alzheimer's syndrome; hypertriglyceridaemia; cystic fibrosis; anorexia;
KW   autoimmune disorder; obesity; cachexia; viral disease; endometriosis;
KW   dyslipidaemia; atopic disorder; diabetes; ELG6; gene; ds.
XX
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OS   Homo sapiens.
XX
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FT                   /product= "ELG6 protein"
XX
PN   WO200244320-A2.
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PD   06-JUN-2002.
XX
PF   29-NOV-2001; 2001WO-CA001705.
XX
PR   29-NOV-2000; 2000US-0253728P.
XX
PA   (XENO-) XENON GENETICS INC.
XX
PI   Winther MD,  Knickle LC,  Haardt M,  De Antueno RJ,  Jenkins DK;
PI   Nwaka SO,  Allen SJ,  Ponton A,  Goldberg YP;
XX
DR   WPI; 2002-547693/58.
DR   P-PSDB; AAE24550.
XX
PT   Novel elongase polypeptide, genes and their control regions useful in
PT   determining compositions for treating polyunsaturated fatty acid disorder
PT   e.g. cardiovascular, inflammation, gastrointestinal disorders and cancer.
XX
PS   Claim 1; Page 160; 173pp; English.
XX
CC   The invention relates to novel elongase polypeptides, genes and their
CC   control regions. Sequences of the invention are used in the diagnosis and
CC   treatment of polyunsaturated fatty acid (PUFA) disorders such as
CC   cardiovascular disorders (e.g. atherosclerosis, coronary artery disease),
CC   inflammatory disorders (e.g. sinusitis, pancreatitis, asthma,
CC   osteoarthritis, rheumatoid arthritis, acne), Sjogren's syndrome, body
CC   weight disorders (e.g. obesity, cachexia and anorexia), viral diseases
CC   and postviral fatigue, gastrointestinal disorders, eczema, psychiatric
CC   disorders, cancer, congenital liver disease, alcoholism, Alzheimer's
CC   syndrome, cystic fibrosis, endometriosis, pre-menstrual syndrome,
CC   hypercholesterolaemia, hypertriglyceridaemia, dyslipidaemia, peripheral
CC   vascular disease, cerebrovascular disease, autoimmune disorders, acute
CC   respiratory distress syndrome, atopic disorders, articular cartilage
CC   degradation, diabetes and diabetic complication. The present sequence is
CC   human elongase gene (ELG6)
XX
SQ   Sequence 813 BP; 196 A; 231 C; 182 G; 204 T; 0 U; 0 Other;

  Query Match             3.3%;  Score 38;  DB 6;  Length 813;
  Best Local Similarity   47.2%;  Pred. No. 2.7;
  Matches  116;  Conservative    0;  Mismatches  130;  Indels    0;  Gaps    0;

Qy         75 CAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACT 134
              ||   | || | |   |  ||     ||||| |     | |||  | |    |  |
Db        480 CAAGAACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCAT 539

Qy        135 CCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCAT 194
              |  ||  ||  || ||   ||| |  | |       ||   | ||     | | || ||||
Db        540 CATGTACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCAT 599

Qy        195 GCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTC 254
              || | |  |   ||| ||  | || | | | | | | || ||| || ||  ||| |  |
Db        600 GCTCATCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCAC 659

Qy        255 GTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCT 314
              || |||       |||   |||| || ||   | | |     |   ||   || | |
Db        660 GTACATCTGGAGGCAGGATCAGGGATGCCACACCACGATGGAACACTTATTCTGGTCCTT 719

Qy        315 CATGTT 320
              |||  ||
Db        720 CATCTT 725


RESULT 14
ABZ22162
ID   ABZ22162 standard; cDNA; 813 BP.
XX
AC   ABZ22162;
XX
DT   12-MAR-2003  (first entry)
XX
DE   Human elongase HSELO1-like protein encoding cDNA SEQ ID NO:1.
XX
KW   Human; elongase; elongase HSELO1-like protein; enzyme; cytostatic;
KW   antidiabetic; antiasthmatic; anti-HIV; antiparkinsonian; nootropic;
KW   neuroprotective; tranquilliser; antimigraine; analgesic; neuroleptic;
KW   cerebroprotective; gene therapy; cancer; diabetes; CNS disorder; asthma;
KW   metabolic disease; central nervous system disorder; COPD; dementia;
KW   Parkinson's disease; multiple sclerosis; stroke; Alzheimer's disease;
KW   Huntington's disease; Creutzfeldt-Jakob disease; HIV; schizophrenia;
KW   psychosis; attention deficit disorder; headache pain; migraine; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /product= "elongase HSELO1-like protein"
XX
PN   WO200262974-A2.
XX
PD   15-AUG-2002.
XX
PF   07-FEB-2002; 2002WO-EP001262.
XX
PR   08-FEB-2001; 2001US-0267135P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Zhu Z;
XX
DR   WPI; 2002-636596/68.
DR   P-PSDB; ABP56418.
XX
PT   New isolated human elongase HSELO1-like polynucleotide and encoded
PT   peptide, useful for treating, preventing and ameliorating diseases such
PT   as COPD, cancer, metabolic disease, diabetes, CNS disorders, or asthma.
XX
PS   Claim 1; Fig 1; 128pp; English.
XX
CC   The present sequence encodes a human elongase HSELO1-like protein (I).
CC   (I) has cytostatic, antidiabetic, antiasthmatic, anti-HIV, nootropic,
CC   antiparkinsonian, neuroprotective, tranquilliser, antimigraine,
CC   analgesic, neuroleptic and cerebroprotective activities, and can be used
CC   in gene therapy. (I) can be used in the treatment of a disease, such as
CC   cancer, diabetes, central nervous system (CNS) disorder, asthma,
CC   metabolic disease or COPD. The human elongase HSELO1-like protein is
CC   useful in preventing, treating or ameliorating the diseases cited above,
CC   including Parkinson's disease, dementia, multiple sclerosis, stroke, HIV,
CC   Alzheimer's disease, Huntington's disease, Creutzfeldt-Jakob disease,
CC   schizophrenia, psychosis, attention deficit disorders, pain associated
CC   with CNS disorders, with cancer, or headache pain, e.g. migraine. It can
CC   also be useful in identifying test compounds that may act as activators
CC   or inhibitors at the enzyme's active site, or in raising specific
CC   antibodies that can block and effectively reduce its activity
XX
SQ   Sequence 813 BP; 196 A; 231 C; 182 G; 204 T; 0 U; 0 Other;

  Query Match             3.3%;  Score 38;  DB 6;  Length 813;
  Best Local Similarity   47.2%;  Pred. No. 2.7;
  Matches  116;  Conservative    0;  Mismatches  130;  Indels    0;  Gaps    0;

Qy         75 CAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACT 134
              ||   | || | |   |  ||     ||||| |     | |||  | |    |  |
Db        480 CAAGAACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCAT 539

Qy        135 CCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCAT 194
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Db        540 CATGTACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCAT 599

Qy        195 GCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTC 254

Db        600 GCTCATCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCAC 659

Qy        255 GTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCT 314

Db        660 GTACATCTGGAGGCAGGATCAGGGATGCCACACCACGATGGAACACTTATTCTGGTCCTT 719

Qy        315 CATGTT 320

Db        720 CATCTT 725
```

RESULT 15
ABN86918
ID ABN86918 standard; cDNA; 815 BP.
XX
AC ABN86918;
XX
DT 29-JUL-2002 (first entry)
XX
DE Human NOV6a encoding cDNA sequence SEQ ID NO:17.
XX
KW Human; NOVX; cytostatic; antiarteriosclerotic; cardiovascular; lymphoma;
KW antidiabetic; immunosuppressive; neuroprotective; gene therapy; cancer;
KW cardiomyopathy; atherosclerosis; cell signal processing; diabetes; AIDS;
KW metabolic pathway modulation; neoplastic; neurological disorder; asthma;
KW adenocarcinoma; prostate cancer; uterus cancer; immune response;
KW Crohn's disease; multiple sclerosis; Graft versus host disease;
KW chromosome 10; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1. .813
FT   /*tag= a
FT   /product= "NOV6a"
FT   /note= "Cold inducible glycoprotein 30-like protein"
XX
PN WO200230974-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US031922.
XX
PR 12-OCT-2000; 2000US-0240113P.
PR 16-OCT-2000; 2000US-0240625P.
PR 16-OCT-2000; 2000US-0240637P.
PR 16-OCT-2000; 2000US-0240648P.
PR 16-OCT-2000; 2000US-0240662P.
PR 16-OCT-2000; 2000US-0240669P.
PR 16-OCT-2000; 2000US-0240703P.
PR 16-OCT-2000; 2000US-0240732P.
PR 16-OCT-2000; 2000US-0241190P.
PR 18-JAN-2001; 2001US-0262455P.
XX
PA (CURA-) CURAGEN CORP.
PA (MILL/) MILLET I.
XX
PI Grosse WM, Alsobrook JP, Lepley DM, Burgess CE, Mishra V;
PI Kekuda R, Li L, Padigaru M, Shimkets RA, Zerhusen BD, Spytek KA;
PI Edinger S, Gerlach V, Macdougall J, Stone D, Gunther E, Ellerman K;
XX
DR WPI; 2002-444172/47.
DR P-PSDB; ABB78812.
XX
PT New NOVX polypeptides and polynucleotides, useful for treating or
PT preventing a NOVX-associated disorder or a pathological state in a
PT subject, particularly a human, e.g. cardiomyopathy, atherosclerosis,
PT cancer or diabetes.
XX
PS Claim 9; Page 51; 227pp; English.
XX
CC The present invention describes novel human proteins designated NOVX
CC (where X is 1, 2a, 2b, 2c, 2d, 3, 4, 5, 6a, 6b, 7, 8, or 9). NOV1 is a
CC tyrosine-protein kinase 6-like protein; NOV2a-d are keratin 4-like
CC proteins; NOV3 is a collagen-like protein; NOV4 is a cystatin B-like
CC protein; NOV5 is a serotonin receptor-like protein; NOV6a and NOV65v are
CC cold inducible glycoprotein 30-like proteins; NOV7 is a matrilin-2-like
CC protein; NOV8 is a leukocyte surface antigen (CD53)-like protein; and
CC NOV9 is a tyrosine kinase-like protein. NOVX sequences have cytostatic,
CC antiarteriosclerotic, cardiovascular, antidiabetic, immunosuppressive and
CC neuroprotective activities, and can be used in gene therapy. The NOVX
CC sequences can be used in therapeutics, particularly for treating,
CC preventing or alleviating a NOVX-associated disorder or a pathological
CC state in a subject, particularly a human. These disorders include
CC cardiomyopathy, atherosclerosis, a disorder related to cell signal
CC processing and metabolic pathway modulation or diabetes. The NOVX
CC sequences are also useful for determining the presence of or
CC predisposition to a disease associated with altered levels of NOVX
CC polypeptide or nucleic acid, particularly cancer. The NOVX sequences are
CC especially useful in therapeutic or prophylactic applications for
CC neoplastic or neurological disorders, and in the treatment of
CC adenocarcinoma, lymphoma, prostate cancer, uterus cancer, immune
CC response, AIDS, asthma, Crohn's disease, multiple sclerosis or Graft
CC versus host disease. The present sequence encodes the human NOV6a protein
CC from the present invention. NOV6a is located to chromosome 10
XX
SQ Sequence 815 BP; 196 A; 231 C; 183 G; 205 T; 0 U; 0 Other;

  Query Match   3.3%; Score 38; DB 6; Length 815;
  Best Local Similarity   47.2%; Pred. No. 2.7;
  Matches 116; Conservative   0; Mismatches 130; Indels   0; Gaps   0;

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Qy         75 CAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACT 134

Db        480 CAAGAACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCAT 539

Qy        135 CCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCAT 194

Db        540 CATGTACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCAT 599

Qy        195 GCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTC 254

Db        600 GCTCATCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCAC 659

Qy        255 GTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCT 314

Db        660 GTACATCTGGAGGCAGGATCAGGGATGCCACACCACGATGGAACACTTATTCTGGTCCTT 719

Qy        315 CATGTT 320

Db        720 CATCTT 725
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Listing first 45 summaries

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SUMMARIES

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	2	676.2	58.8	1142	3	US-08-457-918-9	Sequence 9, Appli
	3	43	3.7	468	1	US-08-236-311-12	Sequence 12, Appl
	4	43	3.7	468	3	US-08-457-918-12	Sequence 12, Appl
c	5	40	3.5	533	6	5482709-5	Patent No. 5482709
c	6	40	3.5	543	6	5273901-6	Patent No. 5273901
c	7	37.4	3.3	688	3	US-08-998-416-915	Sequence 915, App
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	12	36.2	3.1	1140	4	US-09-252-991A-269	Sequence 269, App
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	14	36	3.1	1149	4	US-09-252-991A-7156	Sequence 7156, Ap
	15	35.2	3.1	675	4	US-09-252-991A-7278	Sequence 7278, Ap
	16	35	3.0	627	4	US-09-252-991A-3035	Sequence 3035, Ap
	17	35	3.0	630	4	US-09-252-991A-953	Sequence 953, App
	18	35	3.0	720	4	US-09-252-991A-3133	Sequence 3133, Ap
c	19	35	3.0	777	4	US-09-252-991A-1127	Sequence 1127, Ap
c	20	35	3.0	1147	2	US-08-761-277A-44	Sequence 44, Appl
	21	34.8	3.0	695	4	US-09-221-017B-767	Sequence 767, App
c	22	34.6	3.0	41	3	US-08-891-271-25	Sequence 25, Appl
	23	34.6	3.0	822	4	US-09-252-991A-9029	Sequence 9029, Ap
c	24	34.4	3.0	431	4	US-09-433-241A-1	Sequence 1, Appli
	25	34.4	3.0	1011	4	US-09-252-991A-3833	Sequence 3833, Ap
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c	28	34.2	3.0	927	4	US-09-252-991A-15945	Sequence 15945, A
c	29	34.2	3.0	1080	4	US-09-252-991A-6480	Sequence 6480, Ap
	30	33.8	2.9	1053	4	US-09-252-991A-15787	Sequence 15787, A
	31	33.8	2.9	1134	4	US-09-252-991A-15842	Sequence 15842, A
c	32	33.6	2.9	839	3	US-08-998-416-519	Sequence 519, App
c	33	33	2.9	684	4	US-09-252-991A-230	Sequence 230, App
c	34	32.8	2.9	753	4	US-09-252-991A-10372	Sequence 10372, A
	35	32.8	2.9	819	4	US-09-252-991A-10784	Sequence 10784, A
	36	32.8	2.9	861	4	US-09-252-991A-14249	Sequence 14249, A
	37	32.8	2.9	1089	4	US-09-252-991A-13807	Sequence 13807, A
c	38	32.8	2.9	1092	4	US-09-252-991A-14250	Sequence 14250, A
c	39	32.8	2.9	1125	4	US-09-218-489-1	Sequence 1, Appli
c	40	32.6	2.8	872	1	US-08-381-280-19	Sequence 19, Appl
c	41	32.6	2.8	872	2	US-08-445-533-19	Sequence 19, Appl
c	42	32.6	2.8	872	3	US-09-052-085-19	Sequence 19, Appl
c	43	32.6	2.8	1116	3	US-09-104-308-2	Sequence 2, Appli
c	44	32.6	2.8	1116	3	US-09-321-981-2	Sequence 2, Appli
c	45	32.6	2.8	1116	4	US-09-739-861A-2	Sequence 2, Appli

ALIGNMENTS

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RESULT 1
US-08-236-311-9
; Sequence 9, Application US/08236311
; Patent No. 5565335
;  GENERAL INFORMATION:
;    APPLICANT:  Capon, Daniel J.
;    APPLICANT:  Gregory, Timothy J.
;    TITLE OF INVENTION:  Adheson Variants
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/236,311
;      FILING DATE:  02-MAY-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/936190
;      FILING DATE:  26-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/842777
;      FILING DATE:  18-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/250785
;      FILING DATE:  28-SEP-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/104329
;      FILING DATE:  02-OCT-1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  444P1C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1142 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
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;      TOPOLOGY:  linear
US-08-236-311-9

  Query Match             58.8%;  Score 676.2;  DB 1;  Length 1142;
  Best Local Similarity   98.6%;  Pred. No. 1.9e-175;
  Matches  695;  Conservative    0;  Mismatches    3;  Indels    7;  Gaps    1;

Qy          5 ACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 64
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Db        423 AACTCGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 482

Qy         65 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 542

Qy        125 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 602

Qy        185 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 662

Qy        245 TCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 304
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        663 TCATGTTGTCGTGCATGGCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 722

Qy        305 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGGTAGCTCTTTT 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGGTAGCTCTTTT 782

Qy        365 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 842

Qy        425 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 902

Qy        485 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 962

Qy        545 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 1022

Qy        605 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGAC 657
              |||||||||||||||||||||||||||||||||||       |||||||||||||||||
Db       1023 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGAC 1082

Qy        658 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 702
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1083 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 1127


RESULT 2
US-08-457-918-9
; Sequence 9, Application US/08457918
; Patent No. 6117655
;  GENERAL INFORMATION:
;    APPLICANT:  Capon, Daniel J.
;    APPLICANT:  Gregory, Timothy J.
;    TITLE OF INVENTION:  Adheson Variants
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/457,918
;      FILING DATE:  1-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/236311
;      FILING DATE:  02-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/936190
;      FILING DATE:  26-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/842777
;      FILING DATE:  18-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/250785
;      FILING DATE:  28-SEP-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/104329
;      FILING DATE:  02-OCT-1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kubinec, Jeffrey S.
;      REGISTRATION NUMBER:  36,575
;      REFERENCE/DOCKET NUMBER:  P0444P1C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-8228
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1142 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-457-918-9

  Query Match             58.8%;  Score 676.2;  DB 3;  Length 1142;
  Best Local Similarity   98.6%;  Pred. No. 1.9e-175;
  Matches  695;  Conservative    0;  Mismatches    3;  Indels    7;  Gaps    1;

Qy          5 ACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 AACTCGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 482

Qy         65 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 542

Qy        125 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 602

Qy        185 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 662

Qy        245 TCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 304
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        663 TCATGTTGTCGTGCATGGCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 722

Qy        305 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGGTAGCTCTTTT 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGGTAGCTCTTTT 782

Qy        365 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 842

Qy        425 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        843 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 902

Qy        485 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 962

Qy        545 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 1022

Qy        605 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGAC 657
              |||||||||||||||||||||||||||||||||||       ||||||||||||||||
Db       1023 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGAC 1082

Qy        658 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 702
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1083 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 1127
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RESULT 3
US-08-236-311-12
; Sequence 12, Application US/08236311
; Patent No. 5565335
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,311
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 444P1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-236-311-12

Query Match 3.7%; Score 43; DB 1; Length 468;
Best Local Similarity 49.5%; Pred. No. 0.023;
Matches 143; Conservative 0; Mismatches 140; Indels 6; Gaps 1;

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Qy        394 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 453
              | ||||   || | || | | || |||||    ||  || |||           | ||
Db        127 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 186

Qy        454 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 507
              |  ||||||| | ||   ||||||||||| ||   |  ||  ||||      |||
Db        187 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 246

Qy        508 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 567
              | |      ||  |||  |||  | |  |||      |      |     |  ||| ||
Db        247 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 306

Qy        568 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 627
              |||  |  ||||  |||||  || ||  ||  |||        |   || |   || |||
Db        307 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 366

Qy        628 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 676
              | | | |||   || |  ||| |||  |||  |  | |  |||  |||
Db        367 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 415
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RESULT 4
US-08-457-918-12
; Sequence 12, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0444P1C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 12:

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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  468 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-457-918-12

  Query Match             3.7%;  Score 43;  DB 3;  Length 468;
  Best Local Similarity   49.5%;  Pred. No. 0.023;
  Matches  143;  Conservative    0;  Mismatches  140;  Indels    6;  Gaps    1;

Qy        394 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 453
Db        127 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 186

Qy        454 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 507
Db        187 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 246

Qy        508 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 567
Db        247 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 306

Qy        568 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 627
Db        307 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 366

Qy        628 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 676
Db        367 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 415


RESULT 5
5482709-5/c
;Patent No. 5482709
;    APPLICANT: JACOBSON, JAMES W.;STRAUSBERG, ROBERT L.;WILSON,
;SUSAN D.;POPE, SHARON H.;STRAUSBERG, SUSAN L.;RUFF, MICHAEL D.;
; AUGUSTINE, PATRICIA C.;DANFORTH, HARRY D.
;    TITLE OF INVENTION: EIMERIA ANTIGENIC COMPOSITION WHICH
;ELICITS ANTIBODIES AGAINST AVIAN COCCIDIOSIS
;    NUMBER OF SEQUENCES: 10
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/148,432
;      FILING DATE: 08-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 581,693
;      FILING DATE: 12-SEP-1990
;      APPLICATION NUMBER: 215,162
;      FILING DATE: 05-JUL-1989
;      APPLICATION NUMBER: 746,520
;      FILING DATE: 19-JUN-1985
;      APPLICATION NUMBER: 627,811
;      FILING DATE: 05-JUL-1984
;SEQ ID NO:5:
;      LENGTH: 533
5482709-5

  Query Match             3.5%;  Score 40;  DB 6;  Length 533;
  Best Local Similarity   47.3%;  Pred. No. 0.16;
  Matches  121;  Conservative    0;  Mismatches  135;  Indels    0;  Gaps    0;

Qy        104 TCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGG 163
Db        440 TCCCCCAGGCTTACCTGCTGCTGATGCTGCTGCTGCTCTTGCTGCAGCTGCTGTTGTTGC 381

Qy        164 TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT 223
Db        380 TGCTGTTGCTGCTTGTGTTTTCGCTTTCTCTGCTTCTGCTGCTGCTCCTGCTGCTCCTTC 321

Qy        224 TCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGC 283
Db        320 GGTTTCTGTTCGTGCTTCCGCTGCCTTTGCTGCTCCTGCTGCTCCTGCTGCGGCTGTCGC 261

Qy        284 AGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGG 343
Db        260 TGCAGCTGGTGCTGCTGCAGCTCCTGTTGCTGCTGCTGCTGCTGCAGCTGGTGCTGCTGC 201

Qy        344 AGGGTCGGGGGTAGCT 359
Db        200 AGCTGGTGCTGCAGCT 185


RESULT 6
5273901-6/c
;Patent No. 5273901
;    APPLICANT: JACOBSON, JAMES W.;STRAUSBERG, ROBERT L.;WILSON,
;SUSAN D.;POPE, SHARON H.;STRAUSBERG, SUSAN L.;RUFF,MICHAEL D.;
;AUGUSTINE, PATRICIA C.;DANFORTH, HARRY D.
;    TITLE OF INVENTION: GENETICALLY ENGINEERED COCCIDIOSIS
;SPOROZOITE 21.5 KB ANTIGEN, AC-6B
;    NUMBER OF SEQUENCES: 11
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/581,693
;      FILING DATE: 12-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 215,162
;      FILING DATE: 05-JUL-1988
;      APPLICATION NUMBER: 746,520
;      FILING DATE: 19-JUN-1985
;      APPLICATION NUMBER: 627,811
;      FILING DATE: 05-JUL-1984
;SEQ ID NO:6:
;      LENGTH:543
5273901-6

  Query Match             3.5%;  Score 40;  DB 6;  Length 543;
  Best Local Similarity   47.3%;  Pred. No. 0.16;
  Matches  121;  Conservative    0;  Mismatches  135;  Indels    0;  Gaps    0;

Qy        104 TCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGG 163
Db        450 TCCCCCAGGCTTACCTGCTGCTGATGCTGCTGCTGCTCTTGCTGCAGCTGCTGTTGTTGC 391

Qy        164 TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT 223
Db        390 TGCTGTTGCTGCTTGTGTTTTCGCTTTCTCTGCTTCTGCTGCTGCTCCTGCTGCTCCTTC 331

Qy        224 TCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGC 283
Db        330 GGTTTCTGTTCGTGCTTCCGCTGCCTTTGCTGCTCCTGCTGCTCCTGCTGCGGCTGTCGC 271

Qy        284 AGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGG 343
Db        270 TGCAGCTGGTGCTGCTGCAGCTCCTGTTGCTGCTGCTGCTGCTGCAGCTGGTGCTGCTGC 211

Qy        344 AGGGTCGGGGGTAGCT 359
Db        210 AGCTGGTGCTGCAGCT 195


RESULT 7
US-08-998-416-915/c
; Sequence 915, Application US/08998416
; Patent No. 6239264
;  GENERAL INFORMATION:
;    APPLICANT:  Philippsen, Peter
;    APPLICANT:  Pohlmann, Rainer
;    APPLICANT:  Steiner, Sabine
;    APPLICANT:  Mohr, Christine
;    APPLICANT:  Wendland, Jurgen
;    APPLICANT:  Knechtle, Philipp
;    APPLICANT:  Rebischung, Corinne
;    TITLE OF INVENTION:  GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
;    TITLE OF INVENTION:  AND USES THEREOF
;    NUMBER OF SEQUENCES:  1152
;    CORRESPONDENCE ADDRESS:
```

```
;       ADDRESSEE:  No. 6239264artis Corporation
;       STREET:  3054 Cornwallis Road
;       CITY:  Research Triangle Park
;       STATE:  No. 6239264th Carolina
;       COUNTRY:  USA
;       ZIP:  27709
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/998,416
;       FILING DATE:  24-DEC-1997
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  CH 0016/97
;       FILING DATE:  31-DEC-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Meigs, J. Timothy
;       REGISTRATION NUMBER:  38,241
;       REFERENCE/DOCKET NUMBER:  PF/5-30306/A/CGC1976
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  919-541-8587
;       TELEFAX:  919-541-8689
;   INFORMATION FOR SEQ ID NO:  915:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  688 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     ORIGINAL SOURCE:
;       ORGANISM:  PAG1570RP
US-08-998-416-915

  Query Match             3.3%;  Score 37.4;  DB 3;  Length 688;
  Best Local Similarity   45.0%;  Pred. No. 0.9;
  Matches  140;  Conservative    0;  Mismatches  171;  Indels    0;  Gaps    0;

Qy          63 GGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAG 122
               ||||   |   | |  | |  |  |  |  | | ||  |||| |  | |  ||  | |
Db         547 GGACTTGCTGTGGAACCGGTTGTGGTTGCTGTGATTGTGGTTTCAATTGTGGTTGTGGTT 488

Qy         123 GGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTT 182
               ||  | | | || | |       | |  |  ||||    | |||| |||   || | | |
Db         487 GGTGTTGTGTCTGCTGCTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 428

Qy         183 CAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCT 242
               |    |||  |  | ||  || |   | |    |||  |   |  ||   | ||
Db         427 GCTGCGTCTGCTGCTGCGTCTGCTGCTGCGGTTGTGGTTGTTGCGCCTGCGCCTGCGCCA 368

Qy         243 CGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGA 302
               |   | ||  | |  ||  |  | ||  |  |  || | | |  ||    |||
Db         367 GTTGTGGCTGATGAGGCTGTAAACCAAGCTGTTGTTGTTGTTGTAGTTGCGGTTGAGGTT 308

Qy         303 CTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTT 362
                 | | | ||  ||||   |||   | |||||||  |    |  | | ||| | |
Db         307 GGGGCTGCTGCTGCTGTTGTGGTTGTTGTGGTTGTTGTGTTTGTTGCTGTGGTTGTGGTG 248

Qy         363 TTGGTAGAGGT 373
               |||| | |||
Db         247 GTGGTGGTGGT 237


RESULT 8
US-09-252-991A-16469
; Sequence 16469, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER:  US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 16469
;   LENGTH:  1125
;   TYPE:  DNA
;   ORGANISM:  Pseudomonas aeruginosa
US-09-252-991A-16469

  Query Match             3.2%;  Score 36.4;  DB 4;  Length 1125;
  Best Local Similarity   49.5%;  Pred. No. 2;
  Matches   94;  Conservative    0;  Mismatches   96;  Indels    0;  Gaps    0;

Qy         427 CTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCG 486
               || || | | |       | || |  || |  ||   || |  | |   ||| |  |||
Db         791 CTGCTGGCCGGCAAGGAAGGCCCGCTGGGCAAGAACTACAACATGCGCTGGATCGCCTCG 850

Qy         487 CTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGA 546
                 ||       || ||  || |   |  ||   |||  | | || |||| |  | |||
Db         851 ATGGTCGCCGACGTCCACCGCATCCTGACCCGTGGCGGCGTCTTCATGTACCCGCGCGAC 910

Qy         547 GGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCG 606
               | | ||| | |  |  |||  | |||  |    ||  || |||     ||| | | |||
Db         911 GCCCGCGAGCCGGAGAAGCCCGGCAAGCTGCGCCTGATGTACGAAGCCAACCCGATGTCG 970

Qy         607 TCCACCGTCG 616
               | || | |||
Db         971 TTCATCATCG 980


RESULT 9
US-09-621-976-15639
; Sequence 15639, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 15639
;   LENGTH: 505
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-15639

  Query Match             3.1%;  Score 36.2;  DB 4;  Length 505;
  Best Local Similarity   15.0%;  Pred. No. 1.7;
  Matches   32;  Conservative   94;  Mismatches   87;  Indels    0;  Gaps    0;

Qy          48 GGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCT 107
               :|::   ||:|  ::| :|:   :  :::|: :: :::     :|: || :  :::  :|
Db          38 RGKYGTSGGRCGGSRGWMCSKWGYRYSYWGYKWKSWSKKMKKYSGKMGTSKSTRKYRTYT 97

Qy         108 GTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCT 167
               :: ::    :   :: :    ::: ::::: : : | : :: : :| :   :| | :||:
Db          98 SKCRKTTCKYRGWWSWKWRMWKRRKMYYYRMKCYSCASYSYSYRRCRKYTGMTRGWYGCK 157

Qy         168 TCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTG 227
               :   ::   :: ::|  :: ||||:  : ::|:|: :  :    ::   :|:| ::: :
Db         158 KRMCKSSTRYMTRYTRYWKMTGACYGSKGMSCKGSRSKYYGSWKWYYGKYTMCTSKYKSS 217

Qy         228 TTTCGGCGCCCTCCTCGTCATGTTGTCGTGCAT 260
               :  ::::::|:|:: | :  :  | |::::: |
```

```
Db        218 KMSYKKSSMCYTYMMCYYTYWWCTCTYKKSYYT 250


RESULT 10
US-09-252-991A-242/c
; Sequence 242, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 242
;   LENGTH: 615
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-242

  Query Match             3.1%;  Score 36.2;  DB 4;  Length 615;
  Best Local Similarity   49.2%;  Pred. No. 1.8;
  Matches   95;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy        433 GACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAG 492
              |||  |  |   | || | ||   ||| |||| | |   ||   ||  | | | |||  |
Db        359 GACATGCGCCGCGCCCTGGCGCTATGGCCGGAACTGGCGCCTTGGAGCGAGGCCCTGCTG 300

Qy        493 CGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCAC 552
               | ||   |     |  |   || | |  ||      ||  ||||  | ||||| || |
Db        299 GGCCAGTACCTTGCCGTGCACCCGGGCTTCCAGCGCCTGGCGTTCGCGGGCGGAAGGGTC 240

Qy        553 GACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACC 612
              | |||||  |||| |  |    | |  |||  || |  |  ||| ||   | ||     |
Db        239 GGCCTGACCCTGCTGCTGGGCGATGCCATGGAGTGCCTGCCGCAGCTCGACGCGCGGGTC 180

Qy        613 GTCGTCCCCTTGC 625
              | || |   || |
Db        179 GACGCCTGGTTCC 167


RESULT 11
US-09-252-991A-296
; Sequence 296, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 296
;   LENGTH: 1041
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-296

  Query Match             3.1%;  Score 36.2;  DB 4;  Length 1041;
  Best Local Similarity   49.2%;  Pred. No. 2.2;
  Matches   95;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy        433 GACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAG 492
              |||  |  |   | || | ||   ||| |||| | |   ||   ||  | | | |||  |
Db        338 GACATGCGCCGCGCCCTGGCGCTATGGCCGGAACTGGCGCCTTGGAGCGAGGCCCTGCTG 397

Qy        493 CGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCAC 552
               | ||   |     |  |   || | |  ||      ||  ||||  | ||||| || |
Db        398 GGCCAGTACCTTGCCGTGCACCCGGGCTTCCAGCGCCTGGCGTTCGCGGGCGGAAGGGTC 457

Qy        553 GACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACC 612
              | |||||  |||| |  |    | |  |||  || |  |  ||| ||   | ||     |
Db        458 GGCCTGACCCTGCTGCTGGGCGATGCCATGGAGTGCCTGCCGCAGCTCGACGCGCGGGTC 517

Qy        613 GTCGTCCCCTTGC 625
              | || |   || |
Db        518 GACGCCTGGTTCC 530


RESULT 12
US-09-252-991A-269
; Sequence 269, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 269
;   LENGTH: 1140
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-269

  Query Match             3.1%;  Score 36.2;  DB 4;  Length 1140;
  Best Local Similarity   49.2%;  Pred. No. 2.3;
  Matches   95;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy        433 GACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAG 492
              |||  |  |   | || | ||   ||| |||| | |   ||   ||  | | | |||  |
Db        436 GACATGCGCCGCGCCCTGGCGCTATGGCCGGAACTGGCGCCTTGGAGCGAGGCCCTGCTG 495

Qy        493 CGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCAC 552
               | ||   |     |  |   || | |  ||      ||  ||||  | ||||| || |
Db        496 GGCCAGTACCTTGCCGTGCACCCGGGCTTCCAGCGCCTGGCGTTCGCGGGCGGAAGGGTC 555

Qy        553 GACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACC 612
              | |||||  |||| |  |    | |  |||  || |  |  ||| ||   | ||     |
Db        556 GGCCTGACCCTGCTGCTGGGCGATGCCATGGAGTGCCTGCCGCAGCTCGACGCGCGGGTC 615

Qy        613 GTCGTCCCCTTGC 625
              | || |   || |
Db        616 GACGCCTGGTTCC 628


RESULT 13
US-09-252-991A-7481/c
; Sequence 7481, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
```

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;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7481
;   LENGTH: 909
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7481

  Query Match             3.1%;  Score 36;  DB 4;  Length 909;
  Best Local Similarity   45.4%;  Pred. No. 2.4;
  Matches  129;  Conservative    0;  Mismatches  155;  Indels    0;  Gaps    0;

Qy        809 AATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGG 868
              ||    | ||  |  | |  | | |     | ||  | ||| |      ||   ||  || ||
Db        350 AAACACTGGCCAGGGAAAACGCCTTGATCTTGCACGAGGGCCCCGCCACCCTTGGCCGGG 291

Qy        869 TCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCT 928
              || |  || |||| | |   | |  | || | |     | | | | ||||    ||| |
Db        290 TCGGCAACGGACAGAGGTGGGACATGCGTTTGCGCAGAAGGACGACGTTGCTGCTGGTAT 231

Qy        929 AGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGA 988
                | |||||  |||  |||          ||| |  ||| | | |    ||  |   |
Db        230 TTGCAGTGCTGTTGCTGCTGGCGTTCGGCTACGGCTGGCATGCCTGGCGCAGCCTGTTGC 171

Qy        989 CGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTC 1048
                | | | |||   |    | |  ||      || |||| |     |  || | | | |
Db        170 GCGAGCAGGGTGTCGAGCGCCTGGAGTGGCAAGGCCTGGGCCTGTCCGCCGAAGGCATCG 111

Qy       1049 GTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTC 1092
                |  ||  |  |  |||  | |  || | |  ||  | ||| |
Db        110 GGCTGCGACGGCTGGCGCTGGAGCGGCGCGGCGCGGATGGCGCC 67


RESULT 14
US-09-252-991A-7156
; Sequence 7156, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7156
;   LENGTH: 1149
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7156

  Query Match             3.1%;  Score 36;  DB 4;  Length 1149;
  Best Local Similarity   45.4%;  Pred. No. 2.6;
  Matches  129;  Conservative    0;  Mismatches  155;  Indels    0;  Gaps    0;

Qy        809 AATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGG 868
              ||    | ||  |  | |  | | |     | ||  | ||| |      ||   ||  || ||
Db        159 AAACACTGGCCAGGGAAAACGCCTTGATCTTGCACGAGGGCCCCGCCACCCTTGGCCGGG 218

Qy        869 TCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCT 928
              || |  || |||| | |   | |  | || | |     | | | | ||||    ||| |
Db        219 TCGGCAACGGACAGAGGTGGGACATGCGTTTGCGCAGAAGGACGACGTTGCTGCTGGTAT 278

Qy        929 AGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGA 988
                | |||||  |||  |||          ||| |  ||| | | |    ||  |   |
Db        279 TTGCAGTGCTGTTGCTGCTGGCGTTCGGCTACGGCTGGCATGCCTGGCGCAGCCTGTTGC 338

Qy        989 CGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTC 1048
                | | | |||  |    | |  ||      || |||| |     |  || | | | |
Db        339 GCGAGCAGGGTGTCGAGCGCCTGGAGTGGCAAGGCCTGGGCCTGTCCGCCGAAGGCATCG 398

Qy       1049 GTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTC 1092
                |  ||  |  |  |||  | |  || | |  ||  | ||| |
Db        399 GGCTGCGACGGCTGGCGCTGGAGCGGCGCGGCGCGGATGGCGCC 442


RESULT 15
US-09-252-991A-7278
; Sequence 7278, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7278
;   LENGTH: 675
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7278

  Query Match             3.1%;  Score 35.2;  DB 4;  Length 675;
  Best Local Similarity   46.1%;  Pred. No. 3.6;
  Matches  118;  Conservative    0;  Mismatches  138;  Indels    0;  Gaps    0;

Qy        837 CGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAA 896
              | ||  | ||| |      ||   ||  || |||| |  || |||| | |   | | |
Db          2 CTTGCACGAGGGCCCCGCCACCCTTGGCCGGGTCGGCAACGGACAGAGGTGGGACATGCG 61

Qy        897 TTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCT 956
              || | |     | | | | ||||    ||| |    | |||||  |||  |||
Db         62 TTTGCGCAGAAGGACGACGTTGCTGCTGGTATTTGCAGTGCTGTTGCTGCTGGCGTTCGG 121

Qy        957 GGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACT 1016
                |||  |  |||  | | |     ||  |   |   | | | |||  |    | |  ||
Db        122 CTACGGCTGGCATGCCTGGCGCAGCCTGTTGCGCGAGCAGGGTGTCGAGCGCCTGGAGTG 181

Qy       1017 CTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACG 1076
                || |||| |      |  || | | | | |  || | |  |  |||  | |  ||
Db        182 GCAAGGCCTGGGCCTGTCCGCCGAAGGCATCGGGCTGCGACGGCTGGCGCTGGAGCGGCG 241

Qy       1077 AGACAGGGCAGACGTC 1092
                | |  ||  | ||| |
Db        242 CGGCGCGGATGGCGCC 257


Search completed: May  7, 2004, 12:55:32
Job time : 65.5 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:36 ; Search time 371.25 Seconds
(without alignments)
14032.296 Million cell updates/sec

Title: US-10-679-999-8
Perfect score: 1150
Sequence: 1 GTATACCTTGGGTTTAGAAC.....AGGCCCAACAATTACCTAGG 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 4872186

Minimum DB seq length: 0
Maximum DB seq length: 1150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1150	100.0	1150	13	US-10-679-999-8	Sequence 8, Appli
	2	1134	98.6	1150	13	US-10-679-999-11	Sequence 11, Appl
	3	1117.8	97.2	1135	13	US-10-679-999-14	Sequence 14, Appl
	4	1105	96.1	1135	13	US-10-679-999-17	Sequence 17, Appl
	5	676.2	58.8	1142	15	US-10-097-044A-9	Sequence 9, Appli
	6	440.8	38.3	454	9	US-09-366-133-5	Sequence 5, Appli
	7	440.8	38.3	454	13	US-10-679-999-5	Sequence 5, Appli
	8	440.8	38.3	454	15	US-10-214-037-5	Sequence 5, Appli
	9	378.4	32.9	491	9	US-09-366-133-2	Sequence 2, Appli
	10	378.4	32.9	491	13	US-10-679-999-2	Sequence 2, Appli
	11	378.4	32.9	491	15	US-10-214-037-2	Sequence 2, Appli
	12	43	3.7	468	15	US-10-097-044A-12	Sequence 12, Appl
c	13	42.4	3.7	1116	15	US-10-156-761-6640	Sequence 6640, Ap
c	14	40.4	3.5	486	13	US-10-465-217-13	Sequence 13, Appl
	15	40.4	3.5	754	9	US-09-229-200A-13	Sequence 13, Appl
	16	39.6	3.4	200	13	US-10-399-364-2	Sequence 2, Appli
	17	39.4	3.4	675	15	US-10-156-761-2371	Sequence 2371, Ap
	18	39.4	3.4	1011	13	US-10-152-886-82	Sequence 82, Appl
c	19	38.6	3.4	711	15	US-10-156-761-2558	Sequence 2558, Ap
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	22	38.4	3.3	1049	15	US-10-146-731-358	Sequence 358, App
	23	38.4	3.3	1049	15	US-10-140-472-358	Sequence 358, App
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	32	38.4	3.3	1049	16	US-10-140-864-358	Sequence 358, App
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	37	38	3.3	815	10	US-09-976-782-19	Sequence 19, Appl
	38	38	3.3	945	16	US-10-369-493-42967	Sequence 42967, A
c	39	37.6	3.3	717	15	US-10-133-973-2	Sequence 2, Appli
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	41	37.4	3.3	653	15	US-10-184-644-402	Sequence 402, App
	42	37.4	3.3	653	15	US-10-184-634-402	Sequence 402, App
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	44	37.2	3.2	629	13	US-10-282-122A-11907	Sequence 11907, A
c	45	37	3.2	915	15	US-10-156-761-5089	Sequence 5089, Ap

ALIGNMENTS

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RESULT 1
US-10-679-999-8
; Sequence 8, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
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;             LENGTH: 1150 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-679-999-8

  Query Match           100.0%;  Score 1150;  DB 13;  Length 1150;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1150;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 GAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAG 120
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Qy        121 AGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAG 180
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Db        121 AGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAG 180

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Qy        301 GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 360
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Db        301 GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 360

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Db        361 TTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGT 420

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Db        601 TTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTG 660

Qy        661 TTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAA 720
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Db        661 TTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAA 720

Qy        721 GTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTG 780
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Db        721 GTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTG 780

Qy        781 TGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTG 840

Qy        841 GGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGG 900
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Qy        961 GACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA 1020
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Db        961 GACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA 1020

Qy       1021 GACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGAC 1080
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Qy       1081 AGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACA 1140
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Qy       1141 ATTACCTAGG 1150
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Db       1141 ATTACCTAGG 1150


RESULT 2
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; Sequence 11, Application US/10679999
; Publication No. US20040067520A1
;  GENERAL INFORMATION:
;       APPLICANT: Mann, Michael B.
;                  Hecht, Randy I.
;       TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                           METHODS
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Amgen Inc.
;            STREET: 1840 DeHavilland Drive
;            CITY: Thousand Oaks
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 91320-1789
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/679,999
;            FILING DATE: 06-Oct-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/568,528
;            FILING DATE: 09-May-2000
;            APPLICATION NUMBER: 09/267,517
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Knight, Matthew W.
;            REGISTRATION NUMBER: 36,846
;            REFERENCE/DOCKET NUMBER: A-416
;  INFORMATION FOR SEQ ID NO: 11:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1150 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-679-999-11

  Query Match           98.6%;  Score 1134;  DB 13;  Length 1150;
  Best Local Similarity  99.1%;  Pred. No. 0;
  Matches 1140;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

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Qy       121 AGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAG 180
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Qy       181 TTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTC 240
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Db       181 TTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTC 240

Qy       241 CTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACC 300
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Qy       361 TTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGT 420
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Qy       421 AGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATA 480
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Db       421 AGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATA 480

Qy       481 GGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG 540
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Db       481 GGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG 540

Qy       541 TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTG 600
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Db       601 TTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTG 660

Qy       661 TTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAA 720
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Qy       781 TGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTG 840
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Qy       841 GGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGG 900
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Db       841 GGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGG 900

Qy       901 AGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGAC 960
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Db       901 AGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGAC 960

Qy       961 GACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA 1020
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Qy      1081 AGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACA 1140
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Qy      1141 ATTACCTAGG 1150
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Db      1141 ATTACCTAGG 1150
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RESULT 3
US-10-679-999-14
; Sequence 14, Application US/10679999
; Publication No. US20040067520A1
; GENERAL INFORMATION:
; APPLICANT: Mann, Michael B.
; Hecht, Randy I.
; TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/679,999
; FILING DATE: 06-Oct-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/568,528
; FILING DATE: 09-May-2000
; APPLICATION NUMBER: 09/267,517
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Knight, Matthew W.
; REGISTRATION NUMBER: 36,846
; REFERENCE/DOCKET NUMBER: A-416
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1135 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-679-999-14

Query Match 97.2%; Score 1117.8; DB 13; Length 1135;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1122; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db          7 CTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGAAGTCAG 66

Qy         82 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 141
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Qy        202 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 261
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Db        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246

Qy        262 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 321
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366

Qy        382 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426

Qy        442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486

Qy        502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546

Qy        562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606

Qy        622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 666

Qy        682 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 726

Qy        742 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 786

Qy        802 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 846

Qy        862 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 906

Qy        922 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 966

Qy        982 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1026

Qy       1042 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1086

Qy       1102 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135


RESULT 4
US-10-679-999-17
; Sequence 17, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1135 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-679-999-17

  Query Match             96.1%;  Score 1105;  DB 13;  Length 1135;
  Best Local Similarity   98.7%;  Pred. No. 0;
  Matches 1114;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         22 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 81
              ||||||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db          7 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAG 66

Qy         82 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126

Qy        142 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186

Qy        202 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246

Qy        262 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 321
              |||||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGT 306

Qy        322 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 381
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 ACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366

Qy        382 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426

Qy        442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486

Qy        502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546

Qy        562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
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Qy        622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 666

Qy        682 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 726

Qy        742 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 786

Qy        802 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 846

Qy        862 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 906

Qy        922 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 966

Qy        982 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1026

Qy       1042 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1086

Qy       1102 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
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Db       1087 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
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RESULT 5
US-10-097-044A-9
; Sequence 9, Application US/10097044A
; Publication No. US20030143220A1
;   GENERAL INFORMATION:
;        APPLICANT: Capon, Daniel J.
;                   Gregory, Timothy J.
;        TITLE OF INVENTION: Adheson Variants
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 460 Point San Bruno Blvd
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: patin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/097,044A
;             FILING DATE: 28-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/457,918
;             FILING DATE: 1-JUN-1995
;             APPLICATION NUMBER: 08/236311
;             FILING DATE: 02-MAY-1994
;             APPLICATION NUMBER: 07/936190
;             FILING DATE: 26-AUG-1992
;             APPLICATION NUMBER: 07/842777
;             FILING DATE: 18-FEB-1992
;             APPLICATION NUMBER: 07/250785
;             FILING DATE: 28-SEP-1988
;             APPLICATION NUMBER: 07/104329
;             FILING DATE: 02-OCT-1987
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kubinec, Jeffrey S.
;             REGISTRATION NUMBER: 36,575
;             REFERENCE/DOCKET NUMBER: P0444P1C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415/225-8228
;             TELEFAX: 415/952-9881
;             TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1142 bases
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-097-044A-9

  Query Match             58.8%;  Score 676.2;  DB 15;  Length 1142;
  Best Local Similarity   98.6%;  Pred. No. 3.4e-204;
  Matches  695;  Conservative    0;  Mismatches    3;  Indels    7;  Gaps    1;

Qy          5 ACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 AACTCGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 482

Qy         65 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 542

Qy        125 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 602

Qy        185 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 662

Qy        245 TCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 304
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        663 TCATGTTGTCGTGCATGGCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 722

Qy        305 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 782

Qy        365 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 842

Qy        425 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 902

Qy        485 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 962

Qy        545 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 1022

Qy        605 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGAC 657
              |||||||||||||||||||||||||||||||||||||       ||||||||||||||||||
Db       1023 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGAC 1082

Qy        658 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 702
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1083 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 1127


RESULT 6
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US-09-366-133-5
; Sequence 5, Application US/09366133
; Patent No. US20020009798A1
;  GENERAL INFORMATION:
;    APPLICANT:  Pelleymounter, Mary Ann
;    APPLICANT:  Hecht, Randy I
;    APPLICANT:  Mann, Michael B
;    TITLE OF INVENTION:  OB PROTEIN COMPOSITIONS AND METHODS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  91230-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/366,133
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/920,608
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pessin, Karol M.
;      REFERENCE/DOCKET NUMBER:  A-345
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  454 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-366-133-5

  Query Match             38.3%;  Score 440.8;  DB 9;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 1.8e-129;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
              |||||||||||||||||||||||||||||||||||||||| | ||||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
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Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 7
US-10-679-999-5
; Sequence 5, Application US/10679999
; Publication No. US20040067520A1
;  GENERAL INFORMATION:
;       APPLICANT: Mann, Michael B.
;                  Hecht, Randy I.
;       TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                           METHODS
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Amgen Inc.
;            STREET: 1840 DeHavilland Drive
;            CITY: Thousand Oaks
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 91320-1789
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/679,999
;            FILING DATE: 06-Oct-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/568,528
;            FILING DATE: 09-May-2000
;            APPLICATION NUMBER: 09/267,517
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Knight, Matthew W.
;            REGISTRATION NUMBER: 36,846
;            REFERENCE/DOCKET NUMBER: A-416
;  INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 454 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-679-999-5

  Query Match             38.3%;  Score 440.8;  DB 13;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 1.8e-129;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
              |||||||||||||||||||||||||||||||||||||||| | ||||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302
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Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
              |||||||||||||||||||||||||||||||
Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 8
US-10-214-037-5
; Sequence 5, Application US/10214037
; Publication No. US20030054997A1
;  GENERAL INFORMATION:
;       APPLICANT: Pelleymounter, Mary Ann
;                  Hecht, Randy I
;                  Mann, Michael B
;       TITLE OF INVENTION: OB PROTEIN COMPOSITIONS AND METHODS
;       NUMBER OF SEQUENCES: 6
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Amgen Inc.
;            STREET: 1840 Dehavilland Drive
;            CITY: Thousand Oaks
;            STATE: California
;            COUNTRY: U.S.A.
;            ZIP: 91230-1789
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/214,037
;            FILING DATE: 05-Aug-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/920,608
;            FILING DATE: 07-JUN-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Pessin, Karol M.
;            REFERENCE/DOCKET NUMBER: A-345
;  INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 454 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-214-037-5

  Query Match             38.3%;  Score 440.8;  DB 15;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 1.8e-129;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
              ||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
              |||||||||||||||||||||||||||||||||||||||||||| | ||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
              |||||||||||||||||||||||||||||||
Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 9
US-09-366-133-2
; Sequence 2, Application US/09366133
; Patent No. US20020009798A1
;  GENERAL INFORMATION:
;    APPLICANT:  Pelleymounter, Mary Ann
;    APPLICANT:  Hecht, Randy I
;    APPLICANT:  Mann, Michael B
;    TITLE OF INVENTION:  OB PROTEIN COMPOSITIONS AND METHODS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  91230-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/366,133
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/920,608
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pessin, Karol M.
;      REFERENCE/DOCKET NUMBER:  A-345
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-366-133-2

  Query Match             32.9%;  Score 378.4;  DB 9;  Length 491;
  Best Local Similarity   89.8%;  Pred. No. 1.3e-109;
  Matches  406;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
              ||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              |||||||||||||||||||||||||||||||||   | ||||||||  ||||| || ||
Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
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                    |||||||||||||||||||||||||||| | ||||||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
                |||||||||||| | |||||||| ||||||||  |||||| | |||||| |||||||
Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
                |||||||||||||||||||||||||||| ||||||||||||||||||||||||  ||||||
Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
                  | | |||||||||  |||  | |||  || ||||  ||||||||||||||||||   ||
Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||  |||
Db        400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
                ||||||| | |||||||  ||||||||||||
Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491


RESULT 10
US-10-679-999-2
; Sequence 2, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 491 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-679-999-2

  Query Match             32.9%;  Score 378.4;  DB 13;  Length 491;
  Best Local Similarity   89.8%;  Pred. No. 1.3e-109;
  Matches  406;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;
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Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
                ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
                |||||||||||||||||||||||||||||||    | ||||||||    |||||  ||  ||
Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
                |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
                |||||||||||| | |||||||| ||||||||  |||||| | |||||| |||||||
Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
                |||||||||||||||||||||||||||||| ||||||||||||||||||||||  ||||||
Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
                  | | |||||||||  |||  | |||  || ||||  ||||||||||||||||||   ||
Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||  |||
Db        400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
                ||||||| | |||||||  ||||||||||||
Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491


RESULT 11
US-10-214-037-2
; Sequence 2, Application US/10214037
; Publication No. US20030054997A1
;   GENERAL INFORMATION:
;        APPLICANT: Pelleymounter, Mary Ann
;                   Hecht, Randy I
;                   Mann, Michael B
;        TITLE OF INVENTION: OB PROTEIN COMPOSITIONS AND METHODS
;        NUMBER OF SEQUENCES: 6
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 Dehavilland Drive
;             CITY: Thousand Oaks
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 91230-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/214,037
;             FILING DATE: 05-Aug-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/920,608
;             FILING DATE: 07-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Pessin, Karol M.
;             REFERENCE/DOCKET NUMBER: A-345
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 491 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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US-10-214-037-2

Query Match 32.9%; Score 378.4; DB 15; Length 491;
Best Local Similarity 89.8%; Pred. No. 1.3e-109;
Matches 406; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              ||||||||||||||||||||||||||||||||    | ||||||||   ||||| || ||
Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              |||||||||||||||||||||||||||| | ||||||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
              |||||||||||||  | |||||||||  ||||||| | |||||| |||||||
Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
              |||||||||||||||||||||||||||| ||||||||||||||||||||||  ||||||
Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
                | | |||||||||  |||  | |||  || ||||  ||||||||||||||||||||    ||
Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||  |||
Db        400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
              |||||||  | |||||||  ||||||||||||
Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491
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RESULT 12
US-10-097-044A-12
; Sequence 12, Application US/10097044A
; Publication No. US20030143220A1
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/097,044A
; FILING DATE: 28-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0444P1C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-097-044A-12

Query Match 3.7%; Score 43; DB 15; Length 468;
Best Local Similarity 49.5%; Pred. No. 0.0063;
Matches 143; Conservative 0; Mismatches 140; Indels 6; Gaps 1;

```
Qy        394 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 453
              | ||||   || | || | | || |||||    ||  || |||          | |
Db        127 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 186

Qy        454 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 507
              |    |||||| | ||   ||||||||||||| ||   |   ||  ||||      |||
Db        187 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 246

Qy        508 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 567
              | |       ||  |||  |||  | |  |||       |       |       |  ||| ||
Db        247 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 306

Qy        568 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 627
              |||  |  ||||  |||||  ||  ||  ||  |||       |   || |    || |||
Db        307 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 366

Qy        628 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 676
              | | | |||   ||  |  |||  |||  |||  |   |  |  |||  |||
Db        367 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 415
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RESULT 13
US-10-156-761-6640/c
; Sequence 6640, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 6640
; LENGTH: 1116
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS

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;   LOCATION: (1)..(1116)
US-10-156-761-6640

  Query Match             3.7%;  Score 42.4;  DB 15;  Length 1116;
  Best Local Similarity   51.0%;  Pred. No. 0.014;
  Matches  100;  Conservative    0;  Mismatches   96;  Indels    0;  Gaps    0;

Qy        449 AGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCT 508
              ||  | ||| |  |   ||   | || ||  ||| ||| || |||     | |||| |
Db        706 AGGAGAACTCGGGGTCGAAGACCCGGACGACCGGGGCGCCGTCGCGCTCGCCCACCATGA 647

Qy        509 CGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGA 568
              || | |||||  |    |   | | | || | | | || || | ||| |   |  |
Db        646 CGCTGCCCGTGTGGAGGTCACCGTGGAGCGGGGCCTGCGCGCTCGTCATGAAGACGTGGC 587

Qy        569 GGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGA 628
              ||| |  || ||  ||| |     ||| |  ||   ||   | ||  | | ||  |  |
Db        586 GGAGGTCGGCGACCTCGGTGCGCAGGCGCGGGTCGGCGCGGAACGCGGCCGCCAGGTCGT 527

Qy        629 AGAGTACGAGGCACTA 644
              |||| || ||  | |
Db        526 CGAGTCCGGGGTGCCA 511


RESULT 14
US-10-465-217-13/c
; Sequence 13, Application US/10465217
; Publication No. US20030204859A1
; GENERAL INFORMATION:
;  APPLICANT: Kazemi-Esfarjani, Parsa
;  APPLICANT:  Benzer, Seymour
;  TITLE OF INVENTION: AN ANIMAL MODEL OF POLYGLUTAMINE
;  TITLE OF INVENTION:  TOXICITY, METHODS OF USE, AND MODULATORS OF POLYGLUTAMINE
;  TITLE OF INVENTION:  TOXICITY
;  FILE REFERENCE: 06618-686001
;  CURRENT APPLICATION NUMBER: US/10/465,217
;  CURRENT FILING DATE:  2003-06-18
;  PRIOR APPLICATION NUMBER: US/09/639,207
;  PRIOR FILING DATE: 2000-08-14
;  PRIOR APPLICATION NUMBER: US 60/148,934
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: US 60/148,933
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: US 60/177,047
;  PRIOR FILING DATE: 2000-01-18
;  PRIOR APPLICATION NUMBER: US 60/205,720
;  PRIOR FILING DATE: 2000-05-19
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 486
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-10-465-217-13

  Query Match             3.5%;  Score 40.4;  DB 13;  Length 486;
  Best Local Similarity   45.2%;  Pred. No. 0.043;
  Matches  149;  Conservative    0;  Mismatches  181;  Indels    0;  Gaps    0;

Qy         97 TTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTG 156
              ||    | | |||| |  |      | |  | | |  || | ||    |  | |  ||
Db        375 TTGCTGCTGCTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTG 316

Qy        157 CACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTA 216
              |  | | |||| |||    | | | |  ||||    |||  |||| |   ||  |   |
Db        315 CTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGCTGCTGCTG 256

Qy        217 TTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAG 276
              || | |||  |  ||       | ||  |  |||||  ||   ||    |   || ||| |
Db        255 TTGCTGTTGTTGTTGCTGTTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTGCTG 196

Qy        277 GAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTG 336
              |  |  |     ||  | |||     | | | |  ||||    | | | |  ||||
Db        195 CTGCTGTTGCTGTTGCTGCTGCTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTG 136

Qy        337 TTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTT 396
              |  | |  |  | | |  ||| | | || | | | | |||  |  |  |  ||
Db        135 CTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTG 76

Qy        397 GGTGTCCACATGTGGGACGGGGGTAGGGCC 426
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Db         75 TTGCTGCTGCTGGGGGGTTGACGGTGGGCC 46


RESULT 15
US-09-229-200A-13
; Sequence 13, Application US/09229200A
; Patent No. US20020099179A1
;  GENERAL INFORMATION:
;       APPLICANT: Jolliffe et al.
;       TITLE OF INVENTION: CD4 Specific Recombinant Antibody
;       NUMBER OF SEQUENCES: 28
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Johnson & Johnson
;            STREET: One Johnson & Johnson Plaza
;            CITY: New Brunswick
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 08933-7003
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;            COMPUTER: IBM
;            OPERATING SYSTEM: PC-DOS
;            SOFTWARE: <Unknown>
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/229,200A
;            FILING DATE: 13-Jan-1999
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: John W. Wallen, III
;            REGISTRATION NUMBER: 35,403
;            REFERENCE/DOCKET NUMBER: ORT-948
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (858) 784-3239
;            TELEFAX: (908) 524-2808
;   INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 754
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       ANTI-SENSE: no
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-229-200A-13

  Query Match             3.5%;  Score 40.4;  DB 9;  Length 754;
  Best Local Similarity   49.3%;  Pred. No. 0.052;
  Matches  138;  Conservative    0;  Mismatches  136;  Indels    6;  Gaps    1;

Qy        403 CACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACG 462
              || | || | | || ||||    ||  || |||          | |    |   |||
Db        411 CAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGACAACACACG 470

Qy        463 GACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTCTCGTTACCC 516
              ||| | ||   |||||||||||| ||    |  ||  ||||      |||  | |
Db        471 GACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTATTGCGGGAG 530

Qy        517 GTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAG 576
              || ||| |||  | |  |||          |         |   ||| || ||| | |
Db        531 GTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCGTGGATGTCG 590

Qy        577 GAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACG 636
              |||  |||||  || ||  ||  |||        | ||  |   || |||| | | |||
Db        591 GAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAGATGCGGACG 650
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Qy        637 AGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 676
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Db        651 CTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 690
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Search completed: May 9, 2004, 11:51:56
Job time : 373.25 secs

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Db        430 ACAGAGATCTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGA 371

Qy        989 CGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTC 1048

Db        370 CCAAGGAAGAGCTTTGAAGGCCTGAGGTCTGCGAAAGGTGGGAGGAGGCAGACGCCCTGC 311

Qy       1049 GTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1088

Db        310 GTGGCCCATGGTCGGGGCGTCCACGCCGAGGCCGGCAACA 271


RESULT 10
BW265514/c
LOCUS       BW265514                658 bp    mRNA    linear   EST 09-NOV-2002
DEFINITION  BW265514 Nori Satoh unpublished cDNA library, gastrula and neurula
            Ciona intestinalis cDNA clone cign040o10 5', mRNA sequence.
ACCESSION   BW265514
VERSION     BW265514.1  GI:24845432
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 658)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .658
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cign040o10"
                     /tissue_type="whole body"
                     /dev_stage="gastrula and neurula"
                     /clone_lib="Nori Satoh unpublished cDNA library, gastrula
                     and neurula"
ORIGIN

  Query Match             3.8%;  Score 43.2;  DB 13;  Length 658;
  Best Local Similarity   44.1%;  Pred. No. 33;
  Matches  180;  Conservative    0;  Mismatches  228;  Indels    0;  Gaps    0;

Qy        180 GTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCT 239

Db        566 GTTGTTGTTGTTGTAGTTGCTGCTGCTGCTGTTGTTGTTGCTGTAGTTGGTGGTGATGTG 507

Qy        240 CCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGAC 299

Db        506 TTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATTTCGTGTTGTTGCT 447

Qy        300 CGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCT 359

Db        446 GTTGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTT 387

Qy        360 CTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGG 419

Db        386 CCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTT 327

Qy        420 TAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGAT 479

Db        326 GGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGCTGTTGTTGTT 267

Qy        480 AGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTG 539

Db        266 GGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGTTGTTGTTGTTGTT 207

Qy        540 GTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTT 587

Db        206 GGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGT 159


RESULT 11
BW259047/c
LOCUS       BW259047                663 bp    mRNA    linear   EST 09-NOV-2002
DEFINITION  BW259047 Nori Satoh unpublished cDNA library, gastrula and neurula
            Ciona intestinalis cDNA clone cign001j16 5', mRNA sequence.
ACCESSION   BW259047
VERSION     BW259047.1  GI:24838965
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 663)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .663
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cign001j16"
                     /tissue_type="whole body"
                     /dev_stage="gastrula and neurula"
                     /clone_lib="Nori Satoh unpublished cDNA library, gastrula
                     and neurula"
ORIGIN

  Query Match             3.8%;  Score 43.2;  DB 13;  Length 663;
  Best Local Similarity   44.1%;  Pred. No. 33;
  Matches  180;  Conservative    0;  Mismatches  228;  Indels    0;  Gaps    0;

Qy        180 GTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCT 239

Db        566 GTTGTTGTTGTTGTAGTTGCTGCTGCTGCTGTTGTTGTTGCTGTAGTTGGTGGTGATGTG 507

Qy        240 CCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGAC 299

Db        506 TTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATTTCGTGTTGTTGCT 447

Qy        300 CGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCT 359

Db        446 GTTGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTT 387

Qy        360 CTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGG 419

Db        386 CCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTT 327

Qy        420 TAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGAT 479

Db        326 GGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGCTGTTGTTGTT 267

Qy        480 AGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTG 539

Db        266 GGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGTTGTTGTTGTTGTT 207

Qy        540 GTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTT 587

Db        206 GGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGT 159
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Db        182 GTTGTTGTTGTTGATGTTGTTGGTGCTTCTGTAGTTGCCGCTGTTGATATTGGCGGTGAT 123

Qy        582 GTCGTTCGAGT 592
Db        122 TGCGCTTTTGT 112
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RESULT 8
CA128348
LOCUS CA128348 1039 bp mRNA linear EST 24-SEP-2003
DEFINITION SCJLLR2006A05.g LR2 Saccharum officinarum cDNA clone SCJLLR2006A05 5', mRNA sequence.
ACCESSION CA128348
VERSION CA128348.1 GI:35009126
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE 1 (bases 1 to 1039)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 006 row: A column: 05
Seq primer: T7 Promoter Primer.
FEATURES Location/Qualifiers
source 1. .1039
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCJLLR2006A05"
/lab_host="DH10B"
/clone_lib="LR2"
/note="Organ: Leaf roll from field grown adult plants (small insert library); Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [Leaf roll from field grown adult plants (small insert library)]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
ORIGIN

Query Match 3.8%; Score 43.6; DB 13; Length 1039;
Best Local Similarity 45.6%; Pred. No. 33;
Matches 154; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

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Qy        442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501
Db        303 TCGGTGGAGACGTACAAGATCTACATCTTCAAGGTGCTGAAGCAGGTGCACCCGGACATC 362

Qy        502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561
Db        363 TGCATCTCGTCCAAGGCCATGTCCATCATGAACTTCTTCATCAACGACATCTTCCATAAG 422

Qy        562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621
Db        423 CTGGCGGCGGAGGCGGCCAAACTGGCGCGCTACAACAAGAAGCCCACCATCACGTGCCGC 482

Qy        622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681
Db        483 GAGATCCAGACTTTCGTCCGCCTCGTCCTCCCCGGCGAGCTCGCCAAGCACGCCTTCTTC 542

Qy        682 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 741
Db        543 GAGGTGCACCAAGGCCGTTACCAAGTTCACCAGCTCCTATGCGAGCGATGGGACCTGCCT 602

Qy        742 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGT 779
Db        603 TAGTTTCGTTCATGAAGTACTAGTGTGTTGTCGTGTGT 640
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RESULT 9
AI869699/c
LOCUS AI869699 486 bp mRNA linear EST 07-MAR-2000
DEFINITION wm02f07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2433253 3' similar to gb:J05016 PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AI869699
VERSION AI869699.1 GI:5543667
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 486)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 751 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 282.
FEATURES Location/Qualifiers
source 1. .486
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2433253"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Brn25"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATAGGTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN

Query Match 3.8%; Score 43.2; DB 9; Length 486;
Best Local Similarity 54.4%; Pred. No. 28;
Matches 87; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

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Qy        929 AGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGA 988
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Db        309 TGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGC 250

Qy        482 GGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGT 541

Db        249 TGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGTTGGTGTTGTTGT 190

Qy        542 GCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGT 601

Db        189 TGTTGGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGTGCTTCTGT 130

Qy        602 TCTCGTC 608

Db        129 AGTTGCC 123


RESULT 6
BW192111/c
LOCUS       BW192111                602 bp    mRNA    linear   EST 05-NOV-2002
DEFINITION  BW192111 Nori Satoh unpublished cDNA library, young adult Ciona
            intestinalis cDNA clone ciad095m14 5', mRNA sequence.
ACCESSION   BW192111
VERSION     BW192111.1  GI:24606513
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 602)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .602
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
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                     /clone="ciad095m14"
                     /tissue_type="whole animal"
                     /dev_stage="young adult"
                     /clone_lib="Nori Satoh unpublished cDNA library, young
                     adult"
ORIGIN

  Query Match             4.0%;  Score 45.8;  DB 13;  Length 602;
  Best Local Similarity   45.8%;  Pred. No. 7.9;
  Matches  158;  Conservative    0;  Mismatches  187;  Indels    0;  Gaps    0;

Qy        248 TGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTAC 307

Db        444 TGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGTTCC 385

Qy        308 CGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGT 367

Db        384 TGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGT 325

Qy        368 AGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCC 427

Db        324 TGTTCCTGTTGGTGCCGTTGTTGTCCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGA 265

Qy        428 TACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGC 487

Db        264 TGCTGTTGTTGTTGTTGATGATGCTGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGC 205

Qy        488 TGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAG 547

Db        204 TGTTGTTGTTGGTGTTGCTGTTGTTGGCGCTGCTGTTGTTGTTGTTGATGTTGTTGGTGC 145

Qy        548 GGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGT 592

Db        144 TTCTGTAGTTGCCGCTGTTGATATTGGCGGTGATTGCGCTTTTGT 100


RESULT 7
BW314712/c
LOCUS       BW314712                617 bp    mRNA    linear   EST 11-NOV-2002
DEFINITION  BW314712 Nori Satoh unpublished cDNA library, heart Ciona
            intestinalis cDNA clone ciht039h07 5', mRNA sequence.
ACCESSION   BW314712
VERSION     BW314712.1  GI:24895396
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 617)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .617
                     /organism="Ciona intestinalis"
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                     /db_xref="taxon:7719"
                     /clone="ciht039h07"
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ORIGIN

  Query Match             4.0%;  Score 45.8;  DB 13;  Length 617;
  Best Local Similarity   43.2%;  Pred. No. 8;
  Matches  212;  Conservative    0;  Mismatches  279;  Indels    0;  Gaps    0;

Qy        102 GTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTC 161

Db        602 GTTGCTGTTTCTGTGTTCGGTGTATTNTGTGTTGTTGTTGTTGTNGTAGTTGCTGCTGCT 543

Qy        162 GGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACG 221

Db        542 GCTGTTGTTGTTGCTGTAGTTGGTGGTGATGTGTTTTGTGTTGTTCTTGTATTAGGCGTT 483

Qy        222 GTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTG 281

Db        482 GTTGTTGATGTATTTCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGT 423

Qy        282 GCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCG 341

Db        422 GCTGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCT 363

Qy        342 GGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGT 401

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Qy        402 CCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGAC 461

Db        302 GCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGTTGATGATGCTGTTGTTGTT 243

Qy        462 GGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGG 521

Db        242 GGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGCTGTTGTTGGCGCTGCT 183

Qy        522 CCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGAT 581
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Qy        242 TCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCG 301
Db        506 TGGTGGTGATGTGTTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATT 447

Qy        302 ACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCT 361
Db        446 TCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCC 387

Qy        362 TTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTA 421
Db        386 TGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGT 327

Qy        422 GGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAG 481
Db        326 TGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGC 267

Qy        482 GGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGT 541
Db        266 TGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGTTGTTGT 207

Qy        542 GCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAG 591
Db        206 TGGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGTG 157
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RESULT 4
BW249566/c
LOCUS BW249566 546 bp mRNA linear EST 09-NOV-2002
DEFINITION BW249566 Nori Satoh unpublished cDNA library, tailbud embryo Ciona intestinalis cDNA clone citb082d19 5', mRNA sequence.
ACCESSION BW249566
VERSION BW249566.1 GI:24829484
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 546)
AUTHORS Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
TITLE Expressed genes in Ciona intestinalis (2002c)
JOURNAL Unpublished (2002)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES Location/Qualifiers
source 1. .546
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="citb082d19"
/tissue_type="whole animal"
/dev_stage="tailbud embryo"
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ORIGIN

Query Match 4.1%; Score 47; DB 13; Length 546;
Best Local Similarity 45.5%; Pred. No. 4;
Matches 167; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

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Qy        242 TCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCG 301
Db        512 TGGTGGTGATGTGTTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATT 453

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Db        452 TCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCC 393

Qy        362 TTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTA 421
Db        392 TGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGT 333

Qy        422 GGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAG 481
Db        332 TGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGC 273

Qy        482 GGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGT 541
Db        272 TGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGTTGGTGTTGTTGT 213

Qy        542 GCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGT 601
Db        212 TGTTGGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGTGCTTCTGT 153

Qy        602 TCTCGTC 608
Db        152 AGTTGCC 146
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RESULT 5
BW193819/c
LOCUS BW193819 660 bp mRNA linear EST 05-NOV-2002
DEFINITION BW193819 Nori Satoh unpublished cDNA library, cleaving embryo Ciona intestinalis cDNA clone cicl101p23 5', mRNA sequence.
ACCESSION BW193819
VERSION BW193819.1 GI:24608221
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 660)
AUTHORS Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
TITLE Expressed genes in Ciona intestinalis (2002c)
JOURNAL Unpublished (2002)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES Location/Qualifiers
source 1. .660
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/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cicl101p23"
/tissue_type="whole body"
/dev_stage="cleaving embryo"
/clone_lib="Nori Satoh unpublished cDNA library, cleaving embryo"
ORIGIN

Query Match 4.1%; Score 47; DB 13; Length 660;
Best Local Similarity 45.5%; Pred. No. 4.3;
Matches 167; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

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Db        489 TGGTGGTGATGTGTTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATT 430

Qy        302 ACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCT 361
Db        429 TCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCC 370

Qy        362 TTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTA 421
Db        369 TGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGT 310

Qy        422 GGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAG 481
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/db_xref="taxon:7719"
/clone="cilv05e12"
/tissue_type="whole animal"
/dev_stage="larva"
/clone_lib="Nori Satoh unpublished cDNA library, larva"

ORIGIN

Query Match 4.2%; Score 48.8; DB 9; Length 527;
Best Local Similarity 45.8%; Pred. No. 1.5;
Matches 167; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

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Qy        242 TCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCG 301
Db        476 TGGTGGTGATGTGTTNTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATT 417

Qy        302 ACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCT 361
Db        416 TCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCC 357

Qy        362 TTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTA 421
Db        356 TGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGT 297

Qy        422 GGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAG 481
Db        296 TGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGC 237

Qy        482 GGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGT 541
Db        236 TGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGTTGTTGT 177

Qy        542 GCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGT 601
Db        176 TGGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGTGCTTCTGTAGT 117

Qy        602 TCTCG 606
Db        116 TGCCG 112
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RESULT 2
BW035294/c
LOCUS BW035294 610 bp mRNA linear EST 13-OCT-2002
DEFINITION BW035294 Nori Satoh unpublished cDNA library, blood cells Ciona intestinalis cDNA clone cibd028f16 5', mRNA sequence.
ACCESSION BW035294
VERSION BW035294.1 GI:23951246
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 610)
AUTHORS Satou,Y., Satake,M., Azumi,K., Nonaka,M., Shin-i,T., Kohara,Y. and Satoh,N.
TITLE Expressed genes in Ciona intestinalis (2002)
JOURNAL Unpublished (2002)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES Location/Qualifiers
source 1. .610
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cibd028f16"
/tissue_type="blood cells"
/clone_lib="Nori Satoh unpublished cDNA library, blood cells"

ORIGIN

Query Match 4.2%; Score 48.2; DB 13; Length 610;
Best Local Similarity 45.8%; Pred. No. 2.2;
Matches 167; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

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Qy        242 TCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCG 301
Db        475 TGGTGGTGATGTGTTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGATGTATT 416

Qy        302 ACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCT 361
Db        415 TCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCC 356

Qy        362 TTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTA 421
Db        355 TGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGT 296

Qy        422 GGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAG 481
Db        295 TGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGC 236

Qy        482 GGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGT 541
Db        235 TGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGTTGTTGT 176

Qy        542 GCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGT 601
Db        175 TGGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGTGCTTCTGTAGT 116

Qy        602 TCTCG 606
Db        115 TGCCG 111
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RESULT 3
BW251013/c
LOCUS BW251013 619 bp mRNA linear EST 09-NOV-2002
DEFINITION BW251013 Nori Satoh unpublished cDNA library, tailbud embryo Ciona intestinalis cDNA clone citb088l19 5', mRNA sequence.
ACCESSION BW251013
VERSION BW251013.1 GI:24830931
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 619)
AUTHORS Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
TITLE Expressed genes in Ciona intestinalis (2002c)
JOURNAL Unpublished (2002)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES Location/Qualifiers
source 1. .619
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="citb088l19"
/tissue_type="whole animal"
/dev_stage="tailbud embryo"
/clone_lib="Nori Satoh unpublished cDNA library, tailbud embryo"

ORIGIN

Query Match 4.1%; Score 47.6; DB 13; Length 619;
Best Local Similarity 46.0%; Pred. No. 3.1;
Matches 161; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 13:07:09 ; Search time 2222.5 Seconds
(without alignments)
15451.747 Million cell updates/sec

Title: US-10-679-999-8
Perfect score: 1150
Sequence: 1 GTATACCTTGGGTTTAGAAC.....AGGCCCAACAATTACCTAGG 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 54314686

Minimum DB seq length: 0
Maximum DB seq length: 1150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	48.8	4.2	527	9	AV962678	AV962678 AV962678
c	2	48.2	4.2	610	13	BW035294	BW035294 BW035294
c	3	47.6	4.1	619	13	BW251013	BW251013 BW251013
c	4	47	4.1	546	13	BW249566	BW249566 BW249566
c	5	47	4.1	660	13	BW193819	BW193819 BW193819
c	6	45.8	4.0	602	13	BW192111	BW192111 BW192111
c	7	45.8	4.0	617	13	BW314712	BW314712 BW314712
	8	43.6	3.8	1039	13	CA128348	CA128348 SCJLLR200
c	9	43.2	3.8	486	9	AI869699	AI869699 wm02f07.x
c	10	43.2	3.8	658	13	BW265514	BW265514 BW265514
c	11	43.2	3.8	663	13	BW259047	BW259047 BW259047
	12	43.2	3.8	910	29	CNS006ON	AL065629 Drosophil
c	13	42.8	3.7	509	10	BF593096	BF593096 7o56e02.x
c	14	42.8	3.7	552	14	CA686322	CA686322 wlm96.pk0
c	15	42.8	3.7	587	12	BP504875	BP504875 BP504875
c	16	42.6	3.7	642	13	CA012935	CA012935 HT06O08r
c	17	42.6	3.7	649	14	CD907542	CD907542 G468.107E
c	18	42.6	3.7	673	13	CA014102	CA014102 HT10G06r
c	19	42.6	3.7	725	14	CD910343	CD910343 G550.001A
c	20	42.6	3.7	763	14	CD906072	CD906072 G468.103N
c	21	42.6	3.7	838	12	BI948448	BI948448 HVSME1000
c	22	42.2	3.7	512	9	AI289506	AI289506 qw28e11.x
c	23	42.2	3.7	586	9	AI687271	AI687271 tp94e04.x
c	24	42.2	3.7	659	13	CA014547	CA014547 HT11K11r
	25	42	3.7	645	29	CNS012I3	AL101589 Drosophil
	26	41.8	3.6	343	9	AA330793	AA330793 EST34531
	27	41.8	3.6	1101	29	CNS00LXJ	AL078875 Drosophil
	28	41.6	3.6	337	14	CB047414	CB047414 NISC_gg02
	29	41.6	3.6	340	9	AA302570	AA302570 EST15740
c	30	41.6	3.6	408	14	CA720412	CA720412 wkm2n.pk0
c	31	41.6	3.6	414	12	BJ248630	BJ248630 BJ248630
c	32	41.6	3.6	439	10	BE488609	BE488609 WHE1051_G
c	33	41.6	3.6	442	14	CA719617	CA719617 wkm2n.pk0
c	34	41.6	3.6	443	9	AI582641	AI582641 tn47h04.x
c	35	41.6	3.6	443	14	CA656554	CA656554 wlm0.pk00
c	36	41.6	3.6	447	14	CA687517	CA687517 wlm96.pk0
c	37	41.6	3.6	448	14	CA692819	CA692819 wlm96.pk0
c	38	41.6	3.6	451	9	AI083954	AI083954 oz53b09.x
c	39	41.6	3.6	451	10	AW276084	AW276084 xq45c08.x
c	40	41.6	3.6	455	10	AW590575	AW590575 hg46c10.x
c	41	41.6	3.6	458	9	AW088852	AW088852 xd31e06.x
c	42	41.6	3.6	463	10	BF056551	BF056551 7k06g10.x
	43	41.6	3.6	466	10	AW673691	AW673691 ba56g10.y
c	44	41.6	3.6	467	9	AI752976	AI752976 cr03b09.x
c	45	41.6	3.6	467	9	AI879509	AI879509 au53d05.x

ALIGNMENTS

RESULT 1
AV962678/c
LOCUS AV962678 527 bp mRNA linear EST 14-MAR-2002
DEFINITION AV962678 Nori Satoh unpublished cDNA library, larva Ciona intestinalis cDNA clone cilv05e12 5', mRNA sequence.
ACCESSION AV962678
VERSION AV962678.1 GI:19450977
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 527)
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES Location/Qualifiers
source 1. .527
/organism="Ciona intestinalis"
/mol_type="mRNA"

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RESULT 12
CNS006ON
LOCUS       CNS006ON                910 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR14J21 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL065629
VERSION     AL065629.1  GI:4944698
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 910)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .910
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR14J21"
                     /clone_lib="RPCI-98"
                     /note="end : T7"
ORIGIN

  Query Match             3.8%;  Score 43.2;  DB 29;  Length 910;
  Best Local Similarity   19.2%;  Pred. No. 38;
  Matches   81;  Conservative  159;  Mismatches  180;  Indels    2;  Gaps    1;

Qy        330 GAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG 389
              | ||: |  : ||| ||| :|||||  | | |:|: |  : ||    |:  :::: |
Db        468 GGGGKGGGGKGGGGGGGGGHGGGGGSGGGTDTKTWTGGKSTGGGGGGGSSGGSSSKGGGC 527

Qy        390 GGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCA 449
              |:  :  || |:      : ||| :::| :  :::::: :  : ::| : :   | |:
Db        528 GSGSYGGGGGGYGGTGSGSGGGGSSSSGCSSSSSSSSSSSSCGSSSBGCBSSCGCGSCSY 587

Qy        450 GTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTC 509
              : ::  :||:   | :: :   ::     | :::|:||    : ::: :| : : : :|
Db        588 SSSSTGSTGSCGCGSSSSSSSSSSCSSTSTSSSSTSGCGYSSSGSBSSSCSSTBTSSSTT 647

Qy        510 GTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAG 569
              :|:  : :|:: ::|:|  ||: |:|::: ::|::: : :: ::  : : ::: ::: :
Db        648 BTBTKBTSTYSTSYTST--TTSTTSTBSBTSYGSBBKSTSSTSSSTSSSTSSSSSSSTSS 705

Qy        570 GAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAA 629
                  : : :::::||:   |: : ::|  |:: ::   : :    : : :| : :
Db        706 CTSTKBYSTSTBSYSBTTBTBTTSTSTBBTTSTBYTBBTTBYTKSTTSMTSTYTTBBSTS 765

Qy        630 GAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGA 689
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Db        766 KBSTBTSTBKSTGTKTBTSBTTSCTSSSSSBSTSYSYSTSCBSSBSBSSTSYSBCTSTST 825

Qy        690 CAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTG 749
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Db        826 STSSBBSSBSSSSSCGTSBTSSSTSTTSTCTSTTCKTSTGBSSYGTGTSTYTTBTTTATT 885

Qy        750 CT 751
              :|
Db        886 ST 887


RESULT 13
BF593096/c
LOCUS       BF593096                509 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  7o56e02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578187 3'
            similar to TR:Q29305 Q29305 DISULFIDE ISOMERASE-RELATED PROTEIN ;,
            mRNA sequence.
ACCESSION   BF593096
VERSION     BF593096.1  GI:11685420
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 509)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 405.
FEATURES             Location/Qualifiers
     source          1. .509
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                     /mol_type="mRNA"
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                     /clone="IMAGE:3578187"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Kid11"
                     /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
                     prepared, and ss circles were made in vitro. Following HAP
                     purification, this DNA was used as tracer in a subtractive
                     hybridization reaction. The driver was PCR-amplified cDNAs
                     from a pool of 5,000 clones made from the same library
                     (cloneIDs 1322376-1323911, 1456007-1456775, and
                     1500552-1502855). Subtraction by Bento Soares and M.
                     Fatima Bonaldo. "
ORIGIN

  Query Match             3.7%;  Score 42.8;  DB 10;  Length 509;
  Best Local Similarity   54.4%;  Pred. No. 36;
  Matches   86;  Conservative    0;  Mismatches   72;  Indels    0;  Gaps    0;

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Db        425 AGAAATCTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGACC 366

Qy        991 GTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGT 1050
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Db        365 AAGGAAGAGCTTTGAAGGCCTGAGGTCTGCGGAAGGTGGGAGGAGGCAGACGCCCTGCGT 306

Qy       1051 AGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1088
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Db        305 GGCCCATGGTCGGGGCGTCCACACCGAGGCCGGCAACA 268
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RESULT 14
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LOCUS CA686322 552 bp mRNA linear EST 25-NOV-2002
DEFINITION wlm96.pk032.g24 wlm96 Triticum aestivum cDNA clone wlm96.pk032.g24 5' end, mRNA sequence.
ACCESSION CA686322
VERSION CA686322.1 GI:25275677
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 552)
AUTHORS Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z., Miao,G., Caraher,N. and Hanafey,M.K.
TITLE DuPont Wheat cDNA Sequence
JOURNAL Unpublished (2002)
COMMENT Contact: Scott V. Tingey
Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
FEATURES Location/Qualifiers
source 1. .552
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Stephens"
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/tissue_type="leaf"
/clone_lib="wlm96"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2: XhoI; Wheat (Triticum aestivum L.) seedlings 96 hr after inoculation w/ E. graminis"
ORIGIN

Query Match 3.7%; Score 42.8; DB 14; Length 552;
Best Local Similarity 48.0%; Pred. No. 37;
Matches 119; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

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Qy        417 GGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAA 476
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Qy        477 GATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTT 536
Db        287 GGTGCAGTTGGTGCAGGTGCAGCTGGCGCCGCACTTGCACTTGCCGTCGTTCTCCGCGGC 228

Qy        537 CTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCA 596
Db        227 CTCCTGCACCTCGAAGTGNCTCTTNTCGGTGTCGACCATGACGATGCCGTAGCCGTCGCC 168

Qy        597 CCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGA 656
Db        167 CTTCTTCACGCACTGGGTCTTGTCGGCGCAGTCGCAGTTGCCGCACTTGTCAGCCATGGC 108

Qy        657 CGTGTTGG 664
Db        107 GGTCTTGG 100
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RESULT 15
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LOCUS BP504875 587 bp mRNA linear EST 16-SEP-2003
DEFINITION BP504875 Hydra magnipapillata cDNA library Hydra magnipapillata cDNA clone hm_02377, mRNA sequence.
ACCESSION BP504875
VERSION BP504875.1 GI:34771004
KEYWORDS EST.
SOURCE Hydra magnipapillata
ORGANISM Hydra magnipapillata
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae; Hydridae; Hydra.
REFERENCE 1 (bases 1 to 587)
AUTHORS Hayakawa,S., Hwang,J.S., Nishimiya-Fujisawa,C., Ogura,A., Ikeo,K., Fujisawa,T. and Gojobori,T.
TITLE Hydra EST project
JOURNAL Unpublished (2003)
COMMENT Contact: Jung Shan Hwang
Center for Information Biology and DNA Data Bank of Japan
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-55-981-6847(ex.6898)
Fax: 81-55-981-6848
Email: jhwang@lab.nig.ac.jp, URL:http://www.cib.nig.ac.jp.
FEATURES Location/Qualifiers
source 1. .587
/organism="Hydra magnipapillata"
/mol_type="mRNA"
/strain="105"
/db_xref="taxon:6085"
/clone="hm_02377"
/tissue_type="whole body"
/dev_stage="adult budding stage"
/clone_lib="Hydra magnipapillata cDNA library"
ORIGIN

Query Match 3.7%; Score 42.8; DB 12; Length 587;
Best Local Similarity 46.9%; Pred. No. 38;
Matches 169; Conservative 0; Mismatches 187; Indels 4; Gaps 1;

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Qy         49 GGTCGTGGACTTGAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTG 108
Db        538 GGTGGTGGGCAAGATGGTACGCCTTGCATAACGCAGATATCTGCGCATAGTCGGTGCTTG 479

Qy        109 TGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTT 168
Db        478 TGGTCGTGGTAGAGCGTCTGG----TAGTGATTGTGGTGCTATGGGTCCATTTGGTCCTG 423

Qy        169 CTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGT 228
Db        422 GTGGTCCAATTGGTCCATGTGGTCATGGCACACCTGGTGGTCCTGGTGGTACTGCTGGTC 363

Qy        229 TTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGAC 288
Db        362 CAATGGGTCCTGGTCCTCCTGGTGGTCCGGGTGGTCCAGCTGTAGCTTCTGGTGGTCCTG 303

Qy        289 GTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGT 348
Db        302 GTGGTCCTGGAAGTCCTGGTGGTCCTGGAGGTCCTGGTGGTCCAGGTGGTCCATTAGGTC 243

Qy        349 CGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATG 408
Db        242 CAGCTGGTCCTGGTGCACCTAAAGGTTCTGGGTATCCTGGTGGTCCTCGTGGTGGTCGTG 183
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Job time : 2226.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 13:07:09 ; Search time 3070.75 Seconds
(without alignments)
16232.024 Million cell updates/sec

Title: US-10-679-999-10
Perfect score: 1150
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 5430052

Minimum DB seq length: 0
Maximum DB seq length: 1150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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4: gb_om:*
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6: gb_pat:*
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10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
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26: em_ro:*
27: em_sts:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
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39: em_htgo_hum:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1150	100.0	1150	6	BD056519	BD056519 OB fusion
2	1134	98.6	1150	6	BD056517	BD056517 OB fusion
3	1129	98.2	1135	6	BD056521	BD056521 OB fusion
4	1103.4	95.9	1135	6	BD056523	BD056523 OB fusion
5	680.8	59.2	794	6	AR437913	AR437913 Sequence
6	680.8	59.2	794	6	AX303197	AX303197 Sequence
7	680.8	59.2	812	6	AR437917	AR437917 Sequence
8	680.8	59.2	812	6	AX303207	AX303207 Sequence
9	680.8	59.2	861	6	BD263009	BD263009 Dimeric t
10	680.8	59.2	861	6	AR437914	AR437914 Sequence
11	680.8	59.2	861	6	AX303199	AX303199 Sequence
12	679.2	59.1	1080	6	AR173437	AR173437 Sequence
13	678.8	59.0	748	6	AR437973	AR437973 Sequence
14	678.8	59.0	748	6	AX304259	AX304259 Sequence
15	678.8	59.0	757	6	AR437967	AR437967 Sequence
16	678.8	59.0	757	6	AX304247	AX304247 Sequence
17	678.8	59.0	763	6	AR437969	AR437969 Sequence
18	678.8	59.0	763	6	AX304251	AX304251 Sequence
19	678.8	59.0	859	6	AX327583	AX327583 Sequence
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21	678.8	59.0	990	6	AX047023	AX047023 Sequence
22	678.8	59.0	990	6	AX365185	AX365185 Sequence
23	678.8	59.0	990	6	AX478510	AX478510 Sequence
24	678.8	59.0	990	9	HSA294730	AJ294730 Homo sapi
25	678.4	59.0	762	6	AX556168	AX556168 Sequence
26	678.4	59.0	1019	6	AR137115	AR137115 Sequence
27	678.4	59.0	1019	6	BD271954	BD271954 Cell surf
28	678.4	59.0	1019	6	AR275187	AR275187 Sequence
29	677.8	58.9	684	6	BD262999	BD262999 Dimeric t
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43	676.8	58.9	1077	6	AX716759	AX716759 Sequence
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ALIGNMENTS

RESULT 1
BD056519
LOCUS BD056519 1150 bp DNA linear PAT 27-AUG-2002
DEFINITION OB fusion protein compositions and methods.
ACCESSION BD056519
VERSION BD056519.1 GI:22602125
KEYWORDS JP 2001512417-A/7.
SOURCE Aequorea victoria
ORGANISM Aequorea victoria
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
REFERENCE 1 (bases 1 to 1150)
AUTHORS Mann,M.B. and Hecht,R.I.
TITLE OB fusion protein compositions and methods
JOURNAL Patent: JP 2001512417-A 7 21-AUG-2001;

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            AMGEN INC
COMMENT     PN   JP 2001512417-A/7
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   /note= 'Met = ATG'
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .1150
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ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 3.9e-231;
  Matches 1150;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 CTCCTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120
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Qy        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180
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Db        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180

Qy        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240
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Qy        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300
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Db        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360

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Qy        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660
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Qy        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840
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Qy        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900
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Qy        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960
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Qy        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020
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Db        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020

Qy       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080

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Db       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140

Qy       1141 TAATGGATCC 1150
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Db       1141 TAATGGATCC 1150


RESULT 2
BD056517
LOCUS       BD056517               1150 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056517
VERSION     BD056517.1  GI:22602123
KEYWORDS    JP 2001512417-A/5.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1150)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 5 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/5
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
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            CC   Topology: Linear;
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ORIGIN

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Qy        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180
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Db        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180

Qy        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240
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Db        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240

Qy        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300

Qy        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360

Qy        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420

Qy        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480

Qy        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540

Qy        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600
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Db        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600

Qy        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660

Qy        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720

Qy        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780

Qy        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840
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Db        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840

Qy        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900

Qy        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960

Qy        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020

Qy       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080

Qy       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140
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Qy       1141 TAATGGATCC 1150
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Db       1141 TAATGGATCC 1150
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RESULT 3
BD056521
LOCUS       BD056521                1135 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056521
VERSION     BD056521.1  GI:22602127
KEYWORDS    JP 2001512417-A/9.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1135)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 9 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/9
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   /note= 'Met = ATG'
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .1135
                        /organism="Aequorea victoria"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:6100"
ORIGIN
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  Query Match             98.2%;  Score 1129;  DB 6;  Length 1135;
  Best Local Similarity   100.0%;  Pred. No. 1e-226;
  Matches 1129;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 81
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126

Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246

Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366

Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
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Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741
Db        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726

Qy        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801
Db        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786

Qy        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861
Db        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846

Qy        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921
Db        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906

Qy        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981
Db        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966

Qy        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041
Db        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026

Qy       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101
Db       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086

Qy       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
Db       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
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RESULT 4
BD056523
LOCUS       BD056523               1135 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056523
VERSION     BD056523.1  GI:22602129
KEYWORDS    JP 2001512417-A/11.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1135)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 11 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/11
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
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            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   /note= 'Met = ATG'
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
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                        /organism="Aequorea victoria"
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  Best Local Similarity   98.6%;  Pred. No. 2.4e-221;
  Matches 1113;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 81
Db          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126

Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
Db        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246

Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
Db        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366

Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741
Db        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726

Qy        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801
Db        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786

Qy        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861
Db        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846

Qy        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921
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Db        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906

Qy        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981
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Db        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966

Qy        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026

Qy       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101
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Db       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086

Qy       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
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Db       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135


RESULT 5
AR437913
LOCUS       AR437913                794 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 5 from patent US 6660843.
ACCESSION   AR437913
VERSION     AR437913.1  GI:40203252
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 794)
  AUTHORS   Feige,U. and Liu,C.-F.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: US 6660843-A 5 09-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .794
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ORIGIN

  Query Match           59.2%;  Score 680.8;  DB 6;  Length 794;
  Best Local Similarity   98.3%;  Pred. No. 1.3e-132;
  Matches  688;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
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Db         24 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 83

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
              |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 143

Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
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Db        144 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 203

Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
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Db        204 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 263

Qy        244 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 323

Qy        304 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 363
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Db        324 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 383

Qy        364 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 423
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Db        384 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 443

Qy        424 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 483
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Db        444 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 503

Qy        484 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 543
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Db        504 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 563

Qy        544 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 603
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Db        564 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 623

Qy        604 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 683

Qy        664 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
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Db        684 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 6
AX303197
LOCUS       AX303197                794 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 5 from Patent WO0183525.
ACCESSION   AX303197
VERSION     AX303197.1  GI:17383677
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Feige,U., Liu,C.F., Cheetham,J.C., Boone,T.C. and Gudas,J.M.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: WO 0183525-A 5 08-NOV-2001;
            Amgen Inc., (US)
FEATURES             Location/Qualifiers
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                     KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
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                     QKSLSLSPGKGGGGGIEGPTLRQWLAARA"
ORIGIN

  Query Match           59.2%;  Score 680.8;  DB 6;  Length 794;
  Best Local Similarity   98.3%;  Pred. No. 1.3e-132;
  Matches  688;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
              | |||   | ||  |  ||||||||||||||||||||||||||||||||||||||||||
Db         24 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 83

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
              |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 143

Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
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Db        144 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 203

Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
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Db        204 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 263
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 861)
  AUTHORS   Feige,U. and Liu,C.-F.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: US 6660843-A 7 09-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .861
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                     /mol_type="genomic DNA"
ORIGIN
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Query Match 59.2%; Score 680.8; DB 6; Length 861;
Best Local Similarity 98.3%; Pred. No. 1.3e-132;
Matches 688; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
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Db         24 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 83

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
              |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 143

Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
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Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
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Db        204 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 263

Qy        244 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 303
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Db        264 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 323

Qy        304 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 363
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Db        324 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 383

Qy        364 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 423
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Db        384 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 443

Qy        424 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 483
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Db        444 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 503

Qy        484 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 543
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Db        504 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 563

Qy        544 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 623

Qy        604 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 683

Qy        664 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
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Db        684 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
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RESULT 11
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LOCUS       AX303199                861 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 7 from Patent WO0183525.
ACCESSION   AX303199
VERSION     AX303199.1  GI:17383679
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Feige,U., Liu,C.F., Cheetham,J.C., Boone,T.C. and Gudas,J.M.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: WO 0183525-A 7 08-NOV-2001;
            Amgen Inc., (US)
FEATURES             Location/Qualifiers
     source          1. .861
                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"
                     /note="Fc-TMP-TMP"
     CDS             39. .>842
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                     /db_xref="GI:17383680"
                     /db_xref="REMTREMBL:CAD13103"
                     /translation="MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
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                     KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
                     EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
                     QKSLSLSPGKGGGGGIEGPTLRQWLAARAGGGGGGGIEGPTLRQWLAAR"
ORIGIN
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Query Match 59.2%; Score 680.8; DB 6; Length 861;
Best Local Similarity 98.3%; Pred. No. 1.3e-132;
Matches 688; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
              | |||   | ||  |  ||||||||||||||||||||||||||||||||||||||||||||||
Db         24 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 83

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
              |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 143

Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 203

Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 263

Qy        244 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 303
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Db        264 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 323

Qy        304 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 383

Qy        364 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 443

Qy        424 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 483
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Db        444 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 503

Qy        484 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 543
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Db        504 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 563

Qy        544 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 603
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Db        564 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 623

Qy        604 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 663
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Db        624 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 683

Qy        664 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
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Db        684 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 12
AR173437
LOCUS       AR173437                1080 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 14 from patent US 6306395.
ACCESSION   AR173437
VERSION     AR173437.1  GI:17913757
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1080)
  AUTHORS   Nakamura,N. and Nagata,S.
  TITLE     Fas antigen derivatives
  JOURNAL   Patent: US 6306395-A 14 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .1080
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           59.1%;  Score 679.2;  DB 6;  Length 1080;
  Best Local Similarity   98.1%;  Pred. No. 2.8e-132;
  Matches  687;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          3 TATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACT 62
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Db        381 TAACGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT 440

Qy         63 CCTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC 122
              ||||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC 500

Qy        123 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA 560

Qy        183 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 242
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Db        561 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 620

Qy        243 GCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCT 302
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Qy        303 GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA 362
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Db        681 GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA 740

Qy        363 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC 800

Qy        423 CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC 482
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Db        801 CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC 860

Qy        483 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAC 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAC 920

Qy        543 GCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAA 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 GCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAA 980

Qy        603 GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA 662
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Qy        663 CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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Db       1041 CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1080


RESULT 13
AR437973
LOCUS       AR437973                748 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1067 from patent US 6660843.
ACCESSION   AR437973
VERSION     AR437973.1  GI:40203312
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 748)
  AUTHORS   Feige,U. and Liu,C.-F.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: US 6660843-A 1067 09-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .748
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ORIGIN

  Query Match           59.0%;  Score 678.8;  DB 6;  Length 748;
  Best Local Similarity   99.7%;  Pred. No. 3.5e-132;
  Matches  680;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 81
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Db          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126

Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246

Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
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Db        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366

Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
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Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAG 703
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Db        667 CTCTCCCTGTCTCCGGGTAAAG 688


RESULT 14
AX304259
LOCUS       AX304259                748 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 1067 from Patent WO0183525.
ACCESSION   AX304259
VERSION     AX304259.1  GI:17383760
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Feige,U., Liu,C.F., Cheetham,J.C., Boone,T.C. and Gudas,J.M.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: WO 0183525-A 1067 08-NOV-2001;
            Amgen Inc., (US)
FEATURES             Location/Qualifiers
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                     /db_xref="GI:17383761"
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                     KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
                     EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
                     QKSLSLSPGKGGGGGCTTHWGFTLC"
ORIGIN

  Query Match           59.0%;  Score 678.8;  DB 6;  Length 748;
  Best Local Similarity  99.7%;  Pred. No. 3.5e-132;
  Matches  680;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 81
              |||||||||||||||||||||||||||||||||||||||||||||||||| || ||||||
Db          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126

Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246

Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
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Db        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366

Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
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Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
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Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
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Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAG 703
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Db        667 CTCTCCCTGTCTCCGGGTAAAG 688


RESULT 15
AR437967
LOCUS       AR437967                757 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1055 from patent US 6660843.
ACCESSION   AR437967
VERSION     AR437967.1  GI:40203306
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 757)
  AUTHORS   Feige,U. and Liu,C.-F.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: US 6660843-A 1055 09-DEC-2003;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
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ORIGIN

  Query Match           59.0%;  Score 678.8;  DB 6;  Length 757;
  Best Local Similarity  99.7%;  Pred. No. 3.5e-132;
  Matches  680;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 81
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Db          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
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Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
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Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
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Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
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Job time : 3073.75 secs

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PT   New fusion proteins of OB and Fc - used for treating e.g. excess weight,
PT   diabetes, arterial sclerosis, arterial plaque, high blood lipid level,
PT   gall stones or stroke.
XX
PS   Disclosure; Fig 4A-4C; 107pp; English.
XX
CC   The present sequence represents a recombinant human MetFc-OB variant 1
CC   cDNA which encodes a recombinant human Fc-OB fusion variant 1 protein
CC   having a C6A substitution when compared with the wild-type Fc-OB protein
CC   sequence shown in AAW49073. The invention provides Fc-OB fusion proteins
CC   whereby the Fc region of an immunoglobulin or its analogue is linked,
CC   either directly or indirectly using a linker, to the N-terminus of an OB
CC   protein or its analogue. The Fc-OB fusion proteins are claimed to
CC   demonstrate increased stability and clearance rate and decreased
CC   degradation as compared to OB protein or a fusion of Fc to the C-terminus
CC   of the OB protein. These Fc-OB fusion proteins are also claimed to be
CC   useful for treating excess weight in an individual or animal or for
CC   treating co-morbidities associated with excess fat such as diabetes, high
CC   blood lipid level, arterial sclerosis and stroke
XX
SQ   Sequence 1150 BP; 277 A; 365 C; 285 G; 223 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 1150;  DB 2;  Length 1150;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-251;
  Matches 1150;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 CTCCTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120
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Qy        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780
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Db        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900

Qy        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960
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Db        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960

Qy        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020
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Db        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020

Qy       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080
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Db       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080

Qy       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140
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Qy       1141 TAATGGATCC 1150
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Db       1141 TAATGGATCC 1150


RESULT 2
AAV32900
ID   AAV32900 standard; cDNA; 1150 BP.
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AC   AAV32900;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Recombinant human MetFc-OB cDNA.
XX
KW   Recombinant human MetFc-OB cDNA; chimeric; immunoglobulin; diabetes;
KW   high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
KW   ds.
XX
OS   Homo sapiens.
OS   Synthetic.
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FT                   /note= "Encodes for the OB part of the fusion protein"
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XX
PD   02-JUL-1998.
XX
PF   11-DEC-1997;   97WO-US023183.
XX
PR   20-DEC-1996;   96US-00770973.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Mann MB,  Hecht RI;
XX
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 13:07:09 ; Search time 332.75 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 5810876

Minimum DB seq length: 0
Maximum DB seq length: 1150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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43	677.2	58.9	748	3	AAA69507	Aaa69507 Fc-MMP in
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ALIGNMENTS

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RESULT 1
AAV32901
ID   AAV32901 standard; cDNA; 1150 BP.
XX
AC   AAV32901;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Recombinant human MetFc-OB variant 1 cDNA.
XX
KW   Recombinant human MetFc-OB variant 1 cDNA; chimeric; immunoglobulin;
KW   high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
KW   diabetes; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
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FT   mutation        19. .21
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PN   WO9828427-A1.
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PD   02-JUL-1998.
XX
PF   11-DEC-1997;   97WO-US023183.
XX
PR   20-DEC-1996;   96US-00770973.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Mann MB,  Hecht RI;
XX
DR   WPI; 1998-377658/32.
DR   P-PSDB; AAW49074.
XX
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DR   WPI; 1998-377658/32.
DR   P-PSDB; AAW49073.
XX
PT   New fusion proteins of OB and Fc - used for treating e.g. excess weight,
PT   diabetes, arterial sclerosis, arterial plaque, high blood lipid level,
PT   gall stones or stroke.
XX
PS   Disclosure; Fig 3A-3C; 107pp; English.
XX
CC   The present sequence represents a recombinant human MetFc-OB cDNA which
CC   encodes a recombinant human Fc-OB fusion protein. The invention provides
CC   Fc-OB fusion proteins whereby the Fc region of an immunoglobulin or its
CC   analogue is linked, either directly or indirectly using a linker, to the
CC   N-terminus of an OB protein or its analogue. The Fc-OB fusion proteins
CC   are claimed to demonstrate increased stability and clearance rate and
CC   decreased degradation as compared to OB protein or a fusion of Fc to the
CC   C-terminus of the OB protein. These Fc-OB fusion proteins are also
CC   claimed to be useful for treating excess weight in an individual or
CC   animal or for treating co-morbidities associated with excess fat such as
CC   diabetes, high blood lipid level, arterial sclerosis and stroke
XX
SQ   Sequence 1150 BP; 278 A; 367 C; 286 G; 219 T; 0 U; 0 Other;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840

Qy        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900

Qy        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960

Qy        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020

Qy       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080

Qy       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140

Qy       1141 TAATGGATCC 1150
              ||||||||||
Db       1141 TAATGGATCC 1150
```

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RESULT 3
AAV69685
ID   AAV69685 standard; DNA; 1150 BP.
XX
AC   AAV69685;
XX
DT   05-FEB-1999  (first entry)
XX
DE   Recombinant human metFc-OB protein encoding DNA.
XX
KW   Recombinant; metFc-OB protein; Fc region; immunoglobulin; Ig; OB;
KW   obesity; human; adiposity; blood lipid; diabetes type II; insulin;
KW   hypoglycaemic; antihypertensive; diuretic; appetite suppressant;
KW   suspension; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             4. .1143
FT                   /*tag=  a
FT                   /product= "metFc-OB protein"
XX
PN   WO9846257-A1.
XX
PD   22-OCT-1998.
XX
PF   16-APR-1998;    98WO-US007828.
XX
PR   17-APR-1997;    97US-00843971.
PR   14-APR-1998;    98US-00059467.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Brems DN,  French DL,  Speed MA;
XX
DR   WPI; 1998-594525/50.
DR   P-PSDB; AAW83962.
XX
```

```
PT   Concentrated suspension of fusion of obesity protein with Fc
PT   immunoglobulin fragment - stable at physiological pH, used for e.g.
PT   reduction of weight and blood lipid levels, and for treatment of type II
PT   diabetes.
XX
PS   Disclosure; Fig 5A-C; 47pp; English.
XX
CC   This DNA encodes a recombinant metFc-OB protein which consists of an Fc
CC   region of human immunoglobulin (Ig) fused to a human OB (obesity)
CC   protein. The invention provides a human OB protein suspension that
CC   contains at least 0.5 mg/ml of the human OB protein derivatised by
CC   attachment of the Fc region of an Ig to the N-terminus of OB, and has a
CC   pH 6-8. The suspensions are used to reduce weight, adiposity and blood
CC   lipid levels, to treat or prevent diabetes type II, and to increase lean
CC   mass and insulin sensitivity. They may be used in conjunction with
CC   insulin, hypoglycaemics, antihypertensives, diuretics, appetite
CC   suppressants etc. These suspensions are stable and active at
CC   physiological pH and are ready-for-use formulations that do not require
CC   freezing or freeze drying. As they are very concentrated, only small
CC   volumes are required and they provide a sustained-release effect, with
CC   increased potency and reduced frequency of injection
XX
SQ   Sequence 1150 BP; 278 A; 367 C; 286 G; 219 T; 0 U; 0 Other;

  Query Match             98.6%;  Score 1134;  DB 2;  Length 1150;
  Best Local Similarity   99.1%;  Pred. No. 7.6e-248;
  Matches 1140;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 CATATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAA 60
              |||||||||| ||||||  |||||||||||||||||| ||||| || ||||| || |||
Db          1 CATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA 60

Qy         61 CTCCTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120
              |||||||||| || ||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120

Qy        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180

Qy        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240

Qy        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300

Qy        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360

Qy        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420

Qy        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480

Qy        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540

Qy        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600

Qy        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660

Qy        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720

Qy        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780

Qy        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840

Qy        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900

Qy        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960

Qy        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020

Qy       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080

Qy       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140

Qy       1141 TAATGGATCC 1150
              ||||||||||
Db       1141 TAATGGATCC 1150


RESULT 4
AAV32902
ID   AAV32902 standard; cDNA; 1135 BP.
XX
AC   AAV32902;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Recombinant human MetFc-OB variant 2 cDNA.
XX
KW   Recombinant human MetFc-OB variant 2 cDNA; chimeric; immunoglobulin;
KW   high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
KW   diabetes; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             4. .1128
FT                   /*tag=  a
FT                   /product= "Recombinant human Fc-OB variant 2"
FT   mat_peptide     7. .1125
FT                   /*tag=  b
FT   misc_feature    685. .1125
FT                   /*tag=  c
FT                   /note= "Encodes for the OB part of the fusion protein"
XX
PN   WO9828427-A1.
XX
PD   02-JUL-1998.
XX
PF   11-DEC-1997;   97WO-US023183.
XX
PR   20-DEC-1996;   96US-00770973.
XX
PA   (AMGE-) AMGEN INC.
XX
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PI   Mann MB,  Hecht RI;
XX
DR   WPI; 1998-377658/32.
DR   P-PSDB; AAW49075.
XX
PT   New fusion proteins of OB and Fc - used for treating e.g. excess weight,
PT   diabetes, arterial sclerosis, arterial plaque, high blood lipid level,
PT   gall stones or stroke.
XX
PS   Disclosure; Fig 5A-5C; 107pp; English.
XX
CC   The present sequence represents a recombinant human MetFc-OB variant 2
CC   cDNA which encodes a recombinant human Fc-OB fusion variant 2 protein
CC   having a 5 residue deletion of residues 2-6 of the wild-type Fc-OB
CC   protein sequence shown in AAW49073. The invention provides Fc-OB fusion
CC   proteins whereby the Fc region of an immunoglobulin or its analogue is
CC   linked, either directly or indirectly using a linker, to the N-terminus
CC   of an OB protein or its analogue. The Fc-OB fusion proteins are claimed
CC   to demonstrate increased stability and clearance rate and decreased
CC   degradation as compared to OB protein or a fusion of Fc to the C-terminus
CC   of the OB protein. These Fc-OB fusion proteins are also claimed to be
CC   useful for treating excess weight in an individual or animal or for
CC   treating co-morbidities associated with excess fat such as diabetes, high
CC   blood lipid level, arterial sclerosis and stroke
XX
SQ   Sequence 1135 BP; 271 A; 361 C; 283 G; 220 T; 0 U; 0 Other;

  Query Match             98.2%;  Score 1129;  DB 2;  Length 1135;
  Best Local Similarity   100.0%;  Pred. No. 1e-246;
  Matches 1129;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 81
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126

Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246

Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366

Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726

Qy        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786

Qy        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861
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Db        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846

Qy        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906

Qy        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966

Qy        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041
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Db        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026

Qy       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086

Qy       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135

RESULT 5
AAV69686
ID   AAV69686 standard; DNA; 1135 BP.
XX
AC   AAV69686;
XX
DT   05-FEB-1999  (first entry)
XX
DE   Recombinant human metFc-OB protein variant encoding DNA.
XX
KW   Recombinant; metFc-OB protein; Fc region; immunoglobulin; Ig; OB;
KW   obesity; human; adiposity; blood lipid; diabetes type II; insulin;
KW   hypoglycaemic; antihypertensive; diuretic; appetite suppressant;
KW   suspension; variant; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             4. .1128
FT                   /*tag=  a
FT                   /product= "metFc-OB protein variant"
XX
PN   WO9846257-A1.
XX
PD   22-OCT-1998.
XX
PF   16-APR-1998;   98WO-US007828.
XX
PR   17-APR-1997;   97US-00843971.
PR   14-APR-1998;   98US-00059467.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Brems DN,  French DL,  Speed MA;
XX
DR   WPI; 1998-594525/50.
DR   P-PSDB; AAW83963.
XX
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```
PT   Concentrated suspension of fusion of obesity protein with Fc
PT   immunoglobulin fragment - stable at physiological pH, used for e.g.
PT   reduction of weight and blood lipid levels, and for treatment of type II
PT   diabetes.
XX
PS   Disclosure; Fig 6A-C; 47pp; English.
XX
CC   This DNA encodes a recombinant metFc-OB protein variant which consists of
CC   an Fc region of human immunoglobulin (Ig) fused to a human OB (obesity)
CC   protein. The invention provides a human OB protein suspension that
CC   contains at least 0.5 mg/ml of the human OB protein derivatised by
CC   attachment of the Fc region of an Ig to the N-terminus of OB, and has a
CC   pH 6-8. The suspensions are used to reduce weight, adiposity and blood
CC   lipid levels, to treat or prevent diabetes type II, and to increase lean
CC   mass and insulin sensitivity. They may be used in conjunction with
CC   insulin, hypoglycaemics, antihypertensives, diuretics, appetite
CC   suppressants etc. These suspensions are stable and active at
CC   physiological pH and are ready-for-use formulations that do not require
CC   freezing or freeze drying. As they are very concentrated, only small
CC   volumes are required and they provide a sustained-release effect, with
CC   increased potency and reduced frequency of injection
XX
SQ   Sequence 1135 BP; 271 A; 361 C; 283 G; 220 T; 0 U; 0 Other;

  Query Match             98.2%;  Score 1129;  DB 2;  Length 1135;
  Best Local Similarity   100.0%;  Pred. No. 1e-246;
  Matches 1129;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 81
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126

Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246

Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366

Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726

Qy        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786

Qy        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846

Qy        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906

Qy        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966

Qy        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026

Qy       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086

Qy       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135

RESULT 6
AAV32903
ID   AAV32903 standard; cDNA; 1135 BP.
XX
AC   AAV32903;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Recombinant human MetFc-OB variant 3 cDNA.
XX
KW   Recombinant human MetFc-OB variant 3 cDNA; chimeric; immunoglobulin;
KW   high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
KW   diabetes; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             4. .1128
FT                   /*tag=  a
FT                   /product= "Recombinant human Fc-OB variant 3"
FT   mat_peptide     7. .1125
FT                   /*tag=  b
FT   misc_feature    685. .1125
FT                   /*tag=  c
FT                   /note= "Encodes for the OB part of the fusion protein"
XX
PN   WO9828427-A1.
XX
PD   02-JUL-1998.
XX
PF   11-DEC-1997;   97WO-US023183.
XX
PR   20-DEC-1996;   96US-00770973.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Mann MB,  Hecht RI;
XX
DR   WPI; 1998-377658/32.
DR   P-PSDB; AAW49076.
```

```
XX
PT   New fusion proteins of OB and Fc - used for treating e.g. excess weight,
PT   diabetes, arterial sclerosis, arterial plaque, high blood lipid level,
PT   gall stones or stroke.
XX
PS   Disclosure; Fig 6A-6C; 107pp; English.
XX
CC   The present sequence represents a recombinant human MetFc-OB variant 3
CC   cDNA which encodes a recombinant human Fc-OB fusion variant 3 protein
CC   having the L16E, E99A, K101A and K103A substitutions when compared with
CC   the template protein shown in AAW49075. The invention provides Fc-OB
CC   fusion proteins whereby the Fc region of an immunoglobulin or its
CC   analogue is linked, either directly or indirectly using a linker, to the
CC   N-terminus of an OB protein or its analogue. The Fc-OB fusion proteins
CC   are claimed to demonstrate increased stability and clearance rate and
CC   decreased degradation as compared to OB protein or a fusion of Fc to the
CC   C-terminus of the OB protein. These Fc-OB fusion proteins are also
CC   claimed to be useful for treating excess weight in an individual or
CC   animal or for treating co-morbidities associated with excess fat such as
CC   diabetes, high blood lipid level, arterial sclerosis and stroke
XX
SQ   Sequence 1135 BP; 270 A; 365 C; 283 G; 217 T; 0 U; 0 Other;

  Query Match             95.9%;  Score 1103.4;  DB 2;  Length 1135;
  Best Local Similarity   98.6%;  Pred. No. 6.7e-241;
  Matches 1113;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 81
Db          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126

Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
Db        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246

Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
Db        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366

Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741
Db        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726

Qy        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801
Db        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786

Qy        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861
Db        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846

Qy        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921
Db        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906

Qy        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981
Db        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966

Qy        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041
Db        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026

Qy       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101
Db       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086

Qy       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
Db       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135


RESULT 7
AAA69444
ID   AAA69444 standard; DNA; 794 BP.
XX
AC   AAA69444;
XX
DT   31-OCT-2000  (first entry)
XX
DE   Fc-TMP nucleotide sequence SEQ ID NO:5.
XX
KW   Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW   autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW   immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW   inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW   cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW   vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW   thrombosis; pharmaceutical; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200024782-A2.
XX
PD   04-MAY-2000.
XX
PF   25-OCT-1999;   99WO-US025044.
XX
PR   23-OCT-1998;   98US-0105371P.
PR   22-OCT-1999;   99US-00428082.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C,  Cheetham J,  Boone TC;
XX
DR   WPI; 2000-350702/30.
DR   P-PSDB; AAB16958.
XX
PT   Novel composition of matter comprising an Fc domain and pharmacologically
PT   active peptides, useful for treating cancer and autoimmune diseases.
XX
PS   Example 2; Page 178-179; 608pp; English.
XX
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```
CC   The present invention describes composition of matter (I) comprising an
CC   Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC   (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC   independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC   (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC   P3, and P4 = are each independently sequences of pharmacologically active
CC   peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC   c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC   of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC   thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC   cells from the present invention can be used for producing pharmaceutical
CC   compositions. The compositions are useful for treating cancer, asthma,
CC   thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC   a Fab domain) can provide a longer half-life or incorporate functions
CC   such as Fc receptor binding, protein A binding, complement fixation, and
CC   possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC   AAB18003 represent nucleotide and amino acid sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 794 BP; 195 A; 242 C; 213 G; 144 T; 0 U; 0 Other;

  Query Match           59.2%;  Score 680.8;  DB 3;  Length 794;
  Best Local Similarity  98.3%;  Pred. No. 6.1e-145;
  Matches  688;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
              | |||   | ||  |   ||||||||||||||||||||||||||||||||||||||||||
Db         24 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 83

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
              |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 143

Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 203

Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 263

Qy        244 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 323

Qy        304 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 383

Qy        364 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 443

Qy        424 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 503

Qy        484 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 563

Qy        544 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 623

Qy        604 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 683

Qy        664 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||||||||||||||||||||
Db        684 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
```

```
RESULT 8
ABL35761
ID   ABL35761 standard; DNA; 794 BP.
XX
AC   ABL35761;
XX
DT   05-APR-2002  (first entry)
XX
DE   Fc-TPO mimetic peptide (Fc-TMP) nucleic acid SEQ ID NO:5.
XX
KW   Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW   erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW   TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW   TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW   MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW   cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW   antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW   neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW   cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW   sleep disorder; neurological degenerative disease; anaemia;
KW   thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW   Fanconi's syndrome; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200183525-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US014310.
XX
PR   03-MAY-2000; 2000US-00563286.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C,  Cheetham JC,  Boone TC,  Gudas JM;
XX
DR   WPI; 2002-130313/17.
DR   P-PSDB; ABB73411.
XX
PT   Novel vehicle-peptide molecule or its multimers useful for treating
PT   inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT   diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS   Example 2; Fig 7; 176pp; English.
XX
CC   The present invention describes a vehicle-peptide molecule (I) or its
CC   multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC   cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC   antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC   neuroprotective activities. (I) can be used as a therapeutic or
CC   prophylactic agent as well as for screening purposes. (I) is useful for
CC   diagnosing diseases characterised by dysfunction of their associated
CC   protein of interest, for identifying normal or abnormal proteins of
CC   interest, as a part of diagnostic kit to detect the presence of their
CC   proteins of interest in a biological sample. Additionally, (I) is useful
CC   for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC   rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC   infertility, and neurological degenerative diseases. (I), comprising EPO-
CC   mimetic compounds are useful for treating disorders characterised by low
CC   red blood cell levels such as anaemia. The TPO-mimetic comprising
CC   compounds are useful for treating conditions that involve an existing
CC   megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC   deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC   tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC   and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC   represent amino acid and nucleic acid sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 794 BP; 195 A; 242 C; 213 G; 144 T; 0 U; 0 Other;
```

```
  Query Match             59.2%;  Score 680.8;  DB 6;  Length 794;
  Best Local Similarity   98.3%;  Pred. No. 6.1e-145;
  Matches  688;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
              | |||    | ||   |   ||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 83

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
              |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 143

Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 203

Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 263

Qy        244 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 303
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 323

Qy        304 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 363
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 383

Qy        364 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 423
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 443

Qy        424 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 483
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 503

Qy        484 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 543
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 563

Qy        544 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 603
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 623

Qy        604 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 663
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 683

Qy        664 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||||||||||||||||||||
Db        684 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 9
AAA69448
ID   AAA69448 standard; DNA; 812 BP.
XX
AC   AAA69448;
XX
DT   31-OCT-2000  (first entry)
XX
DE   Fc-EMP nucleotide sequence SEQ ID NO:15.
XX
KW   Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW   autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW   immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW   inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW   cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW   vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW   thrombosis; pharmaceutical; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200024782-A2.
XX
PD   04-MAY-2000.
XX
PF   25-OCT-1999;   99WO-US025044.
XX
PR   23-OCT-1998;   98US-0105371P.
PR   22-OCT-1999;   99US-00428082.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C,  Cheetham J,  Boone TC;
XX
DR   WPI; 2000-350702/30.
DR   P-PSDB; AAB16964.
XX
PT   Novel composition of matter comprising an Fc domain and pharmacologically
PT   active peptides, useful for treating cancer and autoimmune diseases.
XX
PS   Example 3; Page 190-191; 608pp; English.
XX
CC   The present invention describes composition of matter (I) comprising an
CC   Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC   (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC   independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC   (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC   P3, and P4 = are each independently sequences of pharmacologically active
CC   peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC   c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC   of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC   thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC   cells from the present invention can be used for producing pharmaceutical
CC   compositions. The compositions are useful for treating cancer, asthma,
CC   thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC   a Fab domain) can provide a longer half-life or incorporate functions
CC   such as Fc receptor binding, protein A binding, complement fixation, and
CC   possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC   AAB18003 represent nucleotide and amino acid sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 812 BP; 198 A; 246 C; 218 G; 150 T; 0 U; 0 Other;

  Query Match             59.2%;  Score 680.8;  DB 3;  Length 812;
  Best Local Similarity   98.3%;  Pred. No. 6.1e-145;
  Matches  688;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
              | |||    | ||   |   ||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 83

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
              |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 143

Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 203

Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 263

Qy        244 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 303
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 323

Qy        304 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 363
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 383

Qy        364 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 423
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        384 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 443

Qy        424 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 503

Qy        484 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 563

Qy        544 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 623

Qy        604 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 683

Qy        664 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||||||||||||||||||||
Db        684 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 10
ABL35765
ID   ABL35765 standard; DNA; 812 BP.
XX
AC   ABL35765;
XX
DT   05-APR-2002  (first entry)
XX
DE   Fc-EPO mimetic peptide (Fc-EMP) nucleic acid SEQ ID NO:15.
XX
KW   Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW   erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW   TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW   TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW   MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW   cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW   antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW   neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW   cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW   sleep disorder; neurological degenerative disease; anaemia;
KW   thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW   Fanconi's syndrome; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200183525-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US014310.
XX
PR   03-MAY-2000; 2000US-00563286.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C,  Cheetham JC,  Boone TC,  Gudas JM;
XX
DR   WPI; 2002-130313/17.
DR   P-PSDB; ABB73415.
XX
PT   Novel vehicle-peptide molecule or its multimers useful for treating
PT   inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT   diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS   Example 3; Fig 13; 176pp; English.
XX
CC   The present invention describes a vehicle-peptide molecule (I) or its
CC   multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC   cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC   antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC   neuroprotective activities. (I) can be used as a therapeutic or
CC   prophylactic agent as well as for screening purposes. (I) is useful for
CC   diagnosing diseases characterised by dysfunction of their associated
CC   protein of interest, for identifying normal or abnormal proteins of
CC   interest, as a part of diagnostic kit to detect the presence of their
CC   proteins of interest in a biological sample. Additionally, (I) is useful
CC   for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC   rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC   infertility, and neurological degenerative diseases. (I), comprising EPO-
CC   mimetic compounds are useful for treating disorders characterised by low
CC   red blood cell levels such as anaemia. The TPO-mimetic comprising
CC   compounds are useful for treating conditions that involve an existing
CC   megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC   deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC   tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC   and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC   represent amino acid and nucleic acid sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 812 BP; 198 A; 246 C; 218 G; 150 T; 0 U; 0 Other;

  Query Match             59.2%;  Score 680.8;  DB 6;  Length 812;
  Best Local Similarity   98.3%;  Pred. No. 6.1e-145;
  Matches  688;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
              | |||   | ||  |   ||||||||||||||||||||||||||||||||||||||||||
Db         24 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 83

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
              ||||||||  || ||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 143

Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 203

Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 263

Qy        244 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 323

Qy        304 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 383

Qy        364 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 443

Qy        424 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 503

Qy        484 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 563

Qy        544 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 623

Qy        604 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 683

Qy        664 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||||||||||||||||||||
Db        684 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
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RESULT 11
AAA29229
ID   AAA29229 standard; DNA; 861 BP.
XX
AC   AAA29229;
XX
DT   04-SEP-2000  (first entry)
XX
DE   Human IgG1 Fc TMP fusion coding sequence.
XX
KW   Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet;
KW   megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV;
KW   anti-anaemic; dermatological; immunosuppressive; anti-inflammatory; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             39. .848
FT                   /*tag=  a
XX
PN   WO200024770-A2.
XX
PD   04-MAY-2000.
XX
PF   22-OCT-1999;   99WO-US024834.
XX
PR   23-OCT-1998;   98US-0105348P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Liu C,  Feige U,  Cheetham J;
XX
DR   WPI; 2000-365108/31.
DR   P-PSDB; AAY96531.
XX
PT   Thrombopoietic peptides which activate mpl receptors and increase the
PT   production of platelets or platelet precursors, useful for treatment of
PT   diseases which involve thombocytopenia.
XX
PS   Example 2A; Page 49-50; 91pp; English.
XX
CC   A compound which binds to an mpl receptor comprising a thrombopoietin
CC   mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is
CC   new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to
CC   14 residues in length comprising X_2-X_1_0, X_2-X_1_1, X_2-X_1_2, X_2-
CC   X_1_3, X_2-X_1_4, X_1-X_1_0, X_1-X_1_1, X_1-X_1_2, X_1-X_1_3, and X_1-
CC   X_1_4. X_1 = I, A, V, L, S or R; X_2 = E, D, K or V; X_3 = G or A; X_4 =
CC   P; X_5 = T or S; X_6 = L, I, V, A or F; X_7 = R or K; X_8 = Q, N, or E;
CC   X_9 = W, Y or F; X_1_0 = L, I, V, A, F, M, or K; X_1_1 = A, I, V, L, F,
CC   S, T, K, H, or E; X_1_2 = A, I, V, L, F, G, S, or Q; X_1_3 = R, K, T, V,
CC   N, Q or G; X_1_4 = A, I, V, L, F, T, R, E, or G; L_1 = linker comprising
CC   1 to 20 amino acids; and n = 0 or 1. The compounds bind to and activate
CC   the c-Mpl receptor which mediates the activity of endogenous
CC   thrombopoietin. The TMPs are useful for increasing the production of
CC   platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which
CC   is useful for treatment of diseases which involve thombocytopenia, e.g.
CC   aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency
CC   virus associated ITP, and systemic lupus erythematosus
XX
SQ   Sequence 861 BP; 206 A; 259 C; 241 G; 155 T; 0 U; 0 Other;

  Query Match           59.2%;  Score 680.8;  DB 3;  Length 861;
  Best Local Similarity  98.3%;  Pred. No. 6.2e-145;
  Matches  688;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
              | |||   | ||  |   |||||||||||||||||||||||||||||||||||||||||
Db         24 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 83

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
              |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||

Db         84 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 143

Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 203

Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 263

Qy        244 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 323

Qy        304 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 383

Qy        364 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 443

Qy        424 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 503

Qy        484 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 563

Qy        544 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 623

Qy        604 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 683

Qy        664 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||||||||||||||||||||||
Db        684 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 12
AAA69445
ID   AAA69445 standard; DNA; 861 BP.
XX
AC   AAA69445;
XX
DT   31-OCT-2000  (first entry)
XX
DE   Fc-TMP-TMP nucleotide sequence SEQ ID NO:7.
XX
KW   Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW   autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW   immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW   inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW   cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW   vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW   thrombosis; pharmaceutical; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200024782-A2.
XX
PD   04-MAY-2000.
XX
PF   25-OCT-1999;   99WO-US025044.
XX
PR   23-OCT-1998;   98US-0105371P.
PR   22-OCT-1999;   99US-00428082.
XX
```

```
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C,  Cheetham J,  Boone TC;
XX
DR   WPI; 2000-350702/30.
DR   P-PSDB; AAB16959.
XX
PT   Novel composition of matter comprising an Fc domain and pharmacologically
PT   active peptides, useful for treating cancer and autoimmune diseases.
XX
PS   Example 2; Page 180-182; 608pp; English.
XX
CC   The present invention describes composition of matter (I) comprising an
CC   Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC   (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC   independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC   (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC   P3, and P4 = are each independently sequences of pharmacologically active
CC   peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC   c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC   of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC   thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC   cells from the present invention can be used for producing pharmaceutical
CC   compositions. The compositions are useful for treating cancer, asthma,
CC   thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC   a Fab domain) can provide a longer half-life or incorporate functions
CC   such as Fc receptor binding, protein A binding, complement fixation, and
CC   possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC   AAB18003 represent nucleotide and amino acid sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 861 BP; 206 A; 259 C; 241 G; 155 T; 0 U; 0 Other;

  Query Match             59.2%;  Score 680.8;  DB 3;  Length 861;
  Best Local Similarity   98.3%;  Pred. No. 6.2e-145;
  Matches  688;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
              | |||   | ||  |   ||||||||||||||||||||||||||||||||||||||||||
Db         24 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 83

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
              |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 143

Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 203

Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 263

Qy        244 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 323

Qy        304 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 383

Qy        364 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 443

Qy        424 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 503

Qy        484 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 563

Qy        544 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 623

Qy        604 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 683

Qy        664 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||||||||||||||||||||
Db        684 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 13
ABL35762
ID   ABL35762 standard; DNA; 861 BP.
XX
AC   ABL35762;
XX
DT   05-APR-2002  (first entry)
XX
DE   Fc-TMP-TMP nucleic acid SEQ ID NO:7.
XX
KW   Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW   erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW   TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW   TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW   MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW   cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW   antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW   neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW   cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW   sleep disorder; neurological degenerative disease; anaemia;
KW   thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW   Fanconi's syndrome; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200183525-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US014310.
XX
PR   03-MAY-2000; 2000US-00563286.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C,  Cheetham JC,  Boone TC,  Gudas JM;
XX
DR   WPI; 2002-130313/17.
DR   P-PSDB; ABB73412.
XX
PT   Novel vehicle-peptide molecule or its multimers useful for treating
PT   inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT   diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS   Example 2; Fig 8; 176pp; English.
XX
CC   The present invention describes a vehicle-peptide molecule (I) or its
CC   multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC   cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC   antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC   neuroprotective activities. (I) can be used as a therapeutic or
CC   prophylactic agent as well as for screening purposes. (I) is useful for
CC   diagnosing diseases characterised by dysfunction of their associated
CC   protein of interest, for identifying normal or abnormal proteins of
CC   interest, as a part of diagnostic kit to detect the presence of their
CC   proteins of interest in a biological sample. Additionally, (I) is useful
CC   for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC   rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC   infertility, and neurological degenerative diseases. (I), comprising EPO-
```

```
CC   mimetic compounds are useful for treating disorders characterised by low
CC   red blood cell levels such as anaemia. The TPO-mimetic comprising
CC   compounds are useful for treating conditions that involve an existing
CC   megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC   deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC   tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC   and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC   represent amino acid and nucleic acid sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 861 BP; 206 A; 259 C; 241 G; 155 T; 0 U; 0 Other;

  Query Match           59.2%;  Score 680.8;  DB 6;  Length 861;
  Best Local Similarity 98.3%;  Pred. No. 6.2e-145;
  Matches  688;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
              | |||    | ||  |   ||||||||||||||||||||||||||||||||||||||||||
Db         24 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 83

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
              |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 143

Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 203

Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 263

Qy        244 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 323

Qy        304 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 383

Qy        364 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 443

Qy        424 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 503

Qy        484 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 563

Qy        544 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 623

Qy        604 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 683

Qy        664 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||||||||||||||||||||
Db        684 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 14
ADD25646
ID   ADD25646 standard; DNA; 714 BP.
XX
AC   ADD25646;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Binding domain-immunoglobulin fusion protein-associated DNA #107.
XX
KW   ds; Binding domain; immunoglobulin; fusion protein; cytostatic;
KW   antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW   neuroprotective; hinge region; immunoglobulin heavy chain;
KW   CH2 constant region; CH3 constant region; IgG1;
KW   antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW   malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW   rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW   type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS   Unidentified.
XX
PN   US2003118592-A1.
XX
PD   26-JUN-2003.
XX
PF   25-JUL-2002; 2002US-00207655.
XX
PR   17-JAN-2001; 2001US-0367358P.
PR   17-JAN-2002; 2002US-00053530.
PR   03-JUN-2002; 2002US-0385691P.
XX
PA   (GENE-) GENECRAFT INC.
XX
PI   Ledbetter JA,  Hayden-Ledbetter MS,  Thompson PA;
XX
DR   WPI; 2003-801317/75.
XX
PT   New binding domain-immunoglobulin fusion protein, useful for treating a
PT   subject having or suspected of having a malignant condition or a B-cell
PT   disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
PS   Disclosure; SEQ ID NO 207; 157pp; English.
XX
CC   Unidentified
XX
SQ   Sequence 714 BP; 180 A; 231 C; 186 G; 117 T; 0 U; 0 Other;

  Query Match           59.1%;  Score 679.2;  DB 9;  Length 714;
  Best Local Similarity 97.5%;  Pred. No. 1.4e-144;
  Matches  690;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          2 ATATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAAC 61
              ||  ||| || ||||||  ||||||||||||||||| ||||| || ||||| || ||||
Db          5 ATCAGGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC 64

Qy         62 TCCTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCT 121
              |||||||||| || ||||||||||||||||||||||||||||||||||||||||||||||
Db         65 TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCT 124

Qy        122 CCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 CCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA 184

Qy        182 AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG 244

Qy        242 AGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 AGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGC 304

Qy        302 TGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGA 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 TGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGA 364

Qy        362 AAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCAT 421
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 AAACAATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCAT 424

Qy        422 CCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATC 481
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        425 CCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATC 484

Qy        482 CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCA 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCA 544

Qy        542 CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACA 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACA 604

Qy        602 AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACA 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACA 664

Qy        662 ACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGA 709
              |||||||||||||||||||||||||||||||||||  | | |
Db        665 ACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGATCTA 712
```

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RESULT 15
ABL35776
ID   ABL35776 standard; DNA; 748 BP.
XX
AC   ABL35776;
XX
DT   05-APR-2002  (first entry)
XX
DE   Fc-MMP inhibitor fusion amino acid SEQ ID NO:1068.
XX
KW   Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW   erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW   TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW   TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW   MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW   cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW   antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW   neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW   cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW   sleep disorder; neurological degenerative disease; anaemia;
KW   thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW   Fanconi's syndrome; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200183525-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US014310.
XX
PR   03-MAY-2000; 2000US-00563286.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C,  Cheetham JC,  Boone TC,  Gudas JM;
XX
DR   WPI; 2002-130313/17.
DR   P-PSDB; ABB73426.
XX
PT   Novel vehicle-peptide molecule or its multimers useful for treating
PT   inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT   diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS   Example 7; Fig 25A-B; 176pp; English.
XX
CC   The present invention describes a vehicle-peptide molecule (I) or its
CC   multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC   cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC   antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC   neuroprotective activities. (I) can be used as a therapeutic or
CC   prophylactic agent as well as for screening purposes. (I) is useful for
CC   diagnosing diseases characterised by dysfunction of their associated
CC   protein of interest, for identifying normal or abnormal proteins of
CC   interest, as a part of diagnostic kit to detect the presence of their
CC   proteins of interest in a biological sample. Additionally, (I) is useful
CC   for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC   rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC   infertility, and neurological degenerative diseases. (I), comprising EPO-
CC   mimetic compounds are useful for treating disorders characterised by low
CC   red blood cell levels such as anaemia. The TPO-mimetic comprising
CC   compounds are useful for treating conditions that involve an existing
CC   megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC   deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC   tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC   and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC   represent amino acid and nucleic acid sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 748 BP; 180 A; 240 C; 201 G; 127 T; 0 U; 0 Other;
```

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  Query Match           59.0%;  Score 678.8;  DB 6;  Length 748;
  Best Local Similarity 99.7%;  Pred. No. 1.7e-144;
  Matches  680;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 81
              ||||||||||||||||||||||||||||||||||||||||||||||||| || ||||||
Db          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126

Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246

Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366

Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||
Db        667 CTCTCCCTGTCTCCGGGTAAAG 688
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 13:07:09 ; Search time 63.5 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1246516

Minimum DB seq length: 0
Maximum DB seq length: 1150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	680.8	59.2	794	4	US-09-428-082B-5	Sequence 5, Appli
2	680.8	59.2	812	4	US-09-428-082B-15	Sequence 15, Appl
3	680.8	59.2	861	4	US-09-428-082B-7	Sequence 7, Appli
4	679.2	59.1	1080	4	US-09-180-100-14	Sequence 14, Appl
5	678.8	59.0	748	4	US-09-428-082B-1067	Sequence 1067, Ap
6	678.8	59.0	757	4	US-09-428-082B-1055	Sequence 1055, Ap
7	678.8	59.0	763	4	US-09-428-082B-1059	Sequence 1059, Ap
8	678.4	59.0	1019	3	US-09-178-869-1	Sequence 1, Appli
9	678.4	59.0	1019	4	US-09-761-413-1	Sequence 1, Appli
10	677.8	58.9	684	4	US-09-428-082B-1	Sequence 1, Appli
11	677.8	58.9	684	4	US-09-847-249A-1	Sequence 1, Appli
12	676.8	58.9	699	2	US-08-595-043A-49	Sequence 49, Appl
13	675.8	58.8	757	4	US-09-428-082B-1061	Sequence 1061, Ap
14	675.8	58.8	761	4	US-09-428-082B-1057	Sequence 1057, Ap
15	675.8	58.8	763	4	US-09-428-082B-1069	Sequence 1069, Ap
16	675.8	58.8	789	4	US-09-428-082B-11	Sequence 11, Appl
17	675.8	58.8	855	4	US-09-428-082B-9	Sequence 9, Appli
18	675.6	58.7	1135	1	US-08-236-311-8	Sequence 8, Appli
19	675.6	58.7	1135	3	US-08-457-918-8	Sequence 8, Appli
20	675	58.7	807	4	US-09-428-082B-17	Sequence 17, Appl
21	675	58.7	881	4	US-09-428-082B-19	Sequence 19, Appl
22	674	58.6	990	4	US-09-301-593-21	Sequence 21, Appl
23	673.8	58.6	768	2	US-08-284-391B-32	Sequence 32, Appl
24	673.8	58.6	768	3	US-09-218-950-32	Sequence 32, Appl
25	673.6	58.6	705	3	US-09-131-247-5	Sequence 5, Appli
26	673	58.5	773	4	US-09-428-082B-1065	Sequence 1065, Ap
27	672.8	58.5	885	4	US-09-428-082B-21	Sequence 21, Appl
28	672.4	58.5	693	1	US-08-322-805-3	Sequence 3, Appli
29	672.4	58.5	693	2	US-08-429-499-3	Sequence 3, Appli
30	672.4	58.5	693	3	US-09-152-733-3	Sequence 3, Appli
31	670.8	58.3	705	4	US-09-023-655-1223	Sequence 1223, Ap
32	670.8	58.3	773	4	US-09-428-082B-1063	Sequence 1063, Ap
33	669.4	58.2	1050	1	US-07-940-861-42	Sequence 42, Appl
34	669.4	58.2	1050	1	US-08-459-512-42	Sequence 42, Appl
35	669.4	58.2	1050	2	US-08-459-657-42	Sequence 42, Appl
36	669.4	58.2	1050	2	US-08-460-132-42	Sequence 42, Appl
37	669.4	58.2	1050	3	US-08-466-465-7	Sequence 7, Appli
38	669.4	58.2	1050	5	PCT-US92-02050-42	Sequence 42, Appl
39	668.2	58.1	706	4	US-09-122-144-1	Sequence 1, Appli
40	668.2	58.1	745	1	US-07-943-843-7	Sequence 7, Appli
41	668.2	58.1	745	1	US-08-236-918A-14	Sequence 14, Appl
42	668.2	58.1	745	1	US-08-347-003-7	Sequence 7, Appli
43	668.2	58.1	745	4	US-09-150-864A-14	Sequence 14, Appl
44	667.8	58.1	705	1	US-07-797-556-3	Sequence 3, Appli
45	667.8	58.1	705	1	US-08-308-881-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-428-082B-5
; Sequence 5, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 794
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc-TMP
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(779)
; OTHER INFORMATION:
US-09-428-082B-5

Query Match 59.2%; Score 680.8; DB 4; Length 794;
Best Local Similarity 98.3%; Pred. No. 3.8e-167;
Matches 688; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
              | |||   | ||  |   ||||||||||||||||||||||||||||||||||||||||||||
Db         24 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 83

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
              |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 143

Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 203

Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 263

Qy        244 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 303
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;   OTHER INFORMATION: Fc MMP INHIBITOR
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(732)
;   OTHER INFORMATION:
US-09-428-082B-1067

  Query Match             59.0%;  Score 678.8;  DB 4;  Length 748;
  Best Local Similarity   99.7%;  Pred. No. 1.2e-166;
  Matches  680;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 81
              ||||||||||||||||||||||||||||||||||||||||||||||||||| || ||||||
Db          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126

Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246

Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366

Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||
Db        667 CTCTCCCTGTCTCCGGGTAAAG 688


RESULT 6
US-09-428-082B-1055
; Sequence 1055, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/09/428,082B
;  CURRENT FILING DATE:  1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1055
;   LENGTH: 757
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: FC-TNF-ALPA INHIBITORS
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(747)
;   OTHER INFORMATION:
US-09-428-082B-1055

  Query Match             59.0%;  Score 678.8;  DB 4;  Length 757;
  Best Local Similarity   99.7%;  Pred. No. 1.2e-166;
  Matches  680;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 81
              ||||||||||||||||||||||||||||||||||||||||||||||||||| || ||||||
Db          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126

Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246

Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366

Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||
Db        667 CTCTCCCTGTCTCCGGGTAAAG 688


RESULT 7
US-09-428-082B-1059
; Sequence 1059, Application US/09428082B
; Patent No. 6660843
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; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/09/428,082B
;  CURRENT FILING DATE:  1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1059
;   LENGTH: 763
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: FC-IL-1 ANTAGONIST
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(747)
;   OTHER INFORMATION:
US-09-428-082B-1059

  Query Match             59.0%;  Score 678.8;  DB 4;  Length 763;
  Best Local Similarity   99.7%;  Pred. No. 1.3e-166;
  Matches  680;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 81
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Db          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126

Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246

Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366

Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
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Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
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Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||
Db        667 CTCTCCCTGTCTCCGGGTAAAG 688


RESULT 8
US-09-178-869-1
; Sequence 1, Application US/09178869B
; Patent No. 6197294
; GENERAL INFORMATION:
;  APPLICANT: Tao, Weng
;  APPLICANT: Wong, Shou
;  APPLICANT: Hickey, William F
;  APPLICANT: Hammang, Joseph P.
;  APPLICANT: Baetge, E. Edward
;  TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
;  FILE REFERENCE: 17810-043
;  CURRENT APPLICATION NUMBER: US/09/178,869B
;  CURRENT FILING DATE: 1998-10-26
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1019
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: ()..)
;   OTHER INFORMATION: Description of Sequence: Recombinant
;   OTHER INFORMATION: Polynucleotide
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (16)..(1008)
US-09-178-869-1

  Query Match             59.0%;  Score 678.4;  DB 3;  Length 1019;
  Best Local Similarity   98.4%;  Pred. No. 1.8e-166;
  Matches  685;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          7 GAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTG 66
              || || ||||||  ||||||||||||||||||| ||||| || ||||| || |||||||||
Db        313 GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 372

Qy         67 GGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 126
              |||||  || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 432

Qy        127 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 492

Qy        187 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 552

Qy        247 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 612

Qy        307 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 672

Qy        367 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 732

Qy        427 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        733 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 792

Qy        487 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 546
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Db        793 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 852

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Db        853 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 912

Qy        607 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 666
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Db        913 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 972

Qy        667 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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Db        973 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1008


RESULT 9
US-09-761-413-1
; Sequence 1, Application US/09761413
; Patent No. 6506891
; GENERAL INFORMATION:
;  APPLICANT: Tao, Weng
;  APPLICANT:  Wong, Shou
;  APPLICANT:  Hickey, William F
;  APPLICANT:  Hammang, Joseph P.
;  APPLICANT:  Baetge, E. Edward
;  TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
;  FILE REFERENCE: 17810-043
;  CURRENT APPLICATION NUMBER: US/09/761,413
;  CURRENT FILING DATE:  2001-01-16
;  PRIOR APPLICATION NUMBER: US/09/178,869
;  PRIOR FILING DATE: 1998-10-26
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1019
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: ()..)
;   OTHER INFORMATION: Description of Sequence: Recombinant
;   OTHER INFORMATION: Polynucleotide
;   NAME/KEY: CDS
;   LOCATION: (16)..(1008)
US-09-761-413-1

  Query Match           59.0%;  Score 678.4;  DB 4;  Length 1019;
  Best Local Similarity  98.4%;  Pred. No. 1.8e-166;
  Matches  685;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          7 GAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTG 66
              || || ||||||  ||||||||||||||||||| ||||| || |||||| || |||||||||
Db        313 GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 372

Qy         67 GGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 126
              ||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 432

Qy        127 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 492

Qy        187 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 552

Qy        247 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 612

Qy        307 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 672

Qy        367 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 732

Qy        427 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        733 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 792

Qy        487 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        793 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 852

Qy        547 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        853 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 912

Qy        607 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        913 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 972

Qy        667 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||||||||||||||||||||||||||||||||
Db        973 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1008


RESULT 10
US-09-428-082B-1
; Sequence 1, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/09/428,082B
;  CURRENT FILING DATE:  1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 684
;   TYPE: DNA
;   ORGANISM: HUMAN
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(684)
;   OTHER INFORMATION:
US-09-428-082B-1

  Query Match           58.9%;  Score 677.8;  DB 4;  Length 684;
  Best Local Similarity  99.7%;  Pred. No. 2.2e-166;
  Matches  679;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 81
              ||||||||||||||||||||||||||||||||||||||||||||||||||| || ||||||
Db          4 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCAGTC 63

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 123

Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 183

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 243
```

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Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 303

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 363

Qy        382 GGGCAGCCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 GGGCAGCCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 423

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 483

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 543

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 603

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 663

Qy        682 CTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||
Db        664 CTCTCCCTGTCTCCGGGTAAA 684
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RESULT 11
US-09-847-249A-1
; Sequence 1, Application US/09847249A
; Patent No. 6677136
; GENERAL INFORMATION:
; APPLICANT: MARSHALL, WILLIAM S.
; APPLICANT: STARK, KEVIN LEE
; TITLE OF INVENTION: GLUCAGON ANTAGONIST
; FILE REFERENCE: A-693
; CURRENT APPLICATION NUMBER: US/09/847,249A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,436
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(684)
; OTHER INFORMATION:
US-09-847-249A-1

Query Match 58.9%; Score 677.8; DB 4; Length 684;
Best Local Similarity 99.7%; Pred. No. 2.2e-166;
Matches 679; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy         22 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 81
              ||||||||||||||||||||||||||||||||||||||||||||||||| || ||||||
Db          4 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCAGTC 63

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 123

Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 183
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Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 243

Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 303

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 363

Qy        382 GGGCAGCCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 GGGCAGCCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 423

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 483

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 543

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 603

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 663

Qy        682 CTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||
Db        664 CTCTCCCTGTCTCCGGGTAAA 684
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RESULT 12
US-08-595-043A-49
; Sequence 49, Application US/08595043A
; Patent No. 5935824
; GENERAL INFORMATION:
; APPLICANT: SGARLATO, GREGORY D.
; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,043A
; FILING DATE: 31-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: SGAR-00371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 699 base pairs
; TYPE: nucleic acid

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;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..699
US-08-595-043A-49

  Query Match           58.9%;  Score 676.8;  DB 2;  Length 699;
  Best Local Similarity  98.3%;  Pred. No. 4e-166;
  Matches  684;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          7 GAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTG 66
              || || ||||||  ||||||||||||||||||| ||||| || ||||| || |||||||||
Db          1 GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCAGAACTCCTG 60

Qy         67 GGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 126
              ||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 120

Qy        127 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 180

Qy        187 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 240

Qy        247 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 306
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        241 TACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 300

Qy        307 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 360

Qy        367 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 420

Qy        427 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 480

Qy        487 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 540

Qy        547 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 600

Qy        607 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 660

Qy        667 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||
Db        661 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 696


RESULT 13
US-09-428-082B-1061
; Sequence 1061, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/09/428,082B
;  CURRENT FILING DATE:  1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1061
;   LENGTH: 757
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-1 ANTAGONIST-FC
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(747)
;   OTHER INFORMATION:
US-09-428-082B-1061

  Query Match           58.8%;  Score 675.8;  DB 4;  Length 757;
  Best Local Similarity  98.3%;  Pred. No. 7.5e-166;
  Matches  683;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy         18 TGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTC 77
              || |||||||||||||||||||||||| ||||| || |||||||||||||| || ||
Db         63 TGGGGACAAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCGTC 122

Qy         78 AGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGT 137
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 AGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGT 182

Qy        138 CACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGT 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 CACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGT 242

Qy        198 GGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAC 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAC 302

Qy        258 GTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTA 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTA 362

Qy        318 CAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGC 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 CAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGC 422

Qy        378 CAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGAC 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 CAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGAC 482

Qy        438 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT 542

Qy        498 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA 557
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA 602

Qy        558 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 617
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 662

Qy        618 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 677
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        663 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 722

Qy        678 GAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCC 712
              |||||||||||||||||||||||||   |  |||||
Db        723 GAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC 757


RESULT 14
US-09-428-082B-1057
; Sequence 1057, Application US/09428082B
```

; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1057
; LENGTH: 761
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TNF-ALPHA INHIBITOR-Fc
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(747)
; OTHER INFORMATION:
US-09-428-082B-1057

Query Match 58.8%; Score 675.8; DB 4; Length 761;
Best Local Similarity 98.3%; Pred. No. 7.5e-166;
Matches 683; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```
Qy         18 TGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTC 77
              ||  |||||||||||||||||||||||||| ||||| || ||||||||||||||| || ||
Db         63 TGGGGACAAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCGTC 122

Qy         78 AGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGT 137
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 AGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGT 182

Qy        138 CACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGT 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 CACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGT 242

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Db        243 GGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAC 302

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Qy        318 CAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGC 377
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; Sequence 1069, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1069
; LENGTH: 763
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MMP INHIBITOR-Fc
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(753)
; OTHER INFORMATION:
US-09-428-082B-1069

Query Match 58.8%; Score 675.8; DB 4; Length 763;
Best Local Similarity 98.3%; Pred. No. 7.5e-166;
Matches 683; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Search completed: May 7, 2004, 12:55:33
Job time : 64.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:36 ; Search time 371.25 Seconds
(without alignments)
14032.296 Million cell updates/sec

Title: US-10-679-999-10
Perfect score: 1150
Sequence: 1 CATATGGAACCAAAATCTGC.....TCCGGGTTGTTAATGGATCC 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 4872186

Minimum DB seq length: 0
Maximum DB seq length: 1150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	1134	98.6	1150	13	US-10-679-999-7	Sequence 7, Appli
3	1129	98.2	1135	13	US-10-679-999-13	Sequence 13, Appl
4	1103.4	95.9	1135	13	US-10-679-999-16	Sequence 16, Appl
5	680.8	59.2	794	12	US-10-645-761-5	Sequence 5, Appli
6	680.8	59.2	794	13	US-10-609-217-5	Sequence 5, Appli
7	680.8	59.2	794	13	US-10-632-388-5	Sequence 5, Appli
8	680.8	59.2	794	13	US-10-651-723-5	Sequence 5, Appli
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22	679.4	59.1	1094	13	US-10-272-899A-71	Sequence 71, Appl
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ALIGNMENTS

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US-10-679-999-10
; Sequence 10, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;       APPLICANT: Mann, Michael B.
;                  Hecht, Randy I.
;       TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                           METHODS
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Amgen Inc.
;            STREET: 1840 DeHavilland Drive
;            CITY: Thousand Oaks
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 91320-1789
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/679,999
;            FILING DATE: 06-Oct-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/568,528
;            FILING DATE: 09-May-2000
;            APPLICATION NUMBER: 09/267,517
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Knight, Matthew W.
;            REGISTRATION NUMBER: 36,846
;            REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 10:
;       SEQUENCE CHARACTERISTICS:
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;           LENGTH: 1150 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: double
;           TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;           NAME/KEY:  misc_feature
;           LOCATION:  4
;           OTHER INFORMATION:  /note= "Met = ATG"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-679-999-10

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; Publication No. US20040067520A1
;  GENERAL INFORMATION:
;       APPLICANT: Mann, Michael B.
;                  Hecht, Randy I.
;       TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                           METHODS
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Amgen Inc.
;            STREET: 1840 DeHavilland Drive
;            CITY: Thousand Oaks
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 91320-1789
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
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;            APPLICATION NUMBER: US/10/679,999
;            FILING DATE: 06-Oct-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/568,528
;            FILING DATE: 09-May-2000
;            APPLICATION NUMBER: 09/267,517
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Knight, Matthew W.
;            REGISTRATION NUMBER: 36,846
;            REFERENCE/DOCKET NUMBER: A-416
;  INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1150 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
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  Best Local Similarity  99.1%;  Pred. No. 4.8e-309;
  Matches 1140;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 CATATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAA 60
              |||||||||| ||||||  |||||||||||||||||| ||||| || ||||| || |||
Db          1 CATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA 60

Qy         61 CTCCTGGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120
              |||||||||| || ||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120

Qy        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180

Qy        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240

Qy        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300

Qy        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360

Qy        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420

Qy        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480

Qy        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540

Qy        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600

Qy        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660

Qy        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720

Qy        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780

Qy        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840

Qy        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900

Qy        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960

Qy        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020

Qy       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080

Qy       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140

Qy       1141 TAATGGATCC 1150
              ||||||||||
Db       1141 TAATGGATCC 1150
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RESULT 3
US-10-679-999-13
; Sequence 13, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1135 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION:  4
;             OTHER INFORMATION:  /note= "Met = ATG"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-679-999-13

  Query Match           98.2%;  Score 1129;  DB 13;  Length 1135;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-307;
  Matches 1129;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 81
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
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Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246

Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366

Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726

Qy        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786

Qy        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846

Qy        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906

Qy        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966

Qy        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026

Qy       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086

Qy       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135


RESULT 4
US-10-679-999-16
; Sequence 16, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 16:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1135 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION:  4
;             OTHER INFORMATION:  /note= "Met = ATG"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-679-999-16

  Query Match             95.9%;  Score 1103.4;  DB 13;  Length 1135;
  Best Local Similarity   98.6%;  Pred. No. 2e-300;
  Matches 1113;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 81
              |||||||||||||||| ||||| || ||||||||||||||    || ||||| ||||||
Db          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126

Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246

Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
              |||||||||||||||||||||||||||||||||||||||||||||||| | |||||||||
Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
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Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726

Qy        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786

Qy        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846

Qy        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906

Qy        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981
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Db        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966

Qy        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026

Qy       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086

Qy       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
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Db       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135


RESULT 5
US-10-645-761-5
; Sequence 5, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/645,761
;  CURRENT FILING DATE:  2003-08-18
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;  LENGTH: 794
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Fc-TMP
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (39)..(779)
;  OTHER INFORMATION:
US-10-645-761-5

  Query Match             59.2%;  Score 680.8;  DB 12;  Length 794;
  Best Local Similarity   98.3%;  Pred. No. 1.9e-181;
  Matches  688;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
              | |||   | ||  |  ||||||||||||||||||||||||||||||||||||||||||
Db         24 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 83

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
              |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 143

Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 203

Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 263

Qy        244 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 323

Qy        304 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 383

Qy        364 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 443

Qy        424 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 503

Qy        484 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 563

Qy        544 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 623

Qy        604 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 683

Qy        664 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||||||||||||||||||||
Db        684 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 6
US-10-609-217-5
; Sequence 5, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
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;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/609,217
;  CURRENT FILING DATE:  2003-06-27
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 794
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc-TMP
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (39)..(779)
;   OTHER INFORMATION:
US-10-609-217-5

  Query Match             59.2%;  Score 680.8;  DB 13;  Length 794;
  Best Local Similarity   98.3%;  Pred. No. 1.9e-181;
  Matches  688;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
              | |||   | ||  |   |||||||||||||||||||||||||||||||||||||||||
Db         24 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 83

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
              |||||||| || |||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 143

Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 203

Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 263

Qy        244 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 303
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 323

Qy        304 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 363
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 383

Qy        364 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 423
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 443

Qy        424 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 483
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 503

Qy        484 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 543
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 563

Qy        544 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 603
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 623

Qy        604 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 663
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 683

Qy        664 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||||||||||||||||||||||
Db        684 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
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RESULT 7
US-10-632-388-5
; Sequence 5, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/632,388
;  CURRENT FILING DATE:  2003-07-31
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 794
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc-TMP
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (39)..(779)
;   OTHER INFORMATION:
US-10-632-388-5

  Query Match             59.2%;  Score 680.8;  DB 13;  Length 794;
  Best Local Similarity   98.3%;  Pred. No. 1.9e-181;
  Matches  688;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
              | |||   | ||  |   |||||||||||||||||||||||||||||||||||||||||
Db         24 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 83

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
              |||||||| || |||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 143

Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 203

Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 263

Qy        244 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 303
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 323

Qy        304 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 363
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 383

Qy        364 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 423
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 443

Qy        424 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 483
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 503

Qy        484 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 543
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 563
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Qy        544 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 623

Qy        604 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 683

Qy        664 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||||||||||||||||||||
Db        684 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 8
US-10-651-723-5
; Sequence 5, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/651,723
;  CURRENT FILING DATE:  2003-08-29
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 794
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc-TMP
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (39)..(779)
;   OTHER INFORMATION:
US-10-651-723-5

  Query Match             59.2%;  Score 680.8;  DB 13;  Length 794;
  Best Local Similarity   98.3%;  Pred. No. 1.9e-181;
  Matches  688;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
              | |||   | ||  |   ||||||||||||||||||||||||||||||||||||||||||||
Db         24 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 83

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
              |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 143

Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 203

Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 263

Qy        244 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 323

Qy        304 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 383

Qy        364 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 443

Qy        424 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 503

Qy        484 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 563

Qy        544 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 623

Qy        604 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 683

Qy        664 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||||||||||||||||||||
Db        684 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 9
US-10-666-696-5
; Sequence 5, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  APPLICANT:  GUDAS, JEAN MARIE
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527A
;  CURRENT APPLICATION NUMBER: US/10/666,696
;  CURRENT FILING DATE:  2003-09-19
;  PRIOR APPLICATION NUMBER: US/09/563,286C
;  PRIOR FILING DATE: 2000-05-03
;  PRIOR APPLICATION NUMBER: 09/428,082
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1157
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 794
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc-TMP
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (39)..(779)
;   OTHER INFORMATION:
US-10-666-696-5

  Query Match             59.2%;  Score 680.8;  DB 17;  Length 794;
  Best Local Similarity   98.3%;  Pred. No. 1.9e-181;
  Matches  688;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
              | |||   | ||  |   ||||||||||||||||||||||||||||||||||||||||||||
Db         24 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 83

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
              |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 143

Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 203
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Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 263

Qy        244 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 323

Qy        304 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 383

Qy        364 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 443

Qy        424 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 503

Qy        484 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 563

Qy        544 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 623

Qy        604 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 683

Qy        664 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||||||||||||||||||||
Db        684 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 10
US-10-645-761-15
; Sequence 15, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/645,761
;  CURRENT FILING DATE:  2003-08-18
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 812
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc-EMP
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (39)..(797)
;   OTHER INFORMATION:
US-10-645-761-15

  Query Match             59.2%;  Score 680.8;  DB 12;  Length 812;
  Best Local Similarity   98.3%;  Pred. No. 1.9e-181;
  Matches  688;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;
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Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
              | |||    | ||   |    ||||||||||||||||||||||||||||||||||||||
Db         24 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 83

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
              |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 143

Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 203

Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 263

Qy        244 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 323

Qy        304 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 383

Qy        364 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 443

Qy        424 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 503

Qy        484 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 563

Qy        544 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 623

Qy        604 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 683

Qy        664 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||||||||||||||||||||
Db        684 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 11
US-10-609-217-15
; Sequence 15, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/609,217
;  CURRENT FILING DATE:  2003-06-27
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 812
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
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;   OTHER INFORMATION: Fc-EMP
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (39)..(797)
;   OTHER INFORMATION:
US-10-609-217-15

  Query Match             59.2%;  Score 680.8;  DB 13;  Length 812;
  Best Local Similarity   98.3%;  Pred. No. 1.9e-181;
  Matches  688;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
              | |||    | ||   |   ||||||||||||||||||||||||||||||||||||||||||||
Db         24 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 83

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
              |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 143

Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 203

Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 263

Qy        244 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 323

Qy        304 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 383

Qy        364 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 443

Qy        424 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 503

Qy        484 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 563

Qy        544 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 623

Qy        604 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 683

Qy        664 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||||||||||||||||||||
Db        684 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 12
US-10-632-388-15
; Sequence 15, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/632,388
;  CURRENT FILING DATE:  2003-07-31
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 812
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc-EMP
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (39)..(797)
;   OTHER INFORMATION:
US-10-632-388-15

  Query Match             59.2%;  Score 680.8;  DB 13;  Length 812;
  Best Local Similarity   98.3%;  Pred. No. 1.9e-181;
  Matches  688;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
              | |||    | ||   |   ||||||||||||||||||||||||||||||||||||||||||||
Db         24 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 83

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
              |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 143

Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 203

Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 263

Qy        244 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 323

Qy        304 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 383

Qy        364 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 443

Qy        424 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 503

Qy        484 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 563

Qy        544 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 623

Qy        604 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 683

Qy        664 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||||||||||||||||||||
Db        684 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 13
US-10-651-723-15
```

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; Sequence 15, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/651,723
;  CURRENT FILING DATE:  2003-08-29
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 812
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc-EMP
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (39)..(797)
;   OTHER INFORMATION:
US-10-651-723-15

  Query Match            59.2%;  Score 680.8;  DB 13;  Length 812;
  Best Local Similarity  98.3%;  Pred. No. 1.9e-181;
  Matches  688;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
              | |||   | ||  |   ||||||||||||||||||||||||||||||||||||||||||||||
Db         24 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 83

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
              |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 143

Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 203

Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 263

Qy        244 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 323

Qy        304 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 383

Qy        364 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 443

Qy        424 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 503

Qy        484 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 563

Qy        544 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 623

Qy        604 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 683

Qy        664 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||||||||||||||||||||
Db        684 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 14
US-10-666-696-15
; Sequence 15, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  APPLICANT:  GUDAS, JEAN MARIE
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527A
;  CURRENT APPLICATION NUMBER: US/10/666,696
;  CURRENT FILING DATE:  2003-09-19
;  PRIOR APPLICATION NUMBER: US/09/563,286C
;  PRIOR FILING DATE: 2000-05-03
;  PRIOR APPLICATION NUMBER: 09/428,082
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1157
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 812
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: EMP-Fc
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (39)..(797)
;   OTHER INFORMATION:
US-10-666-696-15

  Query Match            59.2%;  Score 680.8;  DB 17;  Length 812;
  Best Local Similarity  98.3%;  Pred. No. 1.9e-181;
  Matches  688;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
              | |||   | ||  |   ||||||||||||||||||||||||||||||||||||||||||||||
Db         24 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 83

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
              |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 143

Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 203

Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 263

Qy        244 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 323

Qy        304 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 383

Qy        364 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        384 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 443

Qy        424 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 503

Qy        484 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 563

Qy        544 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 623

Qy        604 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 683

Qy        664 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||||||||||||||||||||
Db        684 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 15
US-10-269-806-151
; Sequence 151, Application US/10269806
; Publication No. US20030176352A1
; GENERAL INFORMATION:
;  APPLICANT: Min, Hosung
;  APPLICANT:  Sitney, Karen
;  APPLICANT:  Hartley, Cynthia
;  TITLE OF INVENTION: Peptides and Related Compounds Having Thrombopoietic Activity
;  FILE REFERENCE: A-750
;  CURRENT APPLICATION NUMBER: US/10/269,806
;  CURRENT FILING DATE:  2002-10-10
;  NUMBER OF SEQ ID NOS: 199
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 151
;   LENGTH: 837
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthesized Peptide Sequence
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (57)..(785)
;   OTHER INFORMATION:
US-10-269-806-151

  Query Match             59.2%;  Score 680.8;  DB 15;  Length 837;
  Best Local Similarity   98.3%;  Pred. No. 1.9e-181;
  Matches  688;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          4 ATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 63
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Db         42 AAGGAGGAATAACATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTC 101

Qy         64 CTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 123
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Qy        124 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 183
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Qy        184 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 243
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Qy        244 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 303
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Qy        304 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 363
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Qy        364 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 423
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Qy        424 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 521

Qy        484 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 543
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Db        522 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 581

Qy        544 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 603
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Db        582 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 641

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Qy        664 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
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Search completed: May  9, 2004, 11:51:58
Job time : 373.25 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 13:07:09 ; Search time 2222.5 Seconds
(without alignments)
15451.747 Million cell updates/sec

Title: US-10-679-999-10
Perfect score: 1150
Sequence: 1 CATATGGAACCAAAATCTGC.....TCCGGGTTGTTAATGGATCC 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 54314686

Minimum DB seq length: 0
Maximum DB seq length: 1150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
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17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
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22: em_gss_mam:*
23: em_gss_mus:*
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26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	678.8	59.0	871	12	BG753979	BG753979 602709506
2	678.8	59.0	983	13	BQ708975	BQ708975 AGENCOURT
3	678	59.0	843	12	BM007897	BM007897 603617582
4	677.8	58.9	941	13	BQ712021	BQ712021 AGENCOURT
5	677.2	58.9	925	13	BQ709152	BQ709152 AGENCOURT
6	676.4	58.8	973	13	BQ706204	BQ706204 AGENCOURT
7	676.2	58.8	858	13	BX346946	BX346946 BX346946
8	675.6	58.7	919	13	BQ709339	BQ709339 AGENCOURT
9	675	58.7	897	13	BQ709144	BQ709144 AGENCOURT
10	674	58.6	947	13	BQ709771	BQ709771 AGENCOURT
11	673.8	58.6	881	13	BQ711291	BQ711291 AGENCOURT
c 12	671.8	58.4	1013	13	BX360518	BX360518 BX360518
13	671.4	58.4	757	12	BG674795	BG674795 602620925
14	671.4	58.4	914	13	BQ712363	BQ712363 AGENCOURT
15	669.6	58.2	856	13	BQ709859	BQ709859 AGENCOURT
16	666.8	58.0	892	12	BG397723	BG397723 602438784
17	666.8	58.0	897	12	BM008412	BM008412 603617406
18	666.8	58.0	902	13	BU146962	BU146962 AGENCOURT
c 19	665.6	57.9	1015	13	BX367600	BX367600 BX367600
c 20	665.2	57.8	1147	13	BX360330	BX360330 BX360330
c 21	664.8	57.8	860	13	BX437583	BX437583 BX437583
c 22	664.4	57.8	954	12	BG746184	BG746184 602723696
c 23	664.4	57.8	985	13	BX457369	BX457369 BX457369
c 24	664.4	57.8	1034	13	BX337959	BX337959 BX337959
25	663	57.7	940	13	BQ705928	BQ705928 AGENCOURT
c 26	662.8	57.6	1142	13	BX414495	BX414495 BX414495
c 27	662.4	57.6	898	13	BX415442	BX415442 BX415442
28	661.4	57.5	958	13	BQ706140	BQ706140 AGENCOURT
29	661.4	57.5	961	13	BQ710233	BQ710233 AGENCOURT
c 30	660.8	57.5	885	13	BX437308	BX437308 BX437308
c 31	659.4	57.3	879	13	BX336029	BX336029 BX336029
c 32	658.4	57.3	1149	13	BX381020	BX381020 BX381020
33	658.2	57.2	941	13	BQ711680	BQ711680 AGENCOURT
34	658	57.2	926	12	BG755166	BG755166 602711488
35	656.8	57.1	1014	12	BM914505	BM914505 AGENCOURT
c 36	655.4	57.0	1093	13	BX428863	BX428863 BX428863
37	655.2	57.0	873	13	BQ708562	BQ708562 AGENCOURT
c 38	654.8	56.9	951	12	BG746233	BG746233 602723760
c 39	652.8	56.8	1009	13	BX456658	BX456658 BX456658
40	652.6	56.7	925	13	BQ709853	BQ709853 AGENCOURT
c 41	652.4	56.7	883	13	BX454398	BX454398 BX454398
c 42	651.4	56.6	877	13	BX324928	BX324928 BX324928
c 43	651.4	56.6	921	13	BX359858	BX359858 BX359858
c 44	650.8	56.6	1063	13	BX358861	BX358861 BX358861
c 45	649.6	56.5	980	13	BX325701	BX325701 BX325701

ALIGNMENTS

RESULT 1
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LOCUS BG753979 871 bp mRNA linear EST 15-MAY-2001
DEFINITION 602709506F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4846201 5', mRNA sequence.
ACCESSION BG753979
VERSION BG753979.1 GI:14064632
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 871)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1686 row: k column: 02
High quality sequence stop: 848.

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FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           59.0%;  Score 678.8;  DB 12;  Length 871;
  Best Local Similarity  98.3%;  Pred. No. 1.2e-129;
  Matches  686;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          5 TGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCC 64
              | || || ||||||  ||||||||||||||||| ||||| || ||||| || |||||||
Db         20 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 79

Qy         65 TGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
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Db         80 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 139

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
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Db        140 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 199

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
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Db        200 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 259

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
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Db        320 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 379

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
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Db        440 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 499

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Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
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Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
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RESULT 2
BQ708975
LOCUS       BQ708975                983 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8353514 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279683
            5', mRNA sequence.
ACCESSION   BQ708975
VERSION     BQ708975.1  GI:21847874
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 983)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2469  row: k  column: 12
            High quality sequence stop: 604.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match           59.0%;  Score 678.8;  DB 13;  Length 983;
  Best Local Similarity  98.3%;  Pred. No. 1.3e-129;
  Matches  686;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          5 TGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCC 64
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Qy         65 TGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
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Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
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Db        127 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 186

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
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Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
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RESULT 3
BM007897
LOCUS BM007897 843 bp mRNA linear EST 30-OCT-2001
DEFINITION 603617582F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450469 5', mRNA sequence.
ACCESSION BM007897
VERSION BM007897.1 GI:16522238
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 843)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1939 row: d column: 22
High quality sequence stop: 833.
FEATURES Location/Qualifiers
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/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
ORIGIN

Query Match 59.0%; Score 678; DB 12; Length 843;
Best Local Similarity 97.9%; Pred. No. 1.8e-129;
Matches 687; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy          5 TGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCC 64
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Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
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Db        211 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 270

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 330

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Db        331 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 390

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
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Db        391 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 450

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
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Db        451 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 510

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
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Db        511 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 570

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
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Db        571 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 630

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
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Db        631 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 690

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
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Db        691 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 750

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTAC 706
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Db        751 ATTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAC 792
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RESULT 4
BQ712021
LOCUS BQ712021 941 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8418162 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281403 5', mRNA sequence.
ACCESSION BQ712021
VERSION BQ712021.1 GI:21850920
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 941)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2474 row: c column: 04
High quality sequence stop: 638.

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FEATURES             Location/Qualifiers
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                     /clone="IMAGE:6281403"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN
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Query Match 58.9%; Score 677.8; DB 13; Length 941;
Best Local Similarity 98.1%; Pred. No. 2.1e-129;
Matches 685; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy          5 TGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCC 64
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Db         33 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 92

Qy         65 TGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
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Db         93 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 152

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 212

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
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Db        213 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 272

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Db        273 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 332

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
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Db        333 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 392

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
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Db        393 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 452

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 512

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
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Db        513 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 572

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
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Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
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Db        633 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGANGCTCTGCACAACC 692

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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Db        693 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 730
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RESULT 5
BQ709152
LOCUS       BQ709152                925 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8485151 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301245
            5', mRNA sequence.
ACCESSION   BQ709152
VERSION     BQ709152.1  GI:21848051
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 925)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2516  row: m  column: 22
            High quality sequence stop: 739.
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN
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Query Match 58.9%; Score 677.2; DB 13; Length 925;
Best Local Similarity 98.1%; Pred. No. 2.7e-129;
Matches 685; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy          5 TGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCC 64
              | || || ||||||  ||||||||||||||||| ||||| || ||||| || |||||||
Db         31 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 90

Qy         65 TGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
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Db         91 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 150

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 210

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 270

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Db        271 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 330

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
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Db        331 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 390

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
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Db        391 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 450

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
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Db        451 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 510

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
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Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
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Db        571 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 630

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
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Db        631 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 690

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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Db        691 ACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 728


RESULT 6
BQ706204
LOCUS       BQ706204                973 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8352308 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277592
            5', mRNA sequence.
ACCESSION   BQ706204
VERSION     BQ706204.1  GI:21845103
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 973)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2464  row: d  column: 09
            High quality sequence stop: 640.
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                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match           58.8%;  Score 676.4;  DB 13;  Length 973;
  Best Local Similarity   95.0%;  Pred. No. 4e-129;
  Matches  698;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy          5 TGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCC 64
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Db         91 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 150

Qy         65 TGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
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Db        151 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 210

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
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Db        211 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 270

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
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Db        271 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 330

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Db        331 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 390

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
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Db        391 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 450

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
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Db        451 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 510

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
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Db        511 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 570

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
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Db        631 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 690

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
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Db        691 GCAGGTGGCAGCAGGNGAACGTCTTCTCATGCTCCGTGATGCATGAAGCTCTGCACAACC 750

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGG 724
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Db        751 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGCGACGGGCGGGAAAGC 810

Qy        725 ACGACACCAAAACCT 739
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Db        811 CCCCCTCCCCAGGCT 825


RESULT 7
BX346946
LOCUS       BX346946                858 bp    mRNA    linear   EST 05-MAY-2003
DEFINITION  BX346946 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI039YP09 5-PRIME, mRNA sequence.
ACCESSION   BX346946
VERSION     BX346946.1  GI:30377150
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 858)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
```

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            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 7198.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0AT021ZE05_T01957_1&cluster=7198.r.
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0AT021ZE05_T01957_1.
FEATURES              Location/Qualifiers
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                      /db_xref="taxon:9606"
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                      /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
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                      primer. Five prime end enriched, double-strand cDNA was
                      digested with Not I and cloned into the Not I and EcoR V
                      sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             58.8%;  Score 676.2;  DB 13;  Length 858;
  Best Local Similarity   98.0%;  Pred. No. 4.2e-129;
  Matches  684;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          5 TGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCC 64
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Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
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Db        168 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 227

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
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Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
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Db        408 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 467

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 527

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        528 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 587

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        588 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 647

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        648 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTNCGTGATGCATGAGGCTCTGCACAACC 707

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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Db        708 ACTACACGCAGAAGAGCCTCTCCCTGTCTTCGGGTAAA 745


RESULT 8
BQ709339
LOCUS       BQ709339                 919 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_7976429 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214450
            5', mRNA sequence.
ACCESSION   BQ709339
VERSION     BQ709339.1  GI:21848238
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 919)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2381  row: m  column: 11
            High quality sequence stop: 576.
FEATURES              Location/Qualifiers
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                      /clone_lib="NIH_MGC_113"
                      /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                      EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                      into EcoRI/XhoI sites using the following 5' adaptor:
                      GGCACGAG(G). Library constructed by Ling Hong in the
                      laboratory of Gerald M. Rubin (University of California,
                      Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                      Superscript II RT (Life Technologies). Note: this is a
                      NIH_MGC Library."
ORIGIN

  Query Match             58.7%;  Score 675.6;  DB 13;  Length 919;
  Best Local Similarity   98.0%;  Pred. No. 5.8e-129;
  Matches  684;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          5 TGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCC 64
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Db         40 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 99

Qy         65 TGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
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Db        100 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 159

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 219

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 279

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Db        280 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 339
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Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
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Db        340 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 399

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
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Db        400 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 459

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
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Db        460 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 519

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
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Db        520 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 579

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
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Db        580 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 639

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 GCAAGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 699

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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Db        700 ACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 737
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RESULT 9
BQ709144
LOCUS       BQ709144                897 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8474994 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301566
            5', mRNA sequence.
ACCESSION   BQ709144
VERSION     BQ709144.1  GI:21848043
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 897)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2517  row: k  column: 07
            High quality sequence stop: 628.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
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ORIGIN

  Query Match           58.7%;  Score 675;  DB 13;  Length 897;
  Best Local Similarity 97.9%;  Pred. No. 7.6e-129;
  Matches  684;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          5 TGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCC 64
              | || || ||||||  ||||||||||||||||||| ||||| || ||||| || |||||||
Db         33 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 92

Qy         65 TGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 152

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 212

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 272

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 332

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
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Db        333 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 392

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 452

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
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Db        453 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 512

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
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Db        513 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 572

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
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Db        573 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 632

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 692

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
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RESULT 10
BQ709771
LOCUS       BQ709771                947 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8353965 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278583
            5', mRNA sequence.
ACCESSION   BQ709771
VERSION     BQ709771.1  GI:21848670
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 947)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
```

```
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2466  row: m  column: 16
            High quality sequence start: 3
            High quality sequence stop: 675.
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match            58.6%;  Score 674;  DB 13;  Length 947;
  Best Local Similarity  97.9%;  Pred. No. 1.3e-128;
  Matches  683;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          5 TGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCC 64
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Db        180 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 239

Qy         65 TGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 299

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 359

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
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Db        360 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 419

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 479

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
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Db        480 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 539

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
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Db        540 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 599

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
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Db        600 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 659

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
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Db        660 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 719

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
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Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
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Db        780 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACCACC 839

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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Db        840 ACTACACGCAGAAGAGCCTCTCCCTGTCCTCGGGTAAA 877


RESULT 11
BQ711291
LOCUS       BQ711291                881 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8347186 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279096
            5', mRNA sequence.
ACCESSION   BQ711291
VERSION     BQ711291.1  GI:21850190
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 881)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2468  row: c  column: 01
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match            58.6%;  Score 673.8;  DB 13;  Length 881;
  Best Local Similarity  98.3%;  Pred. No. 1.3e-128;
  Matches  681;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          5 TGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCC 64
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Db        120 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 179

Qy         65 TGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
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Db        180 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 239

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
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Db        240 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 299

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
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Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Db        360 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 419

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
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Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
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Db        480 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 539

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
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Db        540 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 599

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
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Db        600 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 659

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 719

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 779

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG 697
              |||||||||||||||||||||||||||||||
Db        780 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG 812
```

```
RESULT 12
BX360518/c
LOCUS       BX360518               1013 bp    mRNA    linear   EST 05-MAY-2003
DEFINITION  BX360518 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI071YG21 3-PRIME, mRNA sequence.
ACCESSION   BX360518
VERSION     BX360518.1  GI:30372442
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1013)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 7198.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI071AD11NP1&cluster=7198.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI071AD11NP1.
FEATURES             Location/Qualifiers
     source          1. .1013
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI071YG21"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
```

```
ORIGIN

  Query Match           58.4%;  Score 671.8;  DB 13;  Length 1013;
  Best Local Similarity 97.0%;  Pred. No. 3.7e-128;
  Matches  677;  Conservative    6;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          5 TGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCC 64
              | || || |||||| ||||||||||||||||||| ||||| || ||||| || |||||||
Db        785 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 726

Qy         65 TGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||| || |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        725 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 666

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        665 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 606

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 546

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              |||||||| :|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 AGTACAACANGMCGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 486

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||:|:|||||||||||||||||||
Db        485 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTMCMAGCCCCCATCGAGAAAA 426

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 366

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTTTATCCCA 306

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 246

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 CTCCCKTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 186

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 126

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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Db        125 ACTACACGCAGAAGAGCCTCTCCCYBTCTCCGGGTAAA 88
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RESULT 13
BG674795
LOCUS       BG674795               757 bp    mRNA    linear   EST 01-MAY-2001
DEFINITION  602620925F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4746150 5',
            mRNA sequence.
ACCESSION   BG674795
VERSION     BG674795.1  GI:13906191
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 757)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
```

```
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
            Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10594  row: b  column: 07
            High quality sequence stop: 755.
FEATURES             Location/Qualifiers
     source          1. .757
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4746150"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Skn3"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match           58.4%;  Score 671.4;  DB 12;  Length 757;
  Best Local Similarity  97.6%;  Pred. No. 4e-128;
  Matches  681;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          5 TGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCC 64
              | || || ||||||  ||||||||||||||||||| ||||| || ||||| || |||||||
Db         20 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 79

Qy         65 TGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 139

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 199

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 259

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
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Db        260 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 319

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 379

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 439

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
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Db        440 GGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 499

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
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Db        500 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 559

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        560 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGA 619

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        620 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAANC 679

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
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Db        680 ACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGTAAA 717


RESULT 14
BQ712363
LOCUS       BQ712363                914 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8475100 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301405
            5', mRNA sequence.
ACCESSION   BQ712363
VERSION     BQ712363.1  GI:21851262
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 914)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2517  row: d  column: 14
            High quality sequence stop: 585.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6301405"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match           58.4%;  Score 671.4;  DB 13;  Length 914;
  Best Local Similarity  97.6%;  Pred. No. 4.3e-128;
  Matches  681;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          5 TGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCC 64
              | || || ||||||  ||||||||||||||||||| ||||| || ||||| || |||||||
Db         52 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 111

Qy         65 TGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 171

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 231

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 291

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 351

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 13:07:09 ; Search time 3070.75 Seconds
(without alignments)
16232.024 Million cell updates/sec

Title: US-10-679-999-11
Perfect score: 1150
Sequence: 1 GTATACCTTGGTTTTAGACG.....AGGCCCAACAATTACCTAGG 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 5430052

Minimum DB seq length: 0
Maximum DB seq length: 1150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
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6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
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22: em_ov:*
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24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		1150	100.0	1150	6	BD056520	BD056520 OB fusion
2		1134	98.6	1150	6	BD056518	BD056518 OB fusion
3		1129	98.2	1135	6	BD056522	BD056522 OB fusion
4		1103.4	95.9	1135	6	BD056524	BD056524 OB fusion
5		680.8	59.2	861	6	BD263010	BD263010 Dimeric t
6		677.8	58.9	684	6	BD263000	BD263000 Dimeric t
7		660.2	57.4	1142	6	I27618	I27618 Sequence 9
8		440.8	38.3	454	6	BD004077	BD004077 Methods o
9		440.8	38.3	454	6	BD056516	BD056516 OB fusion
10		378.4	32.9	491	6	BD004075	BD004075 Methods o
11		378.4	32.9	491	6	BD056514	BD056514 OB fusion
12		50.8	4.4	908	8	AB029092	AB029092 Cucumis s
13		50.8	4.4	1110	8	AB029147	AB029147 Cucumis s
14		43	3.7	468	6	I27620	I27620 Sequence 12
15		43	3.7	746	6	A51599	A51599 Sequence 9
16	c	40.4	3.5	1057	6	E02180	E02180 DNA sequenc
17	c	40.4	3.5	1057	6	E02181	E02181 DNA sequenc
18	c	40	3.5	533	6	AR365256	AR365256 Sequence
19		39.4	3.4	1011	6	AX616829	AX616829 Sequence
20	c	39	3.4	1046	3	AY058495	AY058495 Drosophil
21	c	38.6	3.4	462	10	AY300753	AY300753 Mesocrice
22	c	38.6	3.4	564	10	AY300754	AY300754 Mesocrice
23	c	37.8	3.3	451	10	MUSIR3E2	M10668 Mouse DNA w
24		37.8	3.3	789	6	AX756672	AX756672 Sequence
25		37.8	3.3	810	6	AX575331	AX575331 Sequence
26		37.8	3.3	813	6	AX467493	AX467493 Sequence
27		37.8	3.3	813	6	AX575327	AX575327 Sequence
28		37.8	3.3	815	6	AX527763	AX527763 Sequence
29		37.8	3.3	815	6	AX527765	AX527765 Sequence
30	c	37.8	3.3	1065	1	AY392156	AY392156 Streptomy
31		37.8	3.3	1147	6	AX575332	AX575332 Sequence
32		37.6	3.3	505	6	AR424142	AR424142 Sequence
33		37.6	3.3	505	6	BD119695	BD119695 EST and e
34	c	37.4	3.3	688	6	A86256	A86256 Sequence 91
35	c	37.4	3.3	688	6	AR155749	AR155749 Sequence
36	c	37.4	3.3	688	6	E66274	E66274 Genome DNA
37		37	3.2	900	4	AF510666	AF510666 Equus cab
38	c	36.8	3.2	675	1	USO539323	AJ539323 Unculture
39	c	36.6	3.2	1018	8	AF479764	AF479764 Triticum
40	c	36.4	3.2	744	6	BD180141	BD180141 Highly th
41	c	36.4	3.2	1029	4	TGU65923	U65923 Tupaia glis
42	c	36.2	3.1	393	8	AB101649	AB101649 Oryza sat
43		36.2	3.1	636	3	LTE494984	AJ494984 Liporrhop
44	c	36	3.1	675	1	USO538112	AJ538112 Unculture
45	c	36	3.1	705	6	AX432443	AX432443 Sequence

ALIGNMENTS

RESULT 1
BD056520
LOCUS BD056520 1150 bp DNA linear PAT 27-AUG-2002
DEFINITION OB fusion protein compositions and methods.
ACCESSION BD056520
VERSION BD056520.1 GI:22602126
KEYWORDS JP 2001512417-A/8.
SOURCE Aequorea victoria
ORGANISM Aequorea victoria
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
REFERENCE 1 (bases 1 to 1150)
AUTHORS Mann,M.B. and Hecht,R.I.
TITLE OB fusion protein compositions and methods
JOURNAL Patent: JP 2001512417-A 8 21-AUG-2001;

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            AMGEN INC
COMMENT     PN   JP 2001512417-A/8
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
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                    /mol_type="genomic DNA"
                    /db_xref="taxon:6100"
ORIGIN

  Query Match           100.0%;  Score 1150;  DB 6;  Length 1150;
  Best Local Similarity  100.0%;  Pred. No. 6.8e-269;
  Matches 1150;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATACCTTGGTTTTAGACGACTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTATACCTTGGTTTTAGACGACTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTT 60

Qy         61 GAGGACCCCCCCAGGAAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGGACCCCCCCAGGAAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAG 120

Qy        121 AGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAG 180

Qy        181 TTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTC 240

Qy        241 CTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACC 300

Qy        301 GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 360

Qy        361 TTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGT 420

Qy        421 AGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATA 480

Qy        481 GGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG 540

Qy        541 TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTG 600

Qy        601 TTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTG 660

Qy        661 TTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAA 720

Qy        721 GTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTG 780

Qy        781 TGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTG 840

Qy        841 GGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGG 900

Qy        901 AGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGAC 960

Qy        961 GACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA 1020

Qy       1021 GACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGAC 1080

Qy       1081 AGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACA 1140

Qy       1141 ATTACCTAGG 1150
              ||||||||||
Db       1141 ATTACCTAGG 1150


RESULT 2
BD056518
LOCUS       BD056518               1150 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056518
VERSION     BD056518.1  GI:22602124
KEYWORDS    JP 2001512417-A/6.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1150)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 6 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/6
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES            Location/Qualifiers
     source         1. .1150
                    /organism="Aequorea victoria"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:6100"
ORIGIN

  Query Match           98.6%;  Score 1134;  DB 6;  Length 1150;
  Best Local Similarity  99.1%;  Pred. No. 5.3e-265;
  Matches 1140;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 GTATACCTTGGTTTTAGACGACTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTT 60
              |||||||||| |||||| ||||||||||||||||| ||||| || ||||| || |||
Db          1 GTATACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTT 60
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Qy        61 GAGGACCCCCCAGGAAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAG 120
             |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||||
Db        61 GAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAG 120

Qy       121 AGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 AGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAG 180

Qy       181 TTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 TTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTC 240

Qy       241 CTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACC 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACC 300

Qy       301 GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 360

Qy       361 TTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGT 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 TTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGT 420

Qy       421 AGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATA 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 AGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATA 480

Qy       481 GGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG 540

Qy       541 TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTG 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTG 600

Qy       601 TTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTG 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 TTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTG 660

Qy       661 TTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAA 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 TTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAA 720

Qy       721 GTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTG 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 GTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTG 780

Qy       781 TGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTG 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 TGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTG 840

Qy       841 GGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGG 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 GGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGG 900

Qy       901 AGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGAC 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 AGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGAC 960

Qy       961 GACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 GACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA 1020

Qy      1021 GACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGAC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 GACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGAC 1080

Qy      1081 AGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACA 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 AGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACA 1140

Qy      1141 ATTACCTAGG 1150
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Db      1141 ATTACCTAGG 1150
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RESULT 3
BD056522

LOCUS	BD056522 1135 bp DNA linear PAT 27-AUG-2002
DEFINITION	OB fusion protein compositions and methods.
ACCESSION	BD056522
VERSION	BD056522.1 GI:22602128
KEYWORDS	JP 2001512417-A/10.
SOURCE	Aequorea victoria
ORGANISM	Aequorea victoria Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae; Aequoreidae; Aequorea.
REFERENCE	1 (bases 1 to 1135)
AUTHORS	Mann,M.B. and Hecht,R.I.
TITLE	OB fusion protein compositions and methods
JOURNAL	Patent: JP 2001512417-A 10 21-AUG-2001; AMGEN INC
COMMENT	PN JP 2001512417-A/10 PD 21-AUG-2001 PF 11-DEC-1997 JP 1998528896 PR 20-DEC-1996 US 08/770973 PI MICHAEL BENJAMIN MANN,RANDY IRA HECHT PC C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC A61P43/00, PC C12N15/09,C12N15/00,A61K37/02 CC Strandedness: Double; CC Topology: Linear; FH Key Location/Qualifiers.
FEATURES	Location/Qualifiers
source	1. .1135 /organism="Aequorea victoria" /mol_type="genomic DNA" /db_xref="taxon:6100"
ORIGIN	

Query Match 98.2%; Score 1129; DB 6; Length 1135;
Best Local Similarity 100.0%; Pred. No. 8.8e-264;
Matches 1129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         22 CTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGAAGTCAG 81
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 CTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGAAGTCAG 66

Qy         82 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126

Qy        142 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186

Qy        202 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246

Qy        262 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 306

Qy        322 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366

Qy        382 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426

Qy        442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
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Qy        502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561
Db        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546

Qy        562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621
Db        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606

Qy        622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681
Db        607 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 666

Qy        682 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 741
Db        667 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 726

Qy        742 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 801
Db        727 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 786

Qy        802 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 861
Db        787 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 846

Qy        862 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 921
Db        847 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 906

Qy        922 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 981
Db        907 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 966

Qy        982 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1041
Db        967 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1026

Qy       1042 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1101
Db       1027 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1086

Qy       1102 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
Db       1087 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
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RESULT 4
BD056524
LOCUS       BD056524               1135 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056524
VERSION     BD056524.1  GI:22602130
KEYWORDS    JP 2001512417-A/12.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1135)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 12 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/12
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .1135
                     /organism="Aequorea victoria"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:6100"
ORIGIN

  Query Match           95.9%;  Score 1103.4;  DB 6;  Length 1135;
  Best Local Similarity  98.6%;  Pred. No. 1.5e-257;
  Matches 1113;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         22 CTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGAAGTCAG 81
Db          7 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAG 66

Qy         82 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 141
Db         67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126

Qy        142 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 201
Db        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186

Qy        202 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 261
Db        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246

Qy        262 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 321
Db        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGT 306

Qy        322 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 381
Db        307 ACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366

Qy        382 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 441
Db        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426

Qy        442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501
Db        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486

Qy        502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561
Db        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546

Qy        562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621
Db        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606

Qy        622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681
Db        607 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 666

Qy        682 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 741
Db        667 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 726

Qy        742 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 801
Db        727 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 786

Qy        802 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 861
Db        787 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 846

Qy        862 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 921
Db        847 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 906

Qy        922 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 981
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Db        907 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 966

Qy        982 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1026

Qy       1042 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1086

Qy       1102 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
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RESULT 5
BD263010
LOCUS BD263010 861 bp DNA linear PAT 17-JUL-2003
DEFINITION Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and having thrombopoietic activity.
ACCESSION BD263010
VERSION BD263010.1 GI:33072778
KEYWORDS JP 2002536960-A/12.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 861)
AUTHORS Liu,C.F., Feige,U. and Cheetham,J.
TITLE Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and having thrombopoietic activity
JOURNAL Patent: JP 2002536960-A 12 05-NOV-2002;
AMGEN INC
COMMENT OS Artificial Sequence
PN JP 2002536960-A/12
PD 05-NOV-2002
PF 22-OCT-1999 JP 2000578340
PR 23-OCT-1998 US 60/105348
PI CHUAN FA LIU,ULRICH FEIGE,JANET CHEETHAM
PC C12N15/09,A61K38/00,A61P7/00,C07K14/52,C07K19/00,C12N1/15, PC C12N1/19,
PC C12N1/21,C12N5/10,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC
Description of Artificial Sequence: oligonucleotide FH Key Location/Qualifiers
FT source 1. .861
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .861
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 59.2%; Score 680.8; DB 6; Length 861;
Best Local Similarity 98.3%; Pred. No. 9.3e-155;
Matches 688; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy          4 TACCTTGGTTTTAGACGACTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAG 63
              | |||   | ||  |  ||||||||||||||||||||||||||||||||||||||||||
Db         24 TTCCTCCTTATTGTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAG 83

Qy         64 GACCCCCCAGGAAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGG 123
              |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGG 143

Qy        124 GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC 203

Qy        184 AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC 263

Qy        244 GTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGAC 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGAC 323

Qy        304 TTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 TTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT 383

Qy        364 TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG 443

Qy        424 GCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGG 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 GCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGG 503

Qy        484 TCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGC 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 TCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGC 563

Qy        544 GGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTC 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 GGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTC 623

Qy        604 TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG 683

Qy        664 GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTC 703
              |||||||||||||||||||||||||||||||||||||||
Db        684 GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTC 723
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RESULT 6
BD263000
LOCUS BD263000 684 bp DNA linear PAT 17-JUL-2003
DEFINITION Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and having thrombopoietic activity.
ACCESSION BD263000
VERSION BD263000.1 GI:33072768
KEYWORDS JP 2002536960-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 684)
AUTHORS Liu,C.F., Feige,U. and Cheetham,J.
TITLE Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and having thrombopoietic activity
JOURNAL Patent: JP 2002536960-A 2 05-NOV-2002;
AMGEN INC
COMMENT OS Artificial Sequence
PN JP 2002536960-A/2
PD 05-NOV-2002
PF 22-OCT-1999 JP 2000578340
PR 23-OCT-1998 US 60/105348
PI CHUAN FA LIU,ULRICH FEIGE,JANET CHEETHAM
PC C12N15/09,A61K38/00,A61P7/00,C07K14/52,C07K19/00,C12N1/15, PC C12N1/19,
PC C12N1/21,C12N5/10,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC
Description of Artificial Sequence: oligonucleotide FH Key Location/Qualifiers
FT source 1. .684
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .684
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 58.9%; Score 677.8; DB 6; Length 684;
Best Local Similarity 99.7%; Pred. No. 4.9e-154;
Matches 679; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy         22 CTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGAAGTCAG 81
              ||||||||||||||||||||||||||||||||||||||||||||||||||| || ||||||
Db          4 CTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGTCAG 63

Qy         82 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 123

Qy        142 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 183

Qy        202 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 243

Qy        262 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 303

Qy        322 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 363

Qy        382 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 423

Qy        442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 483

Qy        502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 543

Qy        562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 603

Qy        622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 663

Qy        682 GAGAGGGACAGAGGCCCATTT 702
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Db        664 GAGAGGGACAGAGGCCCATTT 684
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RESULT 7
I27618
LOCUS       I27618                  1142 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 9 from patent US 5565335.
ACCESSION   I27618
VERSION     I27618.1  GI:1818394
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1142)
  AUTHORS   Capon,D.J. and Gregory,T.J.
  TITLE     Adhesion variants
  JOURNAL   Patent: US 5565335-A 9 15-OCT-1996;
FEATURES             Location/Qualifiers
     source          1. .1142
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             57.4%;  Score 660.2;  DB 6;  Length 1142;
  Best Local Similarity   97.2%;  Pred. No. 9.5e-150;
  Matches  685;  Conservative    0;  Mismatches   13;  Indels    7;  Gaps    1;
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Qy          5 ACCTTGGTTTTAGACGACTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGG 64
              | || || ||||||  ||||||||||||||||||| ||||| || ||||| || |||||||
Db        423 AACTCGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 482

Qy         65 ACCCCCCAGGAAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 124
              ||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 542

Qy        125 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 602

Qy        185 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 662

Qy        245 TCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 304
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        663 TCATGTTGTCGTGCATGGCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 722

Qy        305 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 782

Qy        365 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 842

Qy        425 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 902

Qy        485 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 962

Qy        545 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 1022

Qy        605 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGAC 657
              |||||||||||||||||||||||||||||||||||||       ||||||||||||||||||
Db       1023 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGAC 1082

Qy        658 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 702
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1083 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 1127
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RESULT 8
BD004077
LOCUS       BD004077                454 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Methods of increasing sensitivity of an individual to OB protein by
            up-regulating OB protein receptor.
ACCESSION   BD004077
VERSION     BD004077.1  GI:18632038
KEYWORDS    JP 2001501177-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 454)
  AUTHORS   Pelleymounter,M.A.
  TITLE     Methods of increasing sensitivity of an individual to OB protein by
            up-regulating OB protein receptor
  JOURNAL   Patent: JP 2001501177-A 4 30-JAN-2001;
            AMGEN INC
COMMENT     OS   Unidentified
            PN   JP 2001501177-A/4
            PD   30-JAN-2001
            PF   26-AUG-1997 JP 1998511882
            PR   30-AUG-1996 US    08/705981
            PI   MARY ANN PELLEYMOUNTER
            PC   A61K38/00,A61K31/425,A61P1/16,A61P3/04,A61P3/06,A61P3/10, PC
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            A61P9/10,
            PC   A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .454
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .454
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             38.3%;  Score 440.8;  DB 6;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 2.2e-96;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
              ||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||    ||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
              |||||||||||||||||||||||||||||||||||||||||| | ||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
              |||||||||||||||||||||||||||||||
Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 9
BD056516
LOCUS       BD056516                454 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056516
VERSION     BD056516.1  GI:22602122
KEYWORDS    JP 2001512417-A/4.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 454)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 4 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/4
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
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            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .454
                     /organism="Aequorea victoria"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:6100"
ORIGIN

  Query Match             38.3%;  Score 440.8;  DB 6;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 2.2e-96;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
              ||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||    ||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
              |||||||||||||||||||||||||||||||||||||||||| | ||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
              |||||||||||||||||||||||||||||||
Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 10
BD004075
LOCUS       BD004075                491 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Methods of increasing sensitivity of an individual to OB protein by
            up-regulating OB protein receptor.
ACCESSION   BD004075
VERSION     BD004075.1  GI:18632036
KEYWORDS    JP 2001501177-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 491)
  AUTHORS   Pelleymounter,M.A.
  TITLE     Methods of increasing sensitivity of an individual to OB protein by
            up-regulating OB protein receptor
  JOURNAL   Patent: JP 2001501177-A 2 30-JAN-2001;
            AMGEN INC
COMMENT     OS   Unidentified
            PN   JP 2001501177-A/2
            PD   30-JAN-2001
            PF   26-AUG-1997 JP 1998511882
            PR   30-AUG-1996 US    08/705981
            PI   MARY ANN PELLEYMOUNTER
            PC   A61K38/00,A61K31/425,A61P1/16,A61P3/04,A61P3/06,A61P3/10, PC
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            PC   A61K37/02
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            CC   Topology: Linear;
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            FT   source          1. .491
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
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ORIGIN

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  Matches  406;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
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Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
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Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
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Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
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Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
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Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
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Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
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Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491


RESULT 11
BD056514
LOCUS       BD056514                491 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056514
VERSION     BD056514.1  GI:22602120
KEYWORDS    JP 2001512417-A/2.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 491)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 2 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/2
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .491
                      /organism="Aequorea victoria"
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ORIGIN

  Query Match            32.9%;  Score 378.4;  DB 6;  Length 491;
  Best Local Similarity  89.8%;  Pred. No. 3.3e-81;
  Matches  406;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
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Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
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Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
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Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
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Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
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Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
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Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491


RESULT 12
AB029092
LOCUS       AB029092                908 bp    mRNA    linear   PLN 15-APR-2003
DEFINITION  Cucumis sativus mRNA for arabinogalactan protein, complete cds.
ACCESSION   AB029092
VERSION     AB029092.2  GI:29893813
KEYWORDS    .
SOURCE      Cucumis sativus (cucumber)
  ORGANISM  Cucumis sativus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
REFERENCE   1
  AUTHORS   Park,M.H., Suzuki,Y., Chono,M., Knox,J.P. and Yamaguchi,I.
  TITLE     CsAGP1, a Gibberellin-Responsive Gene from Cucumber Hypocotyls,
            Encodes a Classical Arabinogalactan Protein and Is Involved in Stem
            Elongation
  JOURNAL   Plant Physiol. 131 (3), 1450-1459 (2003)
  MEDLINE   22531811
   PUBMED   12644694
REFERENCE   2  (bases 1 to 908)
  AUTHORS   Chono,M., Suzuki,Y. and Yamaguchi,I.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-JUN-1999) Makiko Chono, University of Tokyo, Applied
```

```
            Biological Chemistry; Yayoi 1-1-1, Bunkyo-ku, Tokyo 113-8657, Japan
            (E-mail:mchono@pgr1.ch.a.u-tokyo.ac.jp, Tel:+81-3-5841-5160,
            Fax:+81-3-5841-8025)
COMMENT     On Apr 16, 2003 this sequence version replaced gi:5443647.
FEATURES             Location/Qualifiers
     source          1. .908
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ORIGIN

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Db        283 CACCAGCCAGCACTCCTCCGACTGCTTCCGTTCCTGCCAGCTCTCCTCCGGCTGCTTCCG 342

Qy        193 ATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTG 252
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Db        343 TTCCACCTAGCTCTCCACCAGCTGCTACCGTTCCGGCTAGCTCTCCGCCTGTTCCAGTTC 402

Qy        253 TCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTC 312
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Db        403 CGGTTAGTTCTCCACCAGTTTCAGTACCGGTGAGCTCTCCTCCAGTACCAACTCCAACGG 462

Qy        313 CTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGG 372
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Db        463 AATCTCCTCCCGCTCCCGAAAGTTCTCCTCCTGCCCCAGTCGCGTCGCCTCCTGTTGAGG 522

Qy        373 TTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTC 432
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Db        523 TTCCTGCCCCGGCACCTAGCAAGAAGAAGTCAAAGAAGCACAGAGCACCAGCTCCTTCTC 582

Qy        433 GACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAG 492
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Db        583 CAGCGTTGCTTGGTCCACCTGCGCCTCCTTCTGAAGCTCCTGCAGGAAGCGAGGAAGGTC 642

Qy        493 CGGCACCTCACCCT 506
              | || ||   ||||
Db        643 CTGCGCCCAGCCCT 656


RESULT 13
AB029147
LOCUS       AB029147                1110 bp    mRNA    linear   PLN 23-JUN-1999
DEFINITION  Cucumis sativus mRNA expressed in cucumber hypocotyls, complete
            cds.
ACCESSION   AB029147
VERSION     AB029147.1  GI:5139694
KEYWORDS    .
SOURCE      Cucumis sativus (cucumber)
  ORGANISM  Cucumis sativus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
REFERENCE   1  (bases 1 to 1110)
  AUTHORS   Chono,M., Suzuki,Y. and Yamaguchi,I.
  TITLE     Molecular cloning of genes expressed in cucumber hypocotyls
  JOURNAL   Published Only in DataBase (1999)
REFERENCE   2  (bases 1 to 1110)
  AUTHORS   Chono,M., Suzuki,Y. and Yamaguchi,I.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-JUN-1999) Makiko Chono, University of Tokyo, Applied
            Biological Chemistry; Yayoi 1-1-1, Bunkyo-ku, Tokyo 113-8657, Japan
            (E-mail:mchono@pgr1.ch.a.u-tokyo.ac.jp, Tel:+81-3-5841-5160,
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FEATURES             Location/Qualifiers
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                     /db_xref="GI:5139695"
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Qy        133 CTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACC 192
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Db        283 CACCAGCCAGCACTCCTCCGACTGCTTCCGTTCCTGCCAGCTCTCCTCCGGCTGCTTCCG 342

Qy        193 ATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTG 252
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Db        403 CGGTTAGTTCTCCACCAGTTTCAGTACCGGTGAGCTCTCCTCCAGTACCAACTCCAACGG 462

Qy        313 CTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGG 372
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Qy        493 CGGCACCTCACCCT 506
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Db        643 CTGCGCCCAGCCCT 656


RESULT 14
I27620
LOCUS       I27620                  468 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 12 from patent US 5565335.
ACCESSION   I27620
VERSION     I27620.1  GI:1818396
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 468)
  AUTHORS   Capon,D.J. and Gregory,T.J.
  TITLE     Adhesion variants
  JOURNAL   Patent: US 5565335-A 12 15-OCT-1996;
FEATURES             Location/Qualifiers
     source          1. .468
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ORIGIN

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  Best Local Similarity   49.5%;  Pred. No. 13;
  Matches  143;  Conservative    0;  Mismatches  140;  Indels    6;  Gaps    1;

Qy        394 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 453
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Db        127 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 186

Qy        454 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 507
              |    ||||||| | ||   ||||||||||||| ||   |   ||  ||||       |||
Db        187 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 246

Qy        508 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 567
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Db        247 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 306

Qy        568 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 627
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Db        307 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 366

Qy        628 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 676
              | | | |||   || |  ||| |||  |||  |   | |  |||  |||
Db        367 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 415


RESULT 15
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LOCUS       A51599                   746 bp    DNA     linear   PAT 10-MAR-1997
DEFINITION  Sequence 9 from Patent WO9616990.
ACCESSION   A51599
VERSION     A51599.1  GI:2304408
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 746)
  AUTHORS   Ellis,J.H. and Lewis,A.P.
  TITLE     HUMANIZED ANTIBODIES TO CD38
  JOURNAL   Patent: WO 9616990-A 9 06-JUN-1996;
            WELLCOME FOUND (GB)
COMMENT     Other publication AU 3933695 960619.
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ORIGIN

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Db        429 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 488

Qy        454 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 507
              |    ||||||| | ||   ||||||||||||| ||   |   ||  ||||       |||
Db        489 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 548

Qy        508 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 567
              | |       ||  |||  |||  | |  |||       |       |      |   ||| ||
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Qy        568 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 627
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Db        609 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 668

Qy        628 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 676
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-10-679-999-11
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Sequence: 1 GTATACCTTGGTTTTAGACG.....AGGCCCAACAATTACCTAGG 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 5810876

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	4	40.4	3.5	1057	2	AAQ03405	Aaq03405 Streptomy
	5	40.2	3.5	926	6	ABZ11846	Abz11846 Human pol
c	6	40	3.5	543	2	AAQ23092	Aaq23092 Antigen t
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	18	37.2	3.2	536	9	ADB68842	Adb68842 Minority
	19	37.2	3.2	629	7	ACA24037	Aca24037 Prokaryot
c	20	36	3.1	705	6	ABK73567	Abk73567 Bacillus
	21	35.8	3.1	558	4	AAF61431	Aaf61431 Synthetic
	22	35.8	3.1	558	4	AAF61428	Aaf61428 Synthetic
c	23	35.6	3.1	1098	7	ADA70957	Ada70957 Rice gene
	24	35.4	3.1	1014	4	ABL15657	Abl15657 Drosophil
c	25	35.2	3.1	1005	7	ADA69785	Ada69785 Rice gene
c	26	35	3.0	1147	2	AAT97188	Aat97188 Immunoglo
	27	34.8	3.0	249	2	AAX54615	Aax54615 Endotheli
	28	34.8	3.0	249	3	AAA34062	Aaa34062 Human ade
	29	34.8	3.0	249	3	AAF20184	Aaf20184 Human low
	30	34.8	3.0	249	7	ABZ95878	Abz95878 Human nuc
c	31	34.8	3.0	799	2	AAV55831	Aav55831 Nucleotid
c	32	34.8	3.0	1144	3	AAC56023	Aac56023 Eucalyptu
c	33	34.6	3.0	422	3	AAC79295	Aac79295 Human lun
c	34	34.6	3.0	422	4	AAD23371	Aad23371 Human lun
c	35	34.6	3.0	422	9	ADD66645	Add66645 Human lun
c	36	34.6	3.0	422	9	ADE87899	Ade87899 Human lun
	37	34.6	3.0	950	6	ABK71707	Abk71707 Human dit
c	38	34.4	3.0	431	8	ACD25835	Acd25835 Maize EST
c	39	34.4	3.0	795	2	AAV55830	Aav55830 FLGA inse
	40	34.2	3.0	780	7	ACA37806	Aca37806 Prokaryot
c	41	34	3.0	621	3	AAF11323	Aaf11323 Aspergill
c	42	34	3.0	693	4	AAF87193	Aaf87193 Human ion
c	43	34	3.0	729	8	ADB10435	Adb10435 Alloiococ
c	44	34	3.0	729	8	ADB10437	Adb10437 Alloiococ
	45	33.8	2.9	355	4	AAL01952	Aal01952 Human rep

ALIGNMENTS

RESULT 1
AAL51057
ID AAL51057 standard; DNA; 138 BP.
XX
AC AAL51057;
XX
DT 20-FEB-2003 (first entry)
XX
DE Cyclic single-strand anti-tumour antibody-related coding sequence #6.
XX
KW Cyclic single-strand anti-tumour antibody; anti-tumour Fab; ds;
KW anti-human Cd3 Fab; anti-human CD28 Fab; immunotherapy; tumour;
KW ovarian cancer.
XX
OS Unidentified.
XX
PN WO200283738-A1.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-CN000252.
XX
PR 11-APR-2001; 2001CN-00110554.
XX
PA (GENE-) INST GENETICS CAS.
PA (BEIJ-) BEIJING ABT GENETIC ENG TECHNOLOGY CO LT.
XX
PI Huang H, Cheng J, Wang X, Song L, Zhang Z, Lin Q, Gu Y;
XX
DR WPI; 2003-075525/07.
DR P-PSDB; AAO16031.
XX
PT Cyclic single-strand tri-specific antibody made from antitumor Fab,
PT single-strand antibody and modified anti-human CD3 or CD28 Fab,
PT applicable in early-stage diagnosis, and prevention or treatment of
PT tumors e.g. ovarian cancer.
XX
PS Disclosure; Fig 4A; 49pp; Chinese.
XX
CC The invention comprises a cyclic single-strand anti-tumour antibody, the
CC antibody of the invention is obtained by combining anti-tumour Fab and
CC modified anti-human Cd3 or CD28 Fab. The antibody is useful in the
CC immunotherapy of tumours - particularly ovarian cancer, including the
CC sensitive early-stage diagnosis and post-operative eradication of
CC disease. The present DNA sequence encodes a peptide which was used in the
CC invention

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XX
SQ   Sequence 138 BP; 35 A; 37 C; 39 G; 27 T; 0 U; 0 Other;

  Query Match             4.7%;  Score 53.6;  DB 7;  Length 138;
  Best Local Similarity   93.3%;  Pred. No. 4.5e-05;
  Matches   56;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        250 TTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCG 309
              ||||||||||||||| || || ||||||||||||||| |||||||||||||||||||||||
Db         61 TTGTCGTGCATGGCCCAACATTCGCAGGAGTGGCATGACGTGGTCCTGACCGACTTACCG 120


RESULT 2
AAT20112
ID   AAT20112 standard; cDNA to mRNA; 268 BP.
XX
AC   AAT20112;
XX
DT   29-JUL-1996  (first entry)
XX
DE   Human gene signature HUMGS01256.
XX
KW   Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW   human; cloning; mapping; non-biased library; diagnosis; detection;
KW   cell typing; abnormal cell function; ss.
XX
OS   Homo sapiens.
XX
PN   WO9514772-A1.
XX
PD   01-JUN-1995.
XX
PF   11-NOV-1994;   94WO-JP001916.
XX
PR   12-NOV-1993;   93JP-00355504.
XX
PA   (MATS/) MATSUBARA K.
PA   (OKUB/) OKUBO K.
XX
PI   Matsubara K,  Okubo K;
XX
DR   WPI; 1995-206931/27.
XX
PT   Single-stranded DNA for identifying gene signatures - isolated from 3'-
PT   directed human cDNA library that reflects relative abundance of corresp.
PT   mRNA in specific human tissues.
XX
PS   Claim 1; Page 563; 2245pp; Japanese.
XX
CC   A single-stranded DNA (or its complementary strand or the corresp. double
CC   -stranded DNA) which comprises one of the 7837 "GS" sequences given in
CC   AAT19001-T26837 and which is able to hybridise to part of human genomic
CC   DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were
CC   obtained from 3'-directed cDNA libraries prepared from various human
CC   tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using
CC   poly(T) as the sole primer. Since the 3'- untranslated sequence is unique
CC   to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise
CC   with specific mRNAs. Each library is constructed so as to reflect
CC   accurately the relative abundance of different mRNAs in the particular
CC   tissue from which it was derived. The appearance frequency of a given GS
CC   in a cDNA library can be determined (esp. using primers and probes
CC   derived from the GS sequences) as a means of diagnosing abnormal cell
CC   function or for recognising different cell types
XX
SQ   Sequence 268 BP; 68 A; 54 C; 70 G; 62 T; 0 U; 14 Other;

  Query Match             3.5%;  Score 40.6;  DB 2;  Length 268;
  Best Local Similarity   53.9%;  Pred. No. 0.31;
  Matches   82;  Conservative    0;  Mismatches   70;  Indels    0;  Gaps    0;

Qy        937 CTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGAC 996
              |||||||  |||     | |    || |  || | |   ||   |   |||||   |||
Db          4 CTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGACCAAGGAA 63

Qy        997 GGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCA 1056
              |     ||||  ||  ||   ||||  |    |  | ||    |  |  | |||  ||| | |||
Db         64 GAGCTTTGAAGGCCTGAGGTCTGCGNAAGGTGGGAGGAGGCAGACGCCCTGCGTGGCCCA 123

Qy       1057 ATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1088
              ||||  |||  ||  ||   ||||  |  ||   | |
Db        124 TGGTCGGGGCGTCCACGCCGAGGCCGGCAACA 155


RESULT 3
AAF75507/c
ID   AAF75507 standard; DNA; 486 BP.
XX
AC   AAF75507;
XX
DT   09-MAY-2001  (first entry)
XX
DE   Polyglutamine tract coding sequence #2.
XX
KW   Animal model; polyglutamine tract; neurodegenerative disorder; HDJ1;
KW   heat shock protein 40; tetratricopeptide repeat protein 2; TPR2; stroke;
KW   myeloid leukaemia factor 1; MLF; human; fruit fly; Alzheimer's disease;
KW   Parkinson's disease; CJD; BSE; Huntington's disease; head trauma; cancer;
KW   ds.
XX
OS   Drosophila sp.
XX
PN   WO200112238-A1.
XX
PD   22-FEB-2001.
XX
PF   14-AUG-2000; 2000WO-US022496.
XX
PR   12-AUG-1999;   99US-0148933P.
PR   12-AUG-1999;   99US-0148934P.
PR   18-JAN-2000; 2000US-0177047P.
PR   19-MAY-2000; 2000US-0205720P.
XX
PA   (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
PI   Benzer S,  Kazemi-Esfarjani P;
XX
DR   WPI; 2001-147537/15.
XX
PT   Identifying genes or other compounds that modulate polyglutamine
PT   toxicity, useful for treating Alzheimer's disease, Parkinson's disease
PT   and Creutzfeldt-Jakob disease.
XX
PS   Disclosure; Fig 1A; 275pp; English.
XX
CC   The present invention describes a method of screening for genes which
CC   modulate polyglutamine toxicity using animal models with polyglutamine
CC   sequences that cause toxicity in the animal. The model is preferably
CC   Drosophila, and toxic polyglutamine sequences include the human and
CC   Drosophila heat shock protein 40/HDJ1, tetratricopeptide repeat protein 2
CC   (TPR2) and myeloid leukaemia factor 1 (MLF) genes. The model is useful
CC   for identifying treatments for neurodegenerative and proliferative
CC   disorders, including Alzheimer's disease, Parkinson's disease,
CC   Creutzfeldt-Jacob's disease (CJD), bovine spongiform encephalopathy
CC   (BSE), Huntington's disease, Machado-Joseph disease, spinocerebellar
CC   ataxias, dentatorubropallidoluysian atrophy, Kennedy's disease, stroke,
CC   head trauma and cancer
XX
SQ   Sequence 486 BP; 193 A; 164 C; 108 G; 21 T; 0 U; 0 Other;

  Query Match             3.5%;  Score 40.4;  DB 4;  Length 486;
  Best Local Similarity   45.2%;  Pred. No. 0.45;
  Matches  149;  Conservative    0;  Mismatches  181;  Indels    0;  Gaps    0;

Qy         97 TTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTG 156
              ||   | | |||| |  |    |  |  | |   || | ||    ||  |  |   ||
Db        375 TTGCTGCTGCTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTG 316
```

```
Qy        157 CACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTA 216
Db        315 CTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGCTGCTGCTG 256

Qy        217 TTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAG 276
Db        255 TTGCTGTTGTTGTTGCTGTTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTGCTG 196

Qy        277 GAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTG 336
Db        195 CTGCTGTTGCTGTTGCTGCTGCTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTG 136

Qy        337 TTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTT 396
Db        135 CTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTG 76

Qy        397 GGTGTCCACATGTGGGACGGGGGTAGGGCC 426
Db         75 TTGCTGCTGCTGGGGGGTTGACGGTGGGCC 46
```

RESULT 4
AAQ03405/c
ID AAQ03405 standard; DNA; 1057 BP.
XX
AC AAQ03405;
XX
DT 25-MAR-2003 (revised)
DT 10-MAR-2003 (revised)
DT 19-AUG-1990 (first entry)
XX
DE Streptomyces gene encoding prepro xylanase.
XX
KW Secretory expression vector; actinomycetes; Streptomyces; xylanase gene;
KW endo-1,4-beta-D-xylanase; EC-3.2.1.8; endo-1,3-beta-D-xylanase;
KW EC-3.2.1.32.
XX
OS Streptomyces sp.
XX
FH Key   Location/Qualifiers
FT CDS   416. .475
FT   /*tag= a
XX
PN JP02002377-A.
XX
PD 08-JAN-1990.
XX
PF 08-JUN-1988; 88JP-00140990.
XX
PR 08-JUN-1988; 88JP-00140990.
XX
PA (BANY) BANYU PHARM CO LTD.
XX
DR WPI; 1990-053427/08.
DR P-PSDB; AAR03202.
XX
PT DNA fragment for manifestation secretory vector for actinomycetes - using
PT Streptomyces spp. as host.
XX
PS Page 876; Fig 3; 17pp; Japanese.
XX
CC Streptomyces or E. coli transformed with a secretory expression vector
CC contg. the sequence efficiently secrete the protein into the culture
CC medium. This sequence is identical to that of patent JO 2002-379-A.
CC (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003
CC to correct PR field.)
XX
SQ Sequence 1057 BP; 186 A; 390 C; 336 G; 145 T; 0 U; 0 Other;

Query Match 3.5%; Score 40.4; DB 2; Length 1057;
Best Local Similarity 44.8%; Pred. No. 0.63;
Matches 155; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

```
Qy        270 GTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCA 329
Db        784 GGCGTTGTACCGGGTCGTCTTGTAGATGTCGTAGGTGCCGCCGTCGCTGTGGACGGTGCC 725

Qy        330 GAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG 389
Db        724 CCGGTACTCGCCGGTGGGCCGGTAGCTGCCCCAGTTGTCGACGATGTAGTACTCGACGAG 665

Qy        390 GGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCA 449
Db        664 CGGGTTGGAGGTCCAGCCGTAGAGGCAGCCGTAGCCGTTGCCCGACGGGTTGAACCAGCC 605

Qy        450 GTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTC 509
Db        604 GGTGTACCGGACGGTCCGGCGCCCGCCGTTGGCCCAGCCCTTGCCGGCCACGAAGTTGCC 545

Qy        510 GTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAG 569
Db        544 GCAGTTGGTCCACCGGGTGCTGTAGCTGCCGCCGCCGTTGAGCGTCATGGAGACGGACCC 485

Qy        570 GAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 615
Db        484 GCCGCCGTCGGTCCAGAACGAGTAGTACATGCCGTCGTACCCGGTC 439
```

RESULT 5
ABZ11846
ID ABZ11846 standard; cDNA; 926 BP.
XX
AC ABZ11846;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human polynucleotide SEQ ID NO 728.
XX
KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200270539-A2.
XX
PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-US005095.
XX
PR 05-MAR-2001; 2001US-00799451.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX
DR WPI; 2002-759812/82.
DR P-PSDB; ABP69629.
XX
PT New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.
XX
PS Claim 1; SEQ ID NO 728; 1012pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising a
CC nucleotide sequence selected from any of 948 sequences (ABZ11119-

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CC   ABZ12066) or their mature protein coding portion, active domain coding
CC   protein or complementary sequences. The polynucleotides are useful for
CC   identifying expressed genes or for physical mapping of human genome. The
CC   encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
CC   markers, as a food supplement, for generating antibodies, in medical
CC   imaging, screening and diagnostic assays and for treating cell-
CC   proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC   or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC   diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC   platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC   or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC   arthritis, etc. Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic format
CC   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 926 BP; 159 A; 240 C; 307 G; 220 T; 0 U; 0 Other;

  Query Match             3.5%;  Score 40.2;  DB 6;  Length 926;
  Best Local Similarity   47.8%;  Pred. No. 0.68;
  Matches  117;  Conservative    0;  Mismatches  128;  Indels    0;  Gaps    0;

Qy         92 GGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACC 151
              ||||  |  |||||||||||| | | | |||    | | |||| |||   || |||
Db        510 GGGGGCTGTGGTTCCTGTGGGGGCTCCAAGGGGGGCTGTGGCTCCTGTGGGGGCTCCAAG 569

Qy        152 ACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCC 211
              ||  | | |  |   ||| |||||      | ||   | |   |   || ||
Db        570 GGGGGCTGTGGTTCTTGTGGGGGCTCCAAGGGGGGCTGTGGCTCCTGTGGGGGCTCCAAA 629

Qy        212 ACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGT 271
                |  |||||   |  ||   ||      |   ||| ||  |    |   | ||
Db        630 GGTGGCTGTGGTTCCTGTGGGGGCTCCAAGGGGGGCTGTGGTTCTTGTGGCTGCTCCCAG 689

Qy        272 CGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGA 331
              |||   |  | | | | || | ||| ||  |   | ||  || || | |  |||||
Db        690 TGCAATTGCTGTAAGCCCTGCTGCTGTCCCTCAGGCTGTGGATCCTGCTGCCAGTCCAGC 749

Qy        332 GGTTG 336
                | ||
Db        750 TGCTG 754


RESULT 6
AAQ23092/c
ID   AAQ23092 standard; DNA; 543 BP.
XX
AC   AAQ23092;
XX
DT   25-MAR-2003  (revised)
DT   17-AUG-1992  (first entry)
XX
DE   Antigen tc-7a gene.
XX
KW   Oocysts; MAb 12-07; sporozoite; ss.
XX
OS   Eimeria tenella.
XX
PN   WO9204460-A.
XX
PD   19-MAR-1992.
XX
PF   05-SEP-1991;   91WO-US006430.
XX
PR   12-SEP-1990;   90US-00581693.
XX
PA   (GEMX ) GENEX CORP.
XX
PI   Jacobson JW,  Strausberg RL,  Wilson SD,  Pope SH,  Strausberg SL;
PI   Ruff MD,  Augustine PC,  Danforth HD;
XX
DR   WPI; 1992-114365/14.
DR   P-PSDB; AAR22392.
XX
PT   Vaccine against avian coccidiosis - comprising recombinant eimeria
PT   antigen ac-18 or ac-6b gene, or microorganisms expressing them.
XX
PS   Claim 5; Page 39 + Fig 5; 56pp; English.
XX
CC   To identify antigens of E. tenella, expression libraries were prepd. in
CC   lambda vector, lambda gt11, using cDNA prepd. from polyA mRNA isolated
CC   from E. tenella oocysts. The cDNA expression library was screened with
CC   monoclonal antibody (MAb) 12-07 which was raised against the sporozoite
CC   stage of E. tenella. The library to be screened was plated on a host that
CC   allows lysis and plaque formation. During induction of the antigens
CC   encoded by the phage, the plaques were identified by screening the
CC   filters with Mab 12-07. The cDNA inserts from the MAb 12-07 positive
CC   phage were cloned into bacteriophage M13 and subjected to sequence
CC   analysis. Following sequence analysis, E. tenella antigen tc-7a was
CC   identified. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 543 BP; 229 A; 135 C; 161 G; 18 T; 0 U; 0 Other;

  Query Match             3.5%;  Score 40;  DB 2;  Length 543;
  Best Local Similarity   47.3%;  Pred. No. 0.62;
  Matches  121;  Conservative    0;  Mismatches  135;  Indels    0;  Gaps    0;

Qy        104 TCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGG 163
              |||    ||  |||  |  |      |  || | |     ||  || |  |||  | |
Db        450 TCCCCCAGGCTTACCTGCTGCTGATGCTGCTGCTGCTCTTGCTGCAGCTGCTGTTGTTGC 391

Qy        164 TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT 223
              ||||  ||  ||   |||  | |  |  |||  |||| ||  ||||   |  | |
Db        390 TGCTGTTGCTGCTTGTGTTTTCGCTTTCTCTGCTTCTGCTGCTGCTCCTGCTGCTCCTTC 331

Qy        224 TCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGC 283
                | | |   ||  || |   |    |||  |  | ||   | || |  || ||  ||
Db        330 GGTTTCTGTTCGTGCTTCCGCTGCCTTTGCTGCTCCTGCTGCTCCTGCTGCGGCTGTCGC 271

Qy        284 AGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGG 343
              | |  |||| |||     |  | | ||| ||  || |   | | |||  | || | | |
Db        270 TGCAGCTGGTGCTGCTGCAGCTCCTGTTGCTGCTGCTGCTGCTGCAGCTGGTGCTGCTGC 211

Qy        344 AGGGTCGGGGGTAGCT 359
              ||      |  ||||
Db        210 AGCTGGTGCTGCAGCT 195


RESULT 7
ABS78695
ID   ABS78695 standard; DNA; 1011 BP.
XX
AC   ABS78695;
XX
DT   29-AUG-2003  (revised)
DT   16-DEC-2002  (first entry)
XX
DE   S. aerocolonigenes DNA encoding UNBU.
XX
KW   Enediyne; warhead structure; ds; cancer; cytostatic; PKSE; gene;
KW   polyketide synthase; TEBC; UNBL; UNBV; UNBU; genetic engineering;
KW   thioesterase unique to enediyne biosynthetic loci;
KW   unique to enediyne biosynthetic loci.
XX
OS   Lechevalieria aerocolonigenes.
XX
PN   CA2387401-A1.
XX
PD   04-SEP-2002.
XX
PF   21-MAY-2002; 2002CA-02387401.
XX
PR   21-MAY-2001; 2001US-0291959P.
PR   03-DEC-2001; 2001US-0334604P.
XX
PA   (ECOP-) ECOPIA BIOSCIENCES INC.
XX
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PI Staffa A, Farnet CM, Zazopoulos E;
XX
DR WPI; 2002-692206/75.
DR P-PSDB; ABG97456.
XX
PT New enediyne polyketide synthase polypeptides involved in synthesis of
PT the warhead structure in enediyne compounds useful in design of new
PT enediyne compounds and identification of new enediyne biosynthetic loci.
XX
PS Claim 1; Page 247; 310pp; English.
XX
CC The invention relates to purified/isolated polypeptides involved in
CC synthesis of the warhead structure in enediyne compounds, or their
CC fragments or sequences 75% homologous to them. The polypeptides comprise
CC five families of proteins: PKSE (polyketide synthase), TEBC (thioesterase
CC unique to enediyne biosynthetic loci), UNBL, UNBV and UNBU (unique to
CC enediyne biosynthetic loci L, B and V). The proteins are isolated from 10
CC different micro-organisms. Also included are the nucleic acids encoding
CC the proteins, antibodies specifically binding the polypeptides, and a
CC computer system/computer readable medium comprising the sequences
CC referred to above. The polypeptides and polynucleotides are useful in
CC genetic engineering to design new enediyne compounds (which are potential
CC anti-cancer drugs) and identify new enediyne biosynthetic loci. They can
CC also be used to identify enediyne biosynthesis genes/gene fragments from
CC samples containing genomic DNA e.g. in biomass from an environmental
CC source (such as a mixed microbial culture/population of organisms), pure
CC cultures or genomic libraries obtained from a mixed population of
CC organisms or from pure culture. The present sequence encodes an enzyme of
CC the enediyne warhead structure biosynthetic pathway. (Updated on 29-AUG-
CC 2003 to standardise OS field)
XX
SQ Sequence 1011 BP; 138 A; 331 C; 348 G; 194 T; 0 U; 0 Other;

Query Match 3.4%; Score 39.4; DB 6; Length 1011;
Best Local Similarity 48.4%; Pred. No. 1.2;
Matches 109; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

Qy 111 GGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCT 170
Db 507 GGAGTGGACCAGCGGCGTCGTCGACGCGCTGATCCCCGTCCTCCTGCTCGCGGCCGGCAC 566

Qy 171 GGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTT 230
Db 567 GATGCTCAACGCGAAGCTGACGAAGAAGATCCCGCTGATCCTGGGCTGGGTGGGTGGGTT 626

Qy 231 CGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGT 290
Db 627 CGTCCTGCAGGCCGTGCTGCGTTCGGCCTTCACCGACCTGTCGATCGTCAGTGCGGTCCT 686

Qy 291 GGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTT 335
Db 687 GCCGATCACCGGAACAGCGTTCATCCTGTTCACCAACTACATGAT 731

RESULT 8
ABL09597/c
ID ABL09597 standard; cDNA; 922 BP.
XX
AC ABL09597;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 23273.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB65494.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 23273; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 922 BP; 231 A; 257 C; 238 G; 196 T; 0 U; 0 Other;

Query Match 3.4%; Score 39; DB 4; Length 922;
Best Local Similarity 48.4%; Pred. No. 1.5;
Matches 108; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

Qy 254 CGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCC 313
Db 383 CGTCCATGGGGCAGAACTCGAGAGTGGCGCCGTCCTTGTGCTGTAACACCAGCCGATTCT 324

Qy 314 TCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT 373
Db 323 TGTGGAACACCATGTCGGGCAGGTGGGGCAGCTGCAGGGAGTGCTGGTAGTGGCAGAGGT 264

Qy 374 TTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCG 433
Db 263 CGCAGCGGTCGGCCGAGTCCTTGGGACAGCACTTGGCGGTGCCCAGTTGGCAGCTGCTCT 204

Qy 434 ACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAA 476
Db 203 TCAGGATGTGCGACTTCTCATACTTGATGGCCCAGTCGTGGAA 161

RESULT 9
AAD56497
ID AAD56497 standard; DNA; 789 BP.
XX
AC AAD56497;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human VLCFABE MOOSE00004 DNA from ctg13284.
XX
KW Human; very long chain fatty acid biosynthesis enzyme; VLFA; VLCFABE;
KW non-insulin dependent diabetes mellitus; NIDDM; adrenoleukodystrophy;
KW ALD; autosomal dominant macular dystrophy; adMD; Alzheimer's disease;
KW coronary heart disease; stroke; myocardial infarction; gene therapy;
KW gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .789
FT /*tag= a

```
FT                   /product= "Human VLCFABE protein"
FT                   /note= "No start and stop codon"
FT                   /partial
XX
PN   WO2003040392-A2.
XX
PD   15-MAY-2003.
XX
PF   04-NOV-2002; 2002WO-IB004610.
XX
PR   06-NOV-2001; 2001US-0332864P.
XX
PA   (DECO-) DECODE GENETICS EHF.
XX
PI   Betts M,  Sigurdsson GT;
XX
DR   WPI; 2003-430674/40.
DR   P-PSDB; AAE37330.
XX
PT   New isolated nucleic acid molecule comprising a very long chain fatty
PT   acid biosynthesis enzyme nucleic acid, useful for treating a disease
PT   associated with the biosynthesis enzyme nucleic acid.
XX
PS   Claim 1; Page 86; 90pp; English.
XX
CC   The invention relates to very long chain fatty acid (VLFA) biosynthesis
CC   enzymes (VLCFABE) and polynucleotides encoding such proteins. Sequences
CC   of the invention are useful for treating VLCFABE diseases such as non-
CC   insulin dependent diabetes mellitus (NIDDM), adrenoleukodystrophy (ALD),
CC   autosomal dominant macular dystrophy (adMD), Alzheimer's disease and
CC   coronary heart diseases such as stroke and myocardial infarction. They
CC   are also used in gene therapy. The present sequence is human VLCFABE DNA
XX
SQ   Sequence 789 BP; 204 A; 215 C; 172 G; 198 T; 0 U; 0 Other;

  Query Match             3.3%;  Score 37.8;  DB 7;  Length 789;
  Best Local Similarity   47.3%;  Pred. No. 3.1;
  Matches  114;  Conservative    0;  Mismatches  127;  Indels    0;  Gaps    0;

Qy         80 AGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGT 139
Db        443 ACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCATCATGT 502

Qy        140 GTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACC 199
Db        503 ACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCATGCTCA 562

Qy        200 TGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCA 259
Db        563 TCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCACGTACA 622

Qy        260 TGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGT 319
Db        623 TCTGGAGGCAGGATCAGGGATGCCACACCACGATGGAACACTTATTCTGGTCCTTCATCT 682

Qy        320 T 320
Db        683 T 683


RESULT 10
ABZ22164
ID   ABZ22164 standard; cDNA; 810 BP.
XX
AC   ABZ22164;
XX
DT   12-MAR-2003  (first entry)
XX
DE   Human elongase HSELO1-like protein encoding cDNA SEQ ID NO:5.
XX
KW   Human; elongase; elongase HSELO1-like protein; enzyme; cytostatic;
KW   antidiabetic; antiasthmatic; anti-HIV; antiparkinsonian; nootropic;
KW   neuroprotective; tranquilliser; antimigraine; analgesic; neuroleptic;
KW   cerebroprotective; gene therapy; cancer; diabetes; CNS disorder; asthma;
KW   metabolic disease; central nervous system disorder; COPD; dementia;
KW   Parkinson's disease; multiple sclerosis; stroke; Alzheimer's disease;
KW   Huntington's disease; Creutzfeldt-Jakob disease; HIV; schizophrenia;
KW   psychosis; attention deficit disorder; headache pain; migraine; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .810
FT                   /*tag=  a
FT                   /partial
FT                   /product= "elongase HSELO1-like protein"
FT                   /note= "no stop codon given"
XX
PN   WO200262974-A2.
XX
PD   15-AUG-2002.
XX
PF   07-FEB-2002; 2002WO-EP001262.
XX
PR   08-FEB-2001; 2001US-0267135P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Zhu Z;
XX
DR   WPI; 2002-636596/68.
DR   P-PSDB; ABP56418.
XX
PT   New isolated human elongase HSELO1-like polynucleotide and encoded
PT   peptide, useful for treating, preventing and ameliorating diseases such
PT   as COPD, cancer, metabolic disease, diabetes, CNS disorders, or asthma.
XX
PS   Claim 1; Fig 5; 128pp; English.
XX
CC   The present sequence encodes a human elongase HSELO1-like protein (I).
CC   (I) has cytostatic, antidiabetic, antiasthmatic, anti-HIV, nootropic,
CC   antiparkinsonian, neuroprotective, tranquilliser, antimigraine,
CC   analgesic, neuroleptic and cerebroprotective activities, and can be used
CC   in gene therapy. (I) can be used in the treatment of a disease, such as
CC   cancer, diabetes, central nervous system (CNS) disorder, asthma,
CC   metabolic disease or COPD. The human elongase HSELO1-like protein is
CC   useful in preventing, treating or ameliorating the diseases cited above,
CC   including Parkinson's disease, dementia, multiple sclerosis, stroke, HIV,
CC   Alzheimer's disease, Huntington's disease, Creutzfeldt-Jakob disease,
CC   schizophrenia, psychosis, attention deficit disorders, pain associated
CC   with CNS disorders, with cancer, or headache pain, e.g. migraine. It can
CC   also be useful in identifying test compounds that may act as activators
CC   or inhibitors at the enzyme's active site, or in raising specific
CC   antibodies that can block and effectively reduce its activity
XX
SQ   Sequence 810 BP; 195 A; 231 C; 181 G; 203 T; 0 U; 0 Other;

  Query Match             3.3%;  Score 37.8;  DB 6;  Length 810;
  Best Local Similarity   47.3%;  Pred. No. 3.1;
  Matches  114;  Conservative    0;  Mismatches  127;  Indels    0;  Gaps    0;

Qy         80 AGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGT 139
Db        485 ACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCATCATGT 544

Qy        140 GTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACC 199
Db        545 ACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCATGCTCA 604

Qy        200 TGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCA 259
Db        605 TCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCACGTACA 664

Qy        260 TGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGT 319
Db        665 TCTGGAGGCAGGATCAGGGATGCCACACCACGATGGAACACTTATTCTGGTCCTTCATCT 724
```

```
Qy        320 T 320
              |
Db        725 T 725


RESULT 11
AAD42270
ID   AAD42270 standard; DNA; 813 BP.
XX
AC   AAD42270;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Human ELG6 gene.
XX
KW   Human; elongase; therapy; enzyme; polyunsaturated fatty acid; sinusitis;
KW   PUFA disorder; cardiovascular disorder; articular cartilage degradation;
KW   peripheral vascular disease; atherosclerosis; coronary artery disease;
KW   inflammatory disorder; pancreatitis; asthma; gastrointestinal disorder;
KW   osteoarthritis; rheumatoid arthritis; congenital liver disease; cancer;
KW   acne; Sjogren's syndrome; body weight disorder; cerebrovascular disease;
KW   acute respiratory distress syndrome; hypercholesterolaemia; alcoholism;
KW   postviral fatigue; psychiatric disorder; pre-menstrual syndrome; eczema;
KW   Alzheimer's syndrome; hypertriglyceridaemia; cystic fibrosis; anorexia;
KW   autoimmune disorder; obesity; cachexia; viral disease; endometriosis;
KW   dyslipidaemia; atopic disorder; diabetes; ELG6; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .813
FT                   /*tag=  a
FT                   /product= "ELG6 protein"
XX
PN   WO200244320-A2.
XX
PD   06-JUN-2002.
XX
PF   29-NOV-2001; 2001WO-CA001705.
XX
PR   29-NOV-2000; 2000US-0253728P.
XX
PA   (XENO-) XENON GENETICS INC.
XX
PI   Winther MD,  Knickle LC,  Haardt M,  De Antueno RJ,  Jenkins DK;
PI   Nwaka SO,  Allen SJ,  Ponton A,  Goldberg YP;
XX
DR   WPI; 2002-547693/58.
DR   P-PSDB; AAE24550.
XX
PT   Novel elongase polypeptide, genes and their control regions useful in
PT   determining compositions for treating polyunsaturated fatty acid disorder
PT   e.g. cardiovascular, inflammation, gastrointestinal disorders and cancer.
XX
PS   Claim 1; Page 160; 173pp; English.
XX
CC   The invention relates to novel elongase polypeptides, genes and their
CC   control regions. Sequences of the invention are used in the diagnosis and
CC   treatment of polyunsaturated fatty acid (PUFA) disorders such as
CC   cardiovascular disorders (e.g. atherosclerosis, coronary artery disease),
CC   inflammatory disorders (e.g. sinusitis, pancreatitis, asthma,
CC   osteoarthritis, rheumatoid arthritis, acne), Sjogren's syndrome, body
CC   weight disorders (e.g. obesity, cachexia and anorexia), viral diseases
CC   and postviral fatigue, gastrointestinal disorders, eczema, psychiatric
CC   disorders, cancer, congenital liver disease, alcoholism, Alzheimer's
CC   syndrome, cystic fibrosis, endometriosis, pre-menstrual syndrome,
CC   hypercholesterolaemia, hypertriglyceridaemia, dyslipidaemia, peripheral
CC   vascular disease, cerebrovascular disease, autoimmune disorders, acute
CC   respiratory distress syndrome, atopic disorders, articular cartilage
CC   degradation, diabetes and diabetic complication. The present sequence is
CC   human elongase gene (ELG6)
XX

SQ   Sequence 813 BP; 196 A; 231 C; 182 G; 204 T; 0 U; 0 Other;

  Query Match             3.3%;  Score 37.8;  DB 6;  Length 813;
  Best Local Similarity   47.3%;  Pred. No. 3.1;
  Matches  114;  Conservative    0;  Mismatches  127;  Indels    0;  Gaps    0;

Qy         80 AGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGT 139
              | || | |   |  ||     |||| |      | |||   | |     |   ||  ||
Db        485 ACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCATCATGT 544

Qy        140 GTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACC 199
               ||  || ||   ||| |  | |      ||   | ||      | | || ||||| |
Db        545 ACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCATGCTCA 604

Qy        200 TGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCA 259
              |  |  ||| ||  | || | | | | | | || ||| || ||  ||| |  ||| ||
Db        605 TCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCACGTACA 664

Qy        260 TGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGT 319
              |       |||   |||| || ||   |  | |      |   ||   || | |||| |
Db        665 TCTGGAGGCAGGATCAGGGATGCCACACCACGATGGAACACTTATTCTGGTCCTTCATCT 724

Qy        320 T 320
              |
Db        725 T 725


RESULT 12
ABZ22162
ID   ABZ22162 standard; cDNA; 813 BP.
XX
AC   ABZ22162;
XX
DT   12-MAR-2003  (first entry)
XX
DE   Human elongase HSELO1-like protein encoding cDNA SEQ ID NO:1.
XX
KW   Human; elongase; elongase HSELO1-like protein; enzyme; cytostatic;
KW   antidiabetic; antiasthmatic; anti-HIV; antiparkinsonian; nootropic;
KW   neuroprotective; tranquilliser; antimigraine; analgesic; neuroleptic;
KW   cerebroprotective; gene therapy; cancer; diabetes; CNS disorder; asthma;
KW   metabolic disease; central nervous system disorder; COPD; dementia;
KW   Parkinson's disease; multiple sclerosis; stroke; Alzheimer's disease;
KW   Huntington's disease; Creutzfeldt-Jakob disease; HIV; schizophrenia;
KW   psychosis; attention deficit disorder; headache pain; migraine; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .813
FT                   /*tag=  a
FT                   /product= "elongase HSELO1-like protein"
XX
PN   WO200262974-A2.
XX
PD   15-AUG-2002.
XX
PF   07-FEB-2002; 2002WO-EP001262.
XX
PR   08-FEB-2001; 2001US-0267135P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Zhu Z;
XX
DR   WPI; 2002-636596/68.
DR   P-PSDB; ABP56418.
XX
PT   New isolated human elongase HSELO1-like polynucleotide and encoded
PT   peptide, useful for treating, preventing and ameliorating diseases such
PT   as COPD, cancer, metabolic disease, diabetes, CNS disorders, or asthma.
XX
PS   Claim 1; Fig 1; 128pp; English.
```

```
XX
CC   The present sequence encodes a human elongase HSELO1-like protein (I).
CC   (I) has cytostatic, antidiabetic, antiasthmatic, anti-HIV, nootropic,
CC   antiparkinsonian, neuroprotective, tranquilliser, antimigraine,
CC   analgesic, neuroleptic and cerebroprotective activities, and can be used
CC   in gene therapy. (I) can be used in the treatment of a disease, such as
CC   cancer, diabetes, central nervous system (CNS) disorder, asthma,
CC   metabolic disease or COPD. The human elongase HSELO1-like protein is
CC   useful in preventing, treating or ameliorating the diseases cited above,
CC   including Parkinson's disease, dementia, multiple sclerosis, stroke, HIV,
CC   Alzheimer's disease, Huntington's disease, Creutzfeldt-Jakob disease,
CC   schizophrenia, psychosis, attention deficit disorders, pain associated
CC   with CNS disorders, with cancer, or headache pain, e.g. migraine. It can
CC   also be useful in identifying test compounds that may act as activators
CC   or inhibitors at the enzyme's active site, or in raising specific
CC   antibodies that can block and effectively reduce its activity
XX
SQ   Sequence 813 BP; 196 A; 231 C; 182 G; 204 T; 0 U; 0 Other;

  Query Match             3.3%;  Score 37.8;  DB 6;  Length 813;
  Best Local Similarity   47.3%;  Pred. No. 3.1;
  Matches  114;  Conservative    0;  Mismatches  127;  Indels    0;  Gaps    0;

Qy         80 AGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGT 139
              | || | |   |  ||     ||||| |      | |||   | |     |   ||  ||
Db        485 ACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCATCATGT 544

Qy        140 GTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACC 199
               ||  || ||   ||| |  | |      ||   | ||     | | || ||||||
Db        545 ACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCATGCTCA 604

Qy        200 TGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCA 259
              |  |   ||| ||  | || | | | | | || ||| || ||  |||  |  ||| ||
Db        605 TCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCACGTACA 664

Qy        260 TGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGT 319
              |       |||   ||||  || ||   | | |      |   ||   || | |||| |
Db        665 TCTGGAGGCAGGATCAGGGATGCCACACCACGATGGAACACTTATTCTGGTCCTTCATCT 724

Qy        320 T 320
              |
Db        725 T 725


RESULT 13
ABN86918
ID   ABN86918 standard; cDNA; 815 BP.
XX
AC   ABN86918;
XX
DT   29-JUL-2002  (first entry)
XX
DE   Human NOV6a encoding cDNA sequence SEQ ID NO:17.
XX
KW   Human; NOVX; cytostatic; antiarteriosclerotic; cardiovascular; lymphoma;
KW   antidiabetic; immunosuppressive; neuroprotective; gene therapy; cancer;
KW   cardiomyopathy; atherosclerosis; cell signal processing; diabetes; AIDS;
KW   metabolic pathway modulation; neoplastic; neurological disorder; asthma;
KW   adenocarcinoma; prostate cancer; uterus cancer; immune response;
KW   Crohn's disease; multiple sclerosis; Graft versus host disease;
KW   chromosome 10; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .813
FT                   /*tag=  a
FT                   /product= "NOV6a"
FT                   /note= "Cold inducible glycoprotein 30-like protein"
XX
PN   WO200230974-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US031922.
XX
PR   12-OCT-2000; 2000US-0240113P.
PR   16-OCT-2000; 2000US-0240625P.
PR   16-OCT-2000; 2000US-0240637P.
PR   16-OCT-2000; 2000US-0240648P.
PR   16-OCT-2000; 2000US-0240662P.
PR   16-OCT-2000; 2000US-0240669P.
PR   16-OCT-2000; 2000US-0240703P.
PR   16-OCT-2000; 2000US-0240732P.
PR   16-OCT-2000; 2000US-0241190P.
PR   18-JAN-2001; 2001US-0262455P.
XX
PA   (CURA-) CURAGEN CORP.
PA   (MILL/) MILLET I.
XX
PI   Grosse WM,  Alsobrook JP,  Lepley DM,  Burgess CE,  Mishra V;
PI   Kekuda R,  Li L,  Padigaru M,  Shimkets RA,  Zerhusen BD,  Spytek KA;
PI   Edinger S,  Gerlach V,  Macdougall J,  Stone D,  Gunther E,  Ellerman K;
XX
DR   WPI; 2002-444172/47.
DR   P-PSDB; ABB78812.
XX
PT   New NOVX polypeptides and polynucleotides, useful for treating or
PT   preventing a NOVX-associated disorder or a pathological state in a
PT   subject, particularly a human, e.g. cardiomyopathy, atherosclerosis,
PT   cancer or diabetes.
XX
PS   Claim 9; Page 51; 227pp; English.
XX
CC   The present invention describes novel human proteins designated NOVX
CC   (where X is 1, 2a, 2b, 2c, 2d, 3, 4, 5, 6a, 6b, 7, 8, or 9). NOV1 is a
CC   tyrosine-protein kinase 6-like protein; NOV2a-d are keratin 4-like
CC   proteins; NOV3 is a collagen-like protein; NOV4 is a cystatin B-like
CC   protein; NOV5 is a serotonin receptor-like protein; NOV6a and NOV65v are
CC   cold inducible glycoprotein 30-like proteins; NOV7 is a matrilin-2-like
CC   protein; NOV8 is a leukocyte surface antigen (CD53)-like protein; and
CC   NOV9 is a tyrosine kinase-like protein. NOVX sequences have cytostatic,
CC   antiarteriosclerotic, cardiovascular, antidiabetic, immunosuppressive and
CC   neuroprotective activities, and can be used in gene therapy. The NOVX
CC   sequences can be used in therapeutics, particularly for treating,
CC   preventing or alleviating a NOVX-associated disorder or a pathological
CC   state in a subject, particularly a human. These disorders include
CC   cardiomyopathy, atherosclerosis, a disorder related to cell signal
CC   processing and metabolic pathway modulation or diabetes. The NOVX
CC   sequences are also useful for determining the presence of or
CC   predisposition to a disease associated with altered levels of NOVX
CC   polypeptide or nucleic acid, particularly cancer. The NOVX sequences are
CC   especially useful in therapeutic or prophylactic applications for
CC   neoplastic or neurological disorders, and in the treatment of
CC   adenocarcinoma, lymphoma, prostate cancer, uterus cancer, immune
CC   response, AIDS, asthma, Crohn's disease, multiple sclerosis or Graft
CC   versus host disease. The present sequence encodes the human NOV6a protein
CC   from the present invention. NOV6a is located to chromosome 10
XX
SQ   Sequence 815 BP; 196 A; 231 C; 183 G; 205 T; 0 U; 0 Other;

  Query Match             3.3%;  Score 37.8;  DB 6;  Length 815;
  Best Local Similarity   47.3%;  Pred. No. 3.1;
  Matches  114;  Conservative    0;  Mismatches  127;  Indels    0;  Gaps    0;

Qy         80 AGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGT 139
              | || | |   |  ||     ||||| |      | |||   | |     |   ||  ||
Db        485 ACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCATCATGT 544

Qy        140 GTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACC 199
               ||  || ||   ||| |  | |      ||   | ||     | | || ||||||
Db        545 ACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCATGCTCA 604

Qy        200 TGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCA 259
              |  |   ||| ||  | || | | | | | || ||| || ||  |||  |  ||| ||
Db        605 TCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCACGTACA 664
```

```
Qy        260 TGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGT 319
              |       |||   |||| || ||   | | |       |   ||   || | |||| |
Db        665 TCTGGAGGCAGGATCAGGGATGCCACACCACGATGGAACACTTATTCTGGTCCTTCATCT 724

Qy        320 T 320
              |
Db        725 T 725
```

RESULT 14
ABN86919
ID ABN86919 standard; cDNA; 815 BP.
XX
AC ABN86919;
XX
DT 29-JUL-2002 (first entry)
XX
DE Human NOV6b encoding cDNA sequence SEQ ID NO:19.
XX
KW Human; NOVX; cytostatic; antiarteriosclerotic; cardiovascular; lymphoma;
KW antidiabetic; immunosuppressive; neuroprotective; gene therapy; cancer;
KW cardiomyopathy; atherosclerosis; cell signal processing; diabetes; AIDS;
KW metabolic pathway modulation; neoplastic; neurological disorder; asthma;
KW adenocarcinoma; prostate cancer; uterus cancer; immune response;
KW Crohn's disease; multiple sclerosis; Graft versus host disease;
KW chromosome 10; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1. .813
FT   /*tag= a
FT   /product= "NOV6b"
FT   /note= "Cold inducible glycoprotein 30-like protein"
XX
PN WO200230974-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US031922.
XX
PR 12-OCT-2000; 2000US-0240113P.
PR 16-OCT-2000; 2000US-0240625P.
PR 16-OCT-2000; 2000US-0240637P.
PR 16-OCT-2000; 2000US-0240648P.
PR 16-OCT-2000; 2000US-0240662P.
PR 16-OCT-2000; 2000US-0240669P.
PR 16-OCT-2000; 2000US-0240703P.
PR 16-OCT-2000; 2000US-0240732P.
PR 16-OCT-2000; 2000US-0241190P.
PR 18-JAN-2001; 2001US-0262455P.
XX
PA (CURA-) CURAGEN CORP.
PA (MILL/) MILLET I.
XX
PI Grosse WM, Alsobrook JP, Lepley DM, Burgess CE, Mishra V;
PI Kekuda R, Li L, Padigaru M, Shimkets RA, Zerhusen BD, Spytek KA;
PI Edinger S, Gerlach V, Macdougall J, Stone D, Gunther E, Ellerman K;
XX
DR WPI; 2002-444172/47.
DR P-PSDB; ABB78813.
XX
PT New NOVX polypeptides and polynucleotides, useful for treating or
PT preventing a NOVX-associated disorder or a pathological state in a
PT subject, particularly a human, e.g. cardiomyopathy, atherosclerosis,
PT cancer or diabetes.
XX
PS Claim 9; Page 53; 227pp; English.
XX
CC The present invention describes novel human proteins designated NOVX
CC (where X is 1, 2a, 2b, 2c, 2d, 3, 4, 5, 6a, 6b, 7, 8, or 9). NOV1 is a
CC tyrosine-protein kinase 6-like protein; NOV2a-d are keratin 4-like
CC proteins; NOV3 is a collagen-like protein; NOV4 is a cystatin B-like
CC protein; NOV5 is a serotonin receptor-like protein; NOV6a and NOV65v are
CC cold inducible glycoprotein 30-like proteins; NOV7 is a matrilin-2-like
CC protein; NOV8 is a leukocyte surface antigen (CD53)-like protein; and
CC NOV9 is a tyrosine kinase-like protein. NOVX sequences have cytostatic,
CC antiarteriosclerotic, cardiovascular, antidiabetic, immunosuppressive and
CC neuroprotective activities, and can be used in gene therapy. The NOVX
CC sequences can be used in therapeutics, particularly for treating,
CC preventing or alleviating a NOVX-associated disorder or a pathological
CC state in a subject, particularly a human. These disorders include
CC cardiomyopathy, atherosclerosis, a disorder related to cell signal
CC processing and metabolic pathway modulation or diabetes. The NOVX
CC sequences are also useful for determining the presence of or
CC predisposition to a disease associated with altered levels of NOVX
CC polypeptide or nucleic acid, particularly cancer. The NOVX sequences are
CC especially useful in therapeutic or prophylactic applications for
CC neoplastic or neurological disorders, and in the treatment of
CC adenocarcinoma, lymphoma, prostate cancer, uterus cancer, immune
CC response, AIDS, asthma, Crohn's disease, multiple sclerosis or Graft
CC versus host disease. The present sequence encodes the human NOV6b protein
CC from the present invention. NOV6b is located to chromosome 10
XX
SQ Sequence 815 BP; 196 A; 231 C; 183 G; 205 T; 0 U; 0 Other;

  Query Match   3.3%; Score 37.8; DB 6; Length 815;
  Best Local Similarity   47.3%; Pred. No. 3.1;
  Matches 114; Conservative   0; Mismatches 127; Indels   0; Gaps   0;

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Db        485 ACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCATCATGT 544

Qy        140 GTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACC 199
                ||  ||||   ||| |  | |       ||   | ||      | | || ||||||  |
Db        545 ACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCATGCTCA 604

Qy        200 TGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCA 259
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Db        605 TCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCACGTACA 664

Qy        260 TGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGT 319
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Db        665 TCTGGAGGCAGGATCAGGGATGCCACACCACGATGGAACACTTATTCTGGTCCTTCATCT 724

Qy        320 T 320
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Db        725 T 725
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RESULT 15
ABZ24216
ID ABZ24216 standard; DNA; 818 BP.
XX
AC ABZ24216;
XX
DT 14-APR-2003 (first entry)
XX
DE Human LCE gene related DNA (sequence Id No. 2).
XX
KW LCE; long chain fatty acyl elongase; p53; cytostatic; gene therapy;
KW cancer; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200299068-A2.
XX
PD 12-DEC-2002.
XX
PF 03-JUN-2002; 2002WO-US017739.
XX
PR 05-JUN-2001; 2001US-0296076P.
PR 10-OCT-2001; 2001US-0328605P.
PR 15-FEB-2002; 2002US-0357253P.

PR 01-MAR-2002; 2002US-0361196P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
PI Karim FD, Keyes LN, Koblizek TI;
XX
DR WPI; 2003-167338/16.
XX
PT Identifying a candidate p53 pathway modulating agent for
PT diagnosing/treating cancer comprises detecting a test agent-biased
PT activity of an assay system comprising a purified long chain fatty acyl
PT elongase (LCE) polypeptide or nucleic acid.
XX
PS Disclosure; Page 50; 69pp; English.
XX
CC The invention relates to identifying a candidate p53 pathway modulating
CC agent that involves assaying a purified LCE (long chain fatty acyl
CC elongase) polypeptide or nucleic acid or its functionally active fragment
CC or derivative, with a test agent. The methods are useful for identifying
CC a candidate p53 pathway modulating agent, modulating a p53 pathway of a
CC cell, or a mammalian cell, diagnosing a disease in a patient, identifying
CC a candidate branching morphogenesis modulating agent, and modulating
CC branching morphogenesis in a mammalian cell. The diseases that can be
CC diagnosed are breast, colon, lung or ovary cancer having greater than 25%
CC expression level. The method is useful for manufacturing a medicament for
CC diagnosing or treating breast, colon, lung or ovary cancer. Sequences
CC ABZ24215-222 represent DNA sequences related to human LCE gene
XX
SQ Sequence 818 BP; 198 A; 232 C; 183 G; 205 T; 0 U; 0 Other;

Query Match 3.3%; Score 37.8; DB 7; Length 818;
Best Local Similarity 47.3%; Pred. No. 3.1;
Matches 114; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

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Qy          80 AGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGT 139
               | || | |   |  ||     ||||| |      | |||   | |     |   ||  ||
Db         489 ACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCATCATGT 548

Qy         140 GTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACC 199
                 ||  || ||   ||| |  | |      ||   | ||     | | || ||||||  |
Db         549 ACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCATGCTCA 608

Qy         200 TGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCA 259
               |  |   ||| ||  | || | | | | | | || ||| || ||  |||  |  ||| ||
Db         609 TCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCACGTACA 668

Qy         260 TGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGT 319
               |       |||   ||||  || ||   |  | |      |   ||   || | |||| |
Db         669 TCTGGAGGCAGGATCAGGGATGCCACACCACGATGGAACACTTATTCTGGTCCTTCATCT 728

Qy         320 T 320
               |
Db         729 T 729
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Search completed: May 7, 2004, 06:57:18
Job time : 334 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 13:07:09 ; Search time 63.5 Seconds
(without alignments)
10050.292 Million cell updates/sec

Title: US-10-679-999-11
Perfect score: 1150
Sequence: 1 GTATACCTTGGTTTTAGACG.....AGGCCCAACAATTACCTAGG 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1246516

Minimum DB seq length: 0
Maximum DB seq length: 1150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	660.2	57.4	1142	1	US-08-236-311-9	Sequence 9, Appli
	2	660.2	57.4	1142	3	US-08-457-918-9	Sequence 9, Appli
	3	43	3.7	468	1	US-08-236-311-12	Sequence 12, Appl
	4	43	3.7	468	3	US-08-457-918-12	Sequence 12, Appl
c	5	40	3.5	533	6	5482709-5	Patent No. 5482709
c	6	40	3.5	543	6	5273901-6	Patent No. 5273901
	7	37.6	3.3	505	4	US-09-621-976-15639	Sequence 15639, A
c	8	37.4	3.3	688	3	US-08-998-416-915	Sequence 915, App
	9	36.4	3.2	1125	4	US-09-252-991A-16469	Sequence 16469, A
c	10	36.2	3.1	615	4	US-09-252-991A-242	Sequence 242, App
	11	36.2	3.1	1041	4	US-09-252-991A-296	Sequence 296, App
	12	36.2	3.1	1140	4	US-09-252-991A-269	Sequence 269, App
c	13	36	3.1	909	4	US-09-252-991A-7481	Sequence 7481, Ap
	14	36	3.1	1149	4	US-09-252-991A-7156	Sequence 7156, Ap
	15	35.2	3.1	675	4	US-09-252-991A-7278	Sequence 7278, Ap
	16	35	3.0	627	4	US-09-252-991A-3035	Sequence 3035, Ap
	17	35	3.0	630	4	US-09-252-991A-953	Sequence 953, App
	18	35	3.0	720	4	US-09-252-991A-3133	Sequence 3133, Ap
c	19	35	3.0	777	4	US-09-252-991A-1127	Sequence 1127, Ap
c	20	35	3.0	1147	2	US-08-761-277A-44	Sequence 44, Appl
	21	34.8	3.0	695	4	US-09-221-017B-767	Sequence 767, App
	22	34.6	3.0	822	4	US-09-252-991A-9029	Sequence 9029, Ap
c	23	34.4	3.0	431	4	US-09-433-241A-1	Sequence 1, Appli
	24	34.4	3.0	1011	4	US-09-252-991A-3833	Sequence 3833, Ap
	25	34.2	3.0	846	4	US-09-252-991A-6073	Sequence 6073, Ap
	26	34.2	3.0	882	4	US-09-252-991A-16446	Sequence 16446, A
c	27	34.2	3.0	927	4	US-09-252-991A-15945	Sequence 15945, A
c	28	34.2	3.0	1080	4	US-09-252-991A-6480	Sequence 6480, Ap
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c	31	33.6	2.9	839	3	US-08-998-416-519	Sequence 519, App
c	32	33	2.9	684	4	US-09-252-991A-230	Sequence 230, App
c	33	32.8	2.9	753	4	US-09-252-991A-10372	Sequence 10372, A
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	35	32.8	2.9	861	4	US-09-252-991A-14249	Sequence 14249, A
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c	37	32.8	2.9	1092	4	US-09-252-991A-14250	Sequence 14250, A
c	38	32.8	2.9	1125	4	US-09-218-489-1	Sequence 1, Appli
c	39	32.6	2.8	872	1	US-08-381-280-19	Sequence 19, Appl
c	40	32.6	2.8	872	2	US-08-445-533-19	Sequence 19, Appl
c	41	32.6	2.8	872	3	US-09-052-085-19	Sequence 19, Appl
c	42	32.6	2.8	1116	3	US-09-104-308-2	Sequence 2, Appli
c	43	32.6	2.8	1116	3	US-09-321-981-2	Sequence 2, Appli
c	44	32.6	2.8	1116	4	US-09-739-861A-2	Sequence 2, Appli
c	45	32.6	2.8	1116	4	US-09-795-583-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-236-311-9
; Sequence 9, Application US/08236311
; Patent No. 5565335
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,311
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 444P1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1142 bases
; TYPE: nucleic acid
; STRANDEDNESS: single

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;      TOPOLOGY:  linear
US-08-236-311-9

  Query Match             57.4%;  Score 660.2;  DB 1;  Length 1142;
  Best Local Similarity   97.2%;  Pred. No. 2.3e-171;
  Matches  685;  Conservative    0;  Mismatches   13;  Indels    7;  Gaps    1;

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Qy        125 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 184
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Db        543 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 602

Qy        185 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 244
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Qy        305 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 364
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Db        783 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 842

Qy        425 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 484
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Db        843 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 902

Qy        485 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 544
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Db        963 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 1022

Qy        605 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGAC 657
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Qy        658 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 702
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Db       1083 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 1127


RESULT 2
US-08-457-918-9
; Sequence 9, Application US/08457918
; Patent No. 6117655
;  GENERAL INFORMATION:
;    APPLICANT:  Capon, Daniel J.
;    APPLICANT:  Gregory, Timothy J.
;    TITLE OF INVENTION:  Adheson Variants
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/457,918
;      FILING DATE:  1-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/236311
;      FILING DATE:  02-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/936190
;      FILING DATE:  26-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/842777
;      FILING DATE:  18-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/250785
;      FILING DATE:  28-SEP-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/104329
;      FILING DATE:  02-OCT-1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kubinec, Jeffrey S.
;      REGISTRATION NUMBER:  36,575
;      REFERENCE/DOCKET NUMBER:  P0444P1C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-8228
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1142 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-457-918-9

  Query Match             57.4%;  Score 660.2;  DB 3;  Length 1142;
  Best Local Similarity   97.2%;  Pred. No. 2.3e-171;
  Matches  685;  Conservative    0;  Mismatches   13;  Indels    7;  Gaps    1;

Qy          5 ACCTTGGTTTTAGACGACTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGG 64
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Db        423 AACTCGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 482

Qy         65 ACCCCCCAGGAAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 124
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Db        483 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 542

Qy        125 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 184
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Db        603 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 662

Qy        245 TCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 304
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Db        663 TCATGTTGTCGTGCATGGCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 722

Qy        305 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 364
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Db        723 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 782

Qy        365 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 842

Qy        425 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 484
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Db        843 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 902

Qy        485 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 962

Qy        545 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 604
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Qy        658 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 702
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1083 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 1127
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RESULT 3
US-08-236-311-12
; Sequence 12, Application US/08236311
; Patent No. 5565335
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,311
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 444P1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-236-311-12

Query Match 3.7%; Score 43; DB 1; Length 468;
Best Local Similarity 49.5%; Pred. No. 0.022;
Matches 143; Conservative 0; Mismatches 140; Indels 6; Gaps 1;

```
Qy        394 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 453
              | ||||  || | || | | | || |||||    ||  || |||       | |
Db        127 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 186

Qy        454 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 507
              |   ||||| | ||   ||||||||||| ||   |   ||  ||||      |||
Db        187 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 246

Qy        508 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 567
              | |      ||  ||| ||| | |  |||       |       |   ||| ||
Db        247 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 306

Qy        568 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 627
              ||| |  ||||  ||||| || ||  ||  |||       |   || |   || |||
Db        307 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 366

Qy        628 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 676
              | | | |||   || |  ||| |||  |||  |   | |  |||  |||
Db        367 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 415
```

RESULT 4
US-08-457-918-12
; Sequence 12, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0444P1C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 12:

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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  468 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-457-918-12

  Query Match             3.7%;  Score 43;  DB 3;  Length 468;
  Best Local Similarity   49.5%;  Pred. No. 0.022;
  Matches  143;  Conservative    0;  Mismatches  140;  Indels    6;  Gaps    1;

Qy        394 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 453
Db        127 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 186

Qy        454 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 507
Db        187 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 246

Qy        508 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 567
Db        247 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 306

Qy        568 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 627
Db        307 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 366

Qy        628 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 676
Db        367 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 415


RESULT 5
5482709-5/c
;Patent No. 5482709
;    APPLICANT: JACOBSON, JAMES W.;STRAUSBERG, ROBERT L.;WILSON,
;SUSAN D.;POPE, SHARON H.;STRAUSBERG, SUSAN L.;RUFF, MICHAEL D.;
; AUGUSTINE, PATRICIA C.;DANFORTH, HARRY D.
;    TITLE OF INVENTION: EIMERIA ANTIGENIC COMPOSITION WHICH
;ELICITS ANTIBODIES AGAINST AVIAN COCCIDIOSIS
;    NUMBER OF SEQUENCES: 10
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/148,432
;      FILING DATE: 08-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 581,693
;      FILING DATE: 12-SEP-1990
;      APPLICATION NUMBER: 215,162
;      FILING DATE: 05-JUL-1989
;      APPLICATION NUMBER: 746,520
;      FILING DATE: 19-JUN-1985
;      APPLICATION NUMBER: 627,811
;      FILING DATE: 05-JUL-1984
;SEQ ID NO:5:
;      LENGTH: 533
5482709-5

  Query Match             3.5%;  Score 40;  DB 6;  Length 533;
  Best Local Similarity   47.3%;  Pred. No. 0.16;
  Matches  121;  Conservative    0;  Mismatches  135;  Indels    0;  Gaps    0;

Qy        104 TCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGG 163
Db        440 TCCCCCAGGCTTACCTGCTGCTGATGCTGCTGCTGCTCTTGCTGCAGCTGCTGTTGTTGC 381

Qy        164 TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT 223
Db        380 TGCTGTTGCTGCTTGTGTTTTCGCTTTCTCTGCTTCTGCTGCTGCTCCTGCTGCTCCTTC 321

Qy        224 TCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGC 283
Db        320 GGTTTCTGTTCGTGCTTCCGCTGCCTTTGCTGCTCCTGCTGCTCCTGCTGCGGCTGTCGC 261

Qy        284 AGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGG 343
Db        260 TGCAGCTGGTGCTGCTGCAGCTCCTGTTGCTGCTGCTGCTGCTGCAGCTGGTGCTGCTGC 201

Qy        344 AGGGTCGGGGGTAGCT 359
Db        200 AGCTGGTGCTGCAGCT 185


RESULT 6
5273901-6/c
;Patent No. 5273901
;    APPLICANT: JACOBSON, JAMES W.;STRAUSBERG, ROBERT L.;WILSON,
;SUSAN D.;POPE, SHARON H.;STRAUSBERG, SUSAN L.;RUFF,MICHAEL D.;
;AUGUSTINE, PATRICIA C.;DANFORTH, HARRY D.
;    TITLE OF INVENTION: GENETICALLY ENGINEERED COCCIDIOSIS
;SPOROZOITE 21.5 KB ANTIGEN, AC-6B
;    NUMBER OF SEQUENCES: 11
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/581,693
;      FILING DATE: 12-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 215,162
;      FILING DATE: 05-JUL-1988
;      APPLICATION NUMBER: 746,520
;      FILING DATE: 19-JUN-1985
;      APPLICATION NUMBER: 627,811
;      FILING DATE: 05-JUL-1984
;SEQ ID NO:6:
;      LENGTH:543
5273901-6

  Query Match             3.5%;  Score 40;  DB 6;  Length 543;
  Best Local Similarity   47.3%;  Pred. No. 0.16;
  Matches  121;  Conservative    0;  Mismatches  135;  Indels    0;  Gaps    0;

Qy        104 TCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGG 163
Db        450 TCCCCCAGGCTTACCTGCTGCTGATGCTGCTGCTGCTCTTGCTGCAGCTGCTGTTGTTGC 391

Qy        164 TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT 223
Db        390 TGCTGTTGCTGCTTGTGTTTTCGCTTTCTCTGCTTCTGCTGCTGCTCCTGCTGCTCCTTC 331

Qy        224 TCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGC 283
Db        330 GGTTTCTGTTCGTGCTTCCGCTGCCTTTGCTGCTCCTGCTGCTCCTGCTGCGGCTGTCGC 271

Qy        284 AGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGG 343
Db        270 TGCAGCTGGTGCTGCTGCAGCTCCTGTTGCTGCTGCTGCTGCTGCAGCTGGTGCTGCTGC 211

Qy        344 AGGGTCGGGGGTAGCT 359
Db        210 AGCTGGTGCTGCAGCT 195


RESULT 7
US-09-621-976-15639
; Sequence 15639, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 15639
;   LENGTH: 505
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;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-15639

  Query Match             3.3%;  Score 37.6;  DB 4;  Length 505;
  Best Local Similarity   13.9%;  Pred. No. 0.69;
  Matches   34;  Conservative  108;  Mismatches  102;  Indels    0;  Gaps    0;

Qy         17 GACGACTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGAA 76
              :::: : : : :| :::     :: :  |: :|::   || |  ::| :|:   :: : :
Db          7 SRYRTSSKSKRYGGKYSMYSSRWSMKYYAWGRGKYGTSGGRCGGSRGWMCSKWGYRYSYW 66

Qy         77 GTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCC 136
              |: :: :::     :|: || :  :::  :|:: ::    :   :: :    ::: :::: 
Db         67 GYKWKSWSKKMKKYSGKMGTSKSTRKYRTYTSKCRKTTCKYRGWWSWKWRMWKRRKMYYY 126

Qy        137 AGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGC 196
              : : : | : :: : :| :   :| | :||::   ::  :: ::|  :: ||||:  :
Db        127 RMKCYSCASYSYSYRRCRKYTGMTRGWYGCKKRMCKSSTRYMTRYTRYWKMTGACYGSKG 186

Qy        197 ACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGT 256
              ::|:|: :  :    ::   :|:| :::  ::  ::::::|:|:: | :  :  | |:::
Db        187 MSCKGSRSKYYGSWKWYYGKYTMCTSKYKSSKMSYKKSSMCYTYMMCYYTYWWCTCTYKK 246

Qy        257 GCAT 260
              :: |
Db        247 SYYT 250


RESULT 8
US-08-998-416-915/c
; Sequence 915, Application US/08998416
; Patent No. 6239264
;  GENERAL INFORMATION:
;    APPLICANT:  Philippsen, Peter
;    APPLICANT:  Pohlmann, Rainer
;    APPLICANT:  Steiner, Sabine
;    APPLICANT:  Mohr, Christine
;    APPLICANT:  Wendland, Jurgen
;    APPLICANT:  Knechtle, Philipp
;    APPLICANT:  Rebischung, Corinne
;    TITLE OF INVENTION:  GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
;    TITLE OF INVENTION:  AND USES THEREOF
;    NUMBER OF SEQUENCES:  1152
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6239264artis Corporation
;      STREET:  3054 Cornwallis Road
;      CITY:  Research Triangle Park
;      STATE:  No. 6239264th Carolina
;      COUNTRY:  USA
;      ZIP:  27709
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/998,416
;      FILING DATE:  24-DEC-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  CH 0016/97
;      FILING DATE:  31-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meigs, J. Timothy
;      REGISTRATION NUMBER:  38,241
;      REFERENCE/DOCKET NUMBER:  PF/5-30306/A/CGC1976
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-541-8587
;      TELEFAX:  919-541-8689
;  INFORMATION FOR SEQ ID NO:  915:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  688 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  PAG1570RP
US-08-998-416-915

  Query Match             3.3%;  Score 37.4;  DB 3;  Length 688;
  Best Local Similarity   45.0%;  Pred. No. 0.88;
  Matches  140;  Conservative    0;  Mismatches  171;  Indels    0;  Gaps    0;

Qy         63 GGACCCCCCAGGAAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAG 122
              ||||   |  | | | | | | | | | | | ||| |||| |  | |  || | | 
Db        547 GGACTTGCTGTGGAACCGGTTGTGGTTGCTGTGATTGTGGTTTCAATTGTGGTTGTGGTT 488

Qy        123 GGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTT 182
              ||  | | | || | |       | | |  ||||    | |||| |||   || | | |
Db        487 GGTGTTGTGTCTGCTGCTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 428

Qy        183 CAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCT 242
              |      |||  | | ||  || | | |  |||  |  |  ||  | | |  | ||
Db        427 GCTGCGTCTGCTGCTGCGTCTGCTGCTGCGGTTGTGGTTGTTGCGCCTGCGCCTGCGCCA 368

Qy        243 CGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGA 302
              |  | || | | ||  | | | || | | | | | | | | | | ||   |||
Db        367 GTTGTGGCTGATGAGGCTGTAAACCAAGCTGTTGTTGTTGTTGTAGTTGCGGTTGAGGTT 308

Qy        303 CTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTT 362
              | | | ||  ||||   |||   | |||||||  |   |   | | |||  |   |
Db        307 GGGGCTGCTGCTGCTGTTGTGGTTGTTGTGGTTGTTGTGTTTGTTGCTGTGGTTGTGGTG 248

Qy        363 TTGGTAGAGGT 373
              ||||  | |||
Db        247 GTGGTGGTGGT 237


RESULT 9
US-09-252-991A-16469
; Sequence 16469, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER:  US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 16469
;   LENGTH:  1125
;   TYPE:  DNA
;   ORGANISM:  Pseudomonas aeruginosa
US-09-252-991A-16469

  Query Match             3.2%;  Score 36.4;  DB 4;  Length 1125;
  Best Local Similarity   49.5%;  Pred. No. 2;
  Matches   94;  Conservative    0;  Mismatches   96;  Indels    0;  Gaps    0;

Qy        427 CTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCG 486
              || || | | |       | || |  || |  ||   || |  | |   ||| |  |||
Db        791 CTGCTGGCCGGCAAGGAAGGCCCGCTGGGCAAGAACTACAACATGCGCTGGATCGCCTCG 850

Qy        487 CTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGA 546
              ||       || ||  || |    |  ||   |||  | | || ||||  |  | |||
Db        851 ATGGTCGCCGACGTCCACCGCATCCTGACCCGTGGCGGCGTCTTCATGTACCCGCGCGAC 910

Qy        547 GGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCG 606
              |  | ||| | |  | |||  | |||  |    ||  || |||     ||| | | |||
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Db        911 GCCCGCGAGCCGGAGAAGCCCGGCAAGCTGCGCCTGATGTACGAAGCCAACCCGATGTCG 970

Qy        607 TCCACCGTCG 616
              | || | |||
Db        971 TTCATCATCG 980


RESULT 10
US-09-252-991A-242/c
; Sequence 242, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 242
;   LENGTH: 615
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-242

  Query Match             3.1%;  Score 36.2;  DB 4;  Length 615;
  Best Local Similarity   49.2%;  Pred. No. 1.8;
  Matches   95;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy        433 GACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAG 492
              |||  |  |   | || | ||   ||| |||| | |   ||   ||  | | | |||  |
Db        359 GACATGCGCCGCGCCCTGGCGCTATGGCCGGAACTGGCGCCTTGGAGCGAGGCCCTGCTG 300

Qy        493 CGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCAC 552
              | ||  |     |  |   || | |  ||      ||  ||||  | ||||| ||  |
Db        299 GGCCAGTACCTTGCCGTGCACCCGGGCTTCCAGCGCCTGGCGTTCGCGGGCGGAAGGGTC 240

Qy        553 GACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACC 612
              | ||||| |||| |  |    | |  |||  || | |  ||| ||   | ||      |
Db        239 GGCCTGACCCTGCTGCTGGGCGATGCCATGGAGTGCCTGCCGCAGCTCGACGCGCGGGTC 180

Qy        613 GTCGTCCCCTTGC 625
              | || |   || |
Db        179 GACGCCTGGTTCC 167


RESULT 11
US-09-252-991A-296
; Sequence 296, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 296
;   LENGTH: 1041
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-296

  Query Match             3.1%;  Score 36.2;  DB 4;  Length 1041;
  Best Local Similarity   49.2%;  Pred. No. 2.2;
  Matches   95;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy        433 GACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAG 492
              |||  |  |   | || | ||   ||| |||| | |   ||   ||  | | | |||  |
Db        338 GACATGCGCCGCGCCCTGGCGCTATGGCCGGAACTGGCGCCTTGGAGCGAGGCCCTGCTG 397

Qy        493 CGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCAC 552
              | ||  |     |  |   || | |  ||      ||  ||||  | ||||| ||  |
Db        398 GGCCAGTACCTTGCCGTGCACCCGGGCTTCCAGCGCCTGGCGTTCGCGGGCGGAAGGGTC 457

Qy        553 GACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACC 612
              | ||||| |||| |  |    | |  |||  || | |  ||| ||   | ||      |
Db        458 GGCCTGACCCTGCTGCTGGGCGATGCCATGGAGTGCCTGCCGCAGCTCGACGCGCGGGTC 517

Qy        613 GTCGTCCCCTTGC 625
              | || |   || |
Db        518 GACGCCTGGTTCC 530


RESULT 12
US-09-252-991A-269
; Sequence 269, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 269
;   LENGTH: 1140
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-269

  Query Match             3.1%;  Score 36.2;  DB 4;  Length 1140;
  Best Local Similarity   49.2%;  Pred. No. 2.3;
  Matches   95;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy        433 GACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAG 492
              |||  |  |   | || | ||   ||| |||| | |   ||   ||  | | | |||  |
Db        436 GACATGCGCCGCGCCCTGGCGCTATGGCCGGAACTGGCGCCTTGGAGCGAGGCCCTGCTG 495

Qy        493 CGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCAC 552
              | ||  |     |  |   || | |  ||      ||  ||||  | ||||| ||  |
Db        496 GGCCAGTACCTTGCCGTGCACCCGGGCTTCCAGCGCCTGGCGTTCGCGGGCGGAAGGGTC 555

Qy        553 GACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACC 612
              | ||||| |||| |  |    | |  |||  || | |  ||| ||   | ||      |
Db        556 GGCCTGACCCTGCTGCTGGGCGATGCCATGGAGTGCCTGCCGCAGCTCGACGCGCGGGTC 615

Qy        613 GTCGTCCCCTTGC 625
              | || |   || |
Db        616 GACGCCTGGTTCC 628


RESULT 13
US-09-252-991A-7481/c
; Sequence 7481, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
```

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;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7481
;   LENGTH: 909
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7481

  Query Match             3.1%;  Score 36;  DB 4;  Length 909;
  Best Local Similarity   45.4%;  Pred. No. 2.4;
  Matches  129;  Conservative    0;  Mismatches  155;  Indels    0;  Gaps    0;

Qy        809 AATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGG 868
              ||    | ||  |  | |  | | |      | ||  | ||| |      ||   ||  || ||
Db        350 AAACACTGGCCAGGGAAAACGCCTTGATCTTGCACGAGGGCCCCGCCACCCTTGGCCGGG 291

Qy        869 TCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCT 928
              ||  |  || |||| | |   | |  |  || | |     | | | | ||||    ||| |
Db        290 TCGGCAACGGACAGAGGTGGGACATGCGTTTGCGCAGAAGGACGACGTTGCTGCTGGTAT 231

Qy        929 AGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGA 988
                | |||||  |||  |||          ||| |  ||| | | |    ||  |   |
Db        230 TTGCAGTGCTGTTGCTGCTGGCGTTCGGCTACGGCTGGCATGCCTGGCGCAGCCTGTTGC 171

Qy        989 CGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTC 1048
                | | | |||  |    | |  ||       || |||| |      |  || | | | |
Db        170 GCGAGCAGGGTGTCGAGCGCCTGGAGTGGCAAGGCCTGGGCCTGTCCGCCGAAGGCATCG 111

Qy       1049 GTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTC 1092
              |   || |  |  |  |||  | |  || | |  ||  | ||  |
Db        110 GGCTGCGACGGCTGGCGCTGGAGCGGCGCGGCGCGGATGGCGCC 67


RESULT 14
US-09-252-991A-7156
; Sequence 7156, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER:  US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7156
;   LENGTH: 1149
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7156

  Query Match             3.1%;  Score 36;  DB 4;  Length 1149;
  Best Local Similarity   45.4%;  Pred. No. 2.6;
  Matches  129;  Conservative    0;  Mismatches  155;  Indels    0;  Gaps    0;

Qy        809 AATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGG 868
              ||    | ||  |  | |  | | |      | ||  | ||| |      ||   ||  || ||
Db        159 AAACACTGGCCAGGGAAAACGCCTTGATCTTGCACGAGGGCCCCGCCACCCTTGGCCGGG 218

Qy        869 TCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCT 928
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Db        219 TCGGCAACGGACAGAGGTGGGACATGCGTTTGCGCAGAAGGACGACGTTGCTGCTGGTAT 278

Qy        929 AGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGA 988
                | |||||  |||  |||          ||| |  ||| | | |    ||  |   |
Db        279 TTGCAGTGCTGTTGCTGCTGGCGTTCGGCTACGGCTGGCATGCCTGGCGCAGCCTGTTGC 338

Qy        989 CGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTC 1048
                | | | |||  |    | |  ||       || |||| |      |  || | | | |
Db        339 GCGAGCAGGGTGTCGAGCGCCTGGAGTGGCAAGGCCTGGGCCTGTCCGCCGAAGGCATCG 398

Qy       1049 GTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTC 1092
              |   || |  |  |  |||  | |  || | |  ||  | ||  |
Db        399 GGCTGCGACGGCTGGCGCTGGAGCGGCGCGGCGCGGATGGCGCC 442


RESULT 15
US-09-252-991A-7278
; Sequence 7278, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER:  US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7278
;   LENGTH: 675
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7278

  Query Match             3.1%;  Score 35.2;  DB 4;  Length 675;
  Best Local Similarity   46.1%;  Pred. No. 3.5;
  Matches  118;  Conservative    0;  Mismatches  138;  Indels    0;  Gaps    0;

Qy        837 CGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAA 896
              | ||  | ||| |      ||   ||  || |||| |  || |||| | |   | |  |
Db          2 CTTGCACGAGGGCCCCGCCACCCTTGGCCGGGTCGGCAACGGACAGAGGTGGGACATGCG 61

Qy        897 TTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCT 956
              || | |     | | | | ||||   ||| |   | |||||  |||  |||
Db         62 TTTGCGCAGAAGGACGACGTTGCTGCTGGTATTTGCAGTGCTGTTGCTGCTGGCGTTCGG 121

Qy        957 GGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACT 1016
              |||  |  |||  | | |     ||  |    |  | | | |||  |    |  | ||
Db        122 CTACGGCTGGCATGCCTGGCGCAGCCTGTTGCGCGAGCAGGGTGTCGAGCGCCTGGAGTG 181

Qy       1017 CTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACG 1076
              || |||| |      |  || | | | |   | || |   |  |||  | |  ||
Db        182 GCAAGGCCTGGGCCTGTCCGCCGAAGGCATCGGGCTGCGACGGCTGGCGCTGGAGCGGCG 241

Qy       1077 AGACAGGGCAGACGTC 1092
                | |  ||  | || |
Db        242 CGGCGCGGATGGCGCC 257


Search completed: May  7, 2004, 12:55:34
Job time : 64.5 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:36 ; Search time 371.25 Seconds
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Perfect score: 1150
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 4872186

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	1150	100.0	1150	13	US-10-679-999-11	Sequence 11, Appl
	2	1134	98.6	1150	13	US-10-679-999-8	Sequence 8, Appli
	3	1129	98.2	1135	13	US-10-679-999-14	Sequence 14, Appl
	4	1103.4	95.9	1135	13	US-10-679-999-17	Sequence 17, Appl
	5	660.2	57.4	1142	15	US-10-097-044A-9	Sequence 9, Appli
	6	440.8	38.3	454	9	US-09-366-133-5	Sequence 5, Appli
	7	440.8	38.3	454	13	US-10-679-999-5	Sequence 5, Appli
	8	440.8	38.3	454	15	US-10-214-037-5	Sequence 5, Appli
	9	378.4	32.9	491	9	US-09-366-133-2	Sequence 2, Appli
	10	378.4	32.9	491	13	US-10-679-999-2	Sequence 2, Appli
	11	378.4	32.9	491	15	US-10-214-037-2	Sequence 2, Appli
	12	43	3.7	468	15	US-10-097-044A-12	Sequence 12, Appl
c	13	42.4	3.7	1116	15	US-10-156-761-6640	Sequence 6640, Ap
c	14	40.4	3.5	486	13	US-10-465-217-13	Sequence 13, Appl
	15	40.4	3.5	754	9	US-09-229-200A-13	Sequence 13, Appl
	16	39.4	3.4	675	15	US-10-156-761-2371	Sequence 2371, Ap
	17	39.4	3.4	1011	13	US-10-152-886-82	Sequence 82, Appl
c	18	38.6	3.4	711	15	US-10-156-761-2558	Sequence 2558, Ap
c	19	38.4	3.3	1107	15	US-10-156-761-4247	Sequence 4247, Ap
	20	38	3.3	945	16	US-10-369-493-42967	Sequence 42967, A
c	21	37.8	3.3	459	15	US-10-029-386-26484	Sequence 26484, A
c	22	37.8	3.3	542	15	US-10-029-386-12784	Sequence 12784, A
	23	37.8	3.3	815	10	US-09-976-782-17	Sequence 17, Appl
	24	37.8	3.3	815	10	US-09-976-782-19	Sequence 19, Appl
	25	37.8	3.3	1049	13	US-10-142-426-358	Sequence 358, App
	26	37.8	3.3	1049	15	US-10-123-155-358	Sequence 358, App
	27	37.8	3.3	1049	15	US-10-146-731-358	Sequence 358, App
	28	37.8	3.3	1049	15	US-10-140-472-358	Sequence 358, App
	29	37.8	3.3	1049	15	US-10-141-761-358	Sequence 358, App
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	32	37.8	3.3	1049	16	US-10-137-871-358	Sequence 358, App
	33	37.8	3.3	1049	16	US-10-140-923-358	Sequence 358, App
	34	37.8	3.3	1049	16	US-10-141-756-358	Sequence 358, App
	35	37.8	3.3	1049	16	US-10-141-759-358	Sequence 358, App
	36	37.8	3.3	1049	16	US-10-140-805-358	Sequence 358, App
	37	37.8	3.3	1049	16	US-10-140-864-358	Sequence 358, App
c	38	37.6	3.3	717	15	US-10-133-973-2	Sequence 2, Appli
	39	37.4	3.3	411	15	US-10-156-761-3810	Sequence 3810, Ap
	40	37.4	3.3	653	15	US-10-184-644-402	Sequence 402, App
	41	37.4	3.3	653	15	US-10-184-634-402	Sequence 402, App
	42	37.2	3.2	536	17	US-10-338-110-119	Sequence 119, App
	43	37.2	3.2	629	13	US-10-282-122A-11907	Sequence 11907, A
c	44	37	3.2	915	15	US-10-156-761-5089	Sequence 5089, Ap
	45	36.6	3.2	957	15	US-10-156-761-867	Sequence 867, App

ALIGNMENTS

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RESULT 1
US-10-679-999-11
; Sequence 11, Application US/10679999
; Publication No. US20040067520A1
;  GENERAL INFORMATION:
;       APPLICANT: Mann, Michael B.
;                  Hecht, Randy I.
;       TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                           METHODS
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Amgen Inc.
;            STREET: 1840 DeHavilland Drive
;            CITY: Thousand Oaks
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 91320-1789
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/679,999
;            FILING DATE: 06-Oct-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/568,528
;            FILING DATE: 09-May-2000
;            APPLICATION NUMBER: 09/267,517
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Knight, Matthew W.
;            REGISTRATION NUMBER: 36,846
;            REFERENCE/DOCKET NUMBER: A-416
;  INFORMATION FOR SEQ ID NO: 11:
;       SEQUENCE CHARACTERISTICS:
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;             LENGTH: 1150 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;         SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-679-999-11

  Query Match             100.0%;  Score 1150;  DB 13;  Length 1150;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1150;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATACCTTGGTTTTAGACGACTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTT 60
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Qy         61 GAGGACCCCCCAGGAAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAG 120
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Qy        121 AGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 TTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTC 240
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Db        181 TTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTC 240

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Qy        301 GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 360

Qy        361 TTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        421 AGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        481 GGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG 540

Qy        541 TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTG 600
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Qy        661 TTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAA 720
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        901 AGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGAC 960
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Qy        961 GACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1021 GACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGAC 1080
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Db       1021 GACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGAC 1080

Qy       1081 AGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACA 1140
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;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1150 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-679-999-8

  Query Match             98.6%;  Score 1134;  DB 13;  Length 1150;
  Best Local Similarity   99.1%;  Pred. No. 0;
  Matches 1140;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 GTATACCTTGGTTTTAGACGACTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTT 60
              |||||||||| ||||||  ||||||||||||||||| ||||| || ||||| || |||
Db          1 GTATACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTT 60
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Qy        61 GAGGACCCCCCCAGGAAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAG 120
             ||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 GAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAG 120

Qy       121 AGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 AGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAG 180

Qy       181 TTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 TTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTC 240

Qy       241 CTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACC 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACC 300

Qy       301 GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 360

Qy       361 TTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGT 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 TTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGT 420

Qy       421 AGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATA 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 AGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATA 480

Qy       481 GGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG 540

Qy       541 TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTG 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTG 600

Qy       601 TTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTG 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 TTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTG 660

Qy       661 TTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAA 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 TTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAA 720

Qy       721 GTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTG 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 GTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTG 780

Qy       781 TGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTG 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 TGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTG 840

Qy       841 GGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGG 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 GGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGG 900

Qy       901 AGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGAC 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 AGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGAC 960

Qy       961 GACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 GACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA 1020

Qy      1021 GACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGAC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 GACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGAC 1080

Qy      1081 AGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACA 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 AGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACA 1140

Qy      1141 ATTACCTAGG 1150
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Db      1141 ATTACCTAGG 1150
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RESULT 3
US-10-679-999-14
; Sequence 14, Application US/10679999
; Publication No. US20040067520A1
; GENERAL INFORMATION:
; APPLICANT: Mann, Michael B.
; Hecht, Randy I.
; TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
; METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/679,999
; FILING DATE: 06-Oct-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/568,528
; FILING DATE: 09-May-2000
; APPLICATION NUMBER: 09/267,517
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Knight, Matthew W.
; REGISTRATION NUMBER: 36,846
; REFERENCE/DOCKET NUMBER: A-416
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1135 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-679-999-14

Query Match 98.2%; Score 1129; DB 13; Length 1135;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         22 CTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGAAGTCAG 81
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 CTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGAAGTCAG 66

Qy         82 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126

Qy        142 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186

Qy        202 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246

Qy        262 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 306
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Qy        322 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366

Qy        382 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426

Qy        442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486

Qy        502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546

Qy        562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606

Qy        622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 666

Qy        682 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 726

Qy        742 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 786

Qy        802 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 846

Qy        862 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 906

Qy        922 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 966

Qy        982 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1026

Qy       1042 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1101
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Db       1027 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1086

Qy       1102 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
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Db       1087 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135


RESULT 4
US-10-679-999-17
; Sequence 17, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1135 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-679-999-17

  Query Match             95.9%;  Score 1103.4;  DB 13;  Length 1135;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches 1113;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         22 CTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGAAGTCAG 81
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Db          7 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAG 66

Qy         82 AAGGAGAAGGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 AAGGAGAAGGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126

Qy        142 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 201
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Db        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186

Qy        202 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 261
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Db        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246

Qy        262 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 321
              |||||||||||||||||||||||||||||||||||||||||||||||||| |   |||
Db        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGT 306

Qy        322 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 381
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Db        307 ACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366

Qy        382 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 441
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Db        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426

Qy        442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486

Qy        502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546

Qy        562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621
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Db        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
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Qy        622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681
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Db        607 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 666

Qy        682 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 726

Qy        742 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 786

Qy        802 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 846

Qy        862 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 906

Qy        922 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 966

Qy        982 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1041
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Db        967 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1026

Qy       1042 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1086

Qy       1102 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
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Db       1087 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
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RESULT 5
US-10-097-044A-9
; Sequence 9, Application US/10097044A
; Publication No. US20030143220A1
;   GENERAL INFORMATION:
;        APPLICANT: Capon, Daniel J.
;                   Gregory, Timothy J.
;        TITLE OF INVENTION: Adheson Variants
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 460 Point San Bruno Blvd
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: patin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/097,044A
;             FILING DATE: 28-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/457,918
;             FILING DATE: 1-JUN-1995
;             APPLICATION NUMBER: 08/236311
;             FILING DATE: 02-MAY-1994
;             APPLICATION NUMBER: 07/936190
;             FILING DATE: 26-AUG-1992
;             APPLICATION NUMBER: 07/842777
;             FILING DATE: 18-FEB-1992
;             APPLICATION NUMBER: 07/250785
;             FILING DATE: 28-SEP-1988
;             APPLICATION NUMBER: 07/104329
;             FILING DATE: 02-OCT-1987
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kubinec, Jeffrey S.
;             REGISTRATION NUMBER: 36,575
;             REFERENCE/DOCKET NUMBER: P0444P1C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415/225-8228
;             TELEFAX: 415/952-9881
;             TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1142 bases
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-097-044A-9

  Query Match             57.4%;  Score 660.2;  DB 15;  Length 1142;
  Best Local Similarity   97.2%;  Pred. No. 1.9e-199;
  Matches  685;  Conservative    0;  Mismatches   13;  Indels    7;  Gaps    1;

Qy          5 ACCTTGGTTTTAGACGACTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGG 64
              | || || |||||  ||||||||||||||||| ||||| || ||||| || |||||||
Db        423 AACTCGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 482

Qy         65 ACCCCCCAGGAAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 124
              ||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 542

Qy        125 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 602

Qy        185 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 662

Qy        245 TCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 304
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        663 TCATGTTGTCGTGCATGGCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 722

Qy        305 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 782

Qy        365 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 842

Qy        425 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 902

Qy        485 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 962

Qy        545 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 1022

Qy        605 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGAC 657
              |||||||||||||||||||||||||||||||||||||       ||||||||||||||||||
Db       1023 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGAC 1082

Qy        658 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 702
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1083 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 1127
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RESULT 6

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US-09-366-133-5
; Sequence 5, Application US/09366133
; Patent No. US20020009798A1
;  GENERAL INFORMATION:
;    APPLICANT:  Pelleymounter, Mary Ann
;    APPLICANT:  Hecht, Randy I
;    APPLICANT:  Mann, Michael B
;    TITLE OF INVENTION:  OB PROTEIN COMPOSITIONS AND METHODS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  91230-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/366,133
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/920,608
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pessin, Karol M.
;      REFERENCE/DOCKET NUMBER:  A-345
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  454 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-366-133-5

  Query Match             38.3%;  Score 440.8;  DB 9;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 1.1e-129;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
              ||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
              |||||||||||||||||||||||||||||||||||||| | ||||||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
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Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 7
US-10-679-999-5
; Sequence 5, Application US/10679999
; Publication No. US20040067520A1
;  GENERAL INFORMATION:
;       APPLICANT: Mann, Michael B.
;                  Hecht, Randy I.
;       TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                           METHODS
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Amgen Inc.
;            STREET: 1840 DeHavilland Drive
;            CITY: Thousand Oaks
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 91320-1789
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/679,999
;            FILING DATE: 06-Oct-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/568,528
;            FILING DATE: 09-May-2000
;            APPLICATION NUMBER: 09/267,517
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Knight, Matthew W.
;            REGISTRATION NUMBER: 36,846
;            REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 454 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-679-999-5

  Query Match             38.3%;  Score 440.8;  DB 13;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 1.1e-129;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
              ||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
              |||||||||||||||||||||||||||||||||||||| | ||||||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302
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Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
              |||||||||||||||||||||||||||||||
Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 8
US-10-214-037-5
; Sequence 5, Application US/10214037
; Publication No. US20030054997A1
;   GENERAL INFORMATION:
;        APPLICANT: Pelleymounter, Mary Ann
;                   Hecht, Randy I
;                   Mann, Michael B
;        TITLE OF INVENTION: OB PROTEIN COMPOSITIONS AND METHODS
;        NUMBER OF SEQUENCES: 6
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 Dehavilland Drive
;             CITY: Thousand Oaks
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 91230-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/214,037
;             FILING DATE: 05-Aug-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/920,608
;             FILING DATE: 07-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Pessin, Karol M.
;             REFERENCE/DOCKET NUMBER: A-345
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 454 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-214-037-5

  Query Match            38.3%;  Score 440.8;  DB 15;  Length 454;
  Best Local Similarity  98.5%;  Pred. No. 1.1e-129;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
              |||||||||||||||||||||||||||||||||||||||||||| | ||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
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Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
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Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
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Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 9
US-09-366-133-2
; Sequence 2, Application US/09366133
; Patent No. US20020009798A1
;  GENERAL INFORMATION:
;    APPLICANT:  Pelleymounter, Mary Ann
;    APPLICANT:  Hecht, Randy I
;    APPLICANT:  Mann, Michael B
;    TITLE OF INVENTION:  OB PROTEIN COMPOSITIONS AND METHODS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  91230-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/366,133
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/920,608
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pessin, Karol M.
;      REFERENCE/DOCKET NUMBER:  A-345
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-366-133-2

  Query Match            32.9%;  Score 378.4;  DB 9;  Length 491;
  Best Local Similarity  89.8%;  Pred. No. 8.5e-110;
  Matches  406;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              ||||||||||||||||||||||||||||||||  | ||||||||  ||||| || ||
Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
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                  |||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
                  |||||||||||| | |||||||| |||||||  |||||| | |||||| |||||||
Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
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Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
                  | | |||||||||| |||  | ||| || |||| ||||||||||||||||||   ||
Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
                  ||||||||||||||||||||||||||||||||||||||||||||||||||| |||  |||
Db        400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
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Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491


RESULT 10
US-10-679-999-2
; Sequence 2, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 491 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-679-999-2

  Query Match             32.9%;  Score 378.4;  DB 13;  Length 491;
  Best Local Similarity   89.8%;  Pred. No. 8.5e-110;
  Matches  406;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
                  ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
                  ||||||||||||||||||||||||||||||    | ||||||||    ||||| || ||
Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
                  ||||||||||||||||||||||||||||| | ||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
                  |||||||||||| | |||||||| |||||||  |||||| | |||||| |||||||
Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
                  |||||||||||||||||||||||||| |||||||||||||||||||||  ||||||
Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
                  | | |||||||||| |||  | ||| || |||| ||||||||||||||||||   ||
Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
                  ||||||||||||||||||||||||||||||||||||||||||||||||||| |||  |||
Db        400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
                  ||||||| | |||||||  ||||||||||||
Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491


RESULT 11
US-10-214-037-2
; Sequence 2, Application US/10214037
; Publication No. US20030054997A1
;   GENERAL INFORMATION:
;        APPLICANT: Pelleymounter, Mary Ann
;                   Hecht, Randy I
;                   Mann, Michael B
;        TITLE OF INVENTION: OB PROTEIN COMPOSITIONS AND METHODS
;        NUMBER OF SEQUENCES: 6
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 Dehavilland Drive
;             CITY: Thousand Oaks
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 91230-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/214,037
;             FILING DATE: 05-Aug-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/920,608
;             FILING DATE: 07-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Pessin, Karol M.
;             REFERENCE/DOCKET NUMBER: A-345
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 491 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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US-10-214-037-2

Query Match 32.9%; Score 378.4; DB 15; Length 491;
Best Local Similarity 89.8%; Pred. No. 8.5e-110;
Matches 406; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

```
Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              ||||||||||||||||||||||||||||||    | ||||||||   ||||| || ||
Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              |||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
              |||||||||||| | |||||||| |||||||| ||||| | |||||| |||||||
Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
              |||||||||||||||||||||||||| |||||||||||||||||||||   ||||||
Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
                | | |||||||| ||| | ||| || |||| ||||||||||||||||||   ||
Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||| |||  |||
Db        400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
              ||||||| | ||||||| ||||||||||||
Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491
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RESULT 12
US-10-097-044A-12
; Sequence 12, Application US/10097044A
; Publication No. US20030143220A1
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/097,044A
; FILING DATE: 28-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0444P1C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-097-044A-12

Query Match 3.7%; Score 43; DB 15; Length 468;
Best Local Similarity 49.5%; Pred. No. 0.0062;
Matches 143; Conservative 0; Mismatches 140; Indels 6; Gaps 1;

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Qy        394 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 453
              | ||||   || | || | | || |||||    ||  || |||          | |
Db        127 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 186

Qy        454 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 507
                |    |||||| | ||   |||||||||||| ||   |  || ||||      |||
Db        187 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 246

Qy        508 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 567
              | |       ||  |||  |||  | |  |||       |       |      |  ||| ||
Db        247 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 306

Qy        568 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 627
              |||  |  ||||  |||||  || ||  ||  |||        |   || |    || |||
Db        307 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 366

Qy        628 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 676
              | | | |||   || |  ||| |||  |||  |   |  | |||  |||
Db        367 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 415
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RESULT 13
US-10-156-761-6640/c
; Sequence 6640, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 6640
; LENGTH: 1116
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS

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;   LOCATION: (1)..(1116)
US-10-156-761-6640

  Query Match             3.7%;  Score 42.4;  DB 15;  Length 1116;
  Best Local Similarity   51.0%;  Pred. No. 0.014;
  Matches  100;  Conservative    0;  Mismatches   96;  Indels    0;  Gaps    0;

Qy        449 AGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCT 508
              ||  | ||| |  |     ||   | || ||  ||| ||| || |||     | |||| |
Db        706 AGGAGAACTCGGGGTCGAAGACCCGGACGACCGGGGCGCCGTCGCGCTCGCCCACCATGA 647

Qy        509 CGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGA 568
              || | |||||  |   |  |  |  | ||  | | | || || | ||| |  |  |
Db        646 CGCTGCCCGTGTGGAGGTCACCGTGGAGCGGGGCCTGCGCGCTCGTCATGAAGACGTGGC 587

Qy        569 GGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGA 628
              ||| |  || ||  ||| |     ||| |  ||   ||   | ||  | | || |  |
Db        586 GGAGGTCGGCGACCTCGGTGCGCAGGCGCGGGTCGGCGCGGAACGCGGCCGCCAGGTCGT 527

Qy        629 AGAGTACGAGGCACTA 644
              |||| || ||  | |
Db        526 CGAGTCCGGGGTGCCA 511


RESULT 14
US-10-465-217-13/c
; Sequence 13, Application US/10465217
; Publication No. US20030204859A1
; GENERAL INFORMATION:
;  APPLICANT: Kazemi-Esfarjani, Parsa
;  APPLICANT:  Benzer, Seymour
;  TITLE OF INVENTION: AN ANIMAL MODEL OF POLYGLUTAMINE
;  TITLE OF INVENTION:  TOXICITY, METHODS OF USE, AND MODULATORS OF POLYGLUTAMINE
;  TITLE OF INVENTION:  TOXICITY
;  FILE REFERENCE: 06618-686001
;  CURRENT APPLICATION NUMBER: US/10/465,217
;  CURRENT FILING DATE:  2003-06-18
;  PRIOR APPLICATION NUMBER: US/09/639,207
;  PRIOR FILING DATE: 2000-08-14
;  PRIOR APPLICATION NUMBER: US 60/148,934
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: US 60/148,933
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: US 60/177,047
;  PRIOR FILING DATE: 2000-01-18
;  PRIOR APPLICATION NUMBER: US 60/205,720
;  PRIOR FILING DATE: 2000-05-19
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 486
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-10-465-217-13

  Query Match             3.5%;  Score 40.4;  DB 13;  Length 486;
  Best Local Similarity   45.2%;  Pred. No. 0.042;
  Matches  149;  Conservative    0;  Mismatches  181;  Indels    0;  Gaps    0;

Qy         97 TTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTG 156
              ||   | | |||| |  |     |  |  | |   || | ||    ||  |  |   ||
Db        375 TTGCTGCTGCTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTG 316

Qy        157 CACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTA 216
              |  | | |||| |||     | | | |   ||||    |||  |||| |   || |   |
Db        315 CTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGCTGCTGCTG 256

Qy        217 TTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAG 276
              || | ||| |  ||       | ||  |  |||||  ||   ||    |   || || |
Db        255 TTGCTGTTGTTGTTGCTGTTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTGCTG 196

Qy        277 GAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTG 336
              |  |  |    || | |||       | | | |  | ||||   | | | |  ||||
Db        195 CTGCTGTTGCTGTTGCTGCTGCTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTG 136

Qy        337 TTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTT 396
              | | |  | | | | |||  | | || | | | | ||| |   |   |  ||
Db        135 CTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTG 76

Qy        397 GGTGTCCACATGTGGGACGGGGGTAGGGCC 426
                  | |   || |||   |  |  |||||
Db         75 TTGCTGCTGCTGGGGGGTTGACGGTGGGCC 46


RESULT 15
US-09-229-200A-13
; Sequence 13, Application US/09229200A
; Patent No. US20020099179A1
;  GENERAL INFORMATION:
;       APPLICANT: Jolliffe et al.
;       TITLE OF INVENTION: CD4 Specific Recombinant Antibody
;       NUMBER OF SEQUENCES: 28
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Johnson & Johnson
;            STREET: One Johnson & Johnson Plaza
;            CITY: New Brunswick
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 08933-7003
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;            COMPUTER: IBM
;            OPERATING SYSTEM: PC-DOS
;            SOFTWARE: <Unknown>
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/229,200A
;            FILING DATE: 13-Jan-1999
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: John W. Wallen, III
;            REGISTRATION NUMBER: 35,403
;            REFERENCE/DOCKET NUMBER: ORT-948
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (858) 784-3239
;            TELEFAX: (908) 524-2808
;  INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 754
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       ANTI-SENSE: no
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-229-200A-13

  Query Match             3.5%;  Score 40.4;  DB 9;  Length 754;
  Best Local Similarity   49.3%;  Pred. No. 0.051;
  Matches  138;  Conservative    0;  Mismatches  136;  Indels    6;  Gaps    1;

Qy        403 CACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACG 462
              || | || | | || |||||    ||  || |||           | |     |   |||
Db        411 CAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGACAACACACG 470

Qy        463 GACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTCTCGTTACCC 516
              ||| | ||   ||||||||||||| ||    |   ||  ||||      ||| | |
Db        471 GACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTATTGCGGGAG 530

Qy        517 GTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAG 576
              || |||  ||| | |  |||     |     |     |  ||| || ||| | |
Db        531 GTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCGTGGATGTCG 590

Qy        577 GAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACG 636
              |||  |||||  || ||  ||  |||       |   || |    || |||| | | |||
Db        591 GAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAGATGCGGACG 650
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```
Qy        637 AGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 676
              || |  ||| |||  |||  |   | |  |||  |||
Db        651 CTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 690
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Search completed: May 9, 2004, 11:52:00
Job time : 373.25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 13:07:09 ; Search time 2222.5 Seconds
(without alignments)
15451.747 Million cell updates/sec

Title: US-10-679-999-11
Perfect score: 1150
Sequence: 1 GTATACCTTGGTTTTAGACG.....AGGCCCAACAATTACCTAGG 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 54314686

Minimum DB seq length: 0
Maximum DB seq length: 1150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	48.8	4.2	527	9	AV962678	AV962678 AV962678
c	2	48.2	4.2	610	13	BW035294	BW035294 BW035294
c	3	47.6	4.1	619	13	BW251013	BW251013 BW251013
c	4	47	4.1	546	13	BW249566	BW249566 BW249566
c	5	47	4.1	660	13	BW193819	BW193819 BW193819
c	6	45.8	4.0	602	13	BW192111	BW192111 BW192111
c	7	45.8	4.0	617	13	BW314712	BW314712 BW314712
	8	43.6	3.8	1039	13	CA128348	CA128348 SCJLLR200
c	9	43.2	3.8	486	9	AI869699	AI869699 wm02f07.x
c	10	43.2	3.8	658	13	BW265514	BW265514 BW265514
c	11	43.2	3.8	663	13	BW259047	BW259047 BW259047
	12	43.2	3.8	910	29	CNS006ON	AL065629 Drosophil
c	13	42.8	3.7	509	10	BF593096	BF593096 7o56e02.x
c	14	42.8	3.7	552	14	CA686322	CA686322 wlm96.pk0
c	15	42.6	3.7	642	13	CA012935	CA012935 HT06O08r
c	16	42.6	3.7	649	14	CD907542	CD907542 G468.107E
c	17	42.6	3.7	673	13	CA014102	CA014102 HT10G06r
c	18	42.6	3.7	725	14	CD910343	CD910343 G550.001A
c	19	42.6	3.7	763	14	CD906072	CD906072 G468.103N
c	20	42.6	3.7	838	12	BI948448	BI948448 HVSME1000
c	21	42.2	3.7	512	9	AI289506	AI289506 qw28e11.x
c	22	42.2	3.7	586	9	AI687271	AI687271 tp94e04.x
c	23	42.2	3.7	659	13	CA014547	CA014547 HT11K11r
	24	42	3.7	645	29	CNS012I3	AL101589 Drosophil
	25	41.8	3.6	343	9	AA330793	AA330793 EST34531
	26	41.8	3.6	1101	29	CNS00LXJ	AL078875 Drosophil
	27	41.6	3.6	337	14	CB047414	CB047414 NISC_gg02
	28	41.6	3.6	340	9	AA302570	AA302570 EST15740
c	29	41.6	3.6	408	14	CA720412	CA720412 wkm2n.pk0
c	30	41.6	3.6	414	12	BJ248630	BJ248630 BJ248630
c	31	41.6	3.6	439	10	BE488609	BE488609 WHE1051_G
c	32	41.6	3.6	442	14	CA719617	CA719617 wkm2n.pk0
c	33	41.6	3.6	443	9	AI582641	AI582641 tn47h04.x
c	34	41.6	3.6	443	14	CA656554	CA656554 wlm0.pk00
c	35	41.6	3.6	447	14	CA687517	CA687517 wlm96.pk0
c	36	41.6	3.6	448	14	CA692819	CA692819 wlm96.pk0
c	37	41.6	3.6	451	9	AI083954	AI083954 oz53b09.x
c	38	41.6	3.6	451	10	AW276084	AW276084 xq45c08.x
c	39	41.6	3.6	455	10	AW590575	AW590575 hg46c10.x
c	40	41.6	3.6	458	9	AW088852	AW088852 xd31e06.x
c	41	41.6	3.6	463	10	BF056551	BF056551 7k06g10.x
	42	41.6	3.6	466	10	AW673691	AW673691 ba56g10.y
c	43	41.6	3.6	467	9	AI752976	AI752976 cr03b09.x
c	44	41.6	3.6	467	9	AI879509	AI879509 au53d05.x
c	45	41.6	3.6	469	9	AI088760	AI088760 qa16h11.x

ALIGNMENTS

RESULT 1
AV962678/c
LOCUS AV962678 527 bp mRNA linear EST 14-MAR-2002
DEFINITION AV962678 Nori Satoh unpublished cDNA library, larva Ciona intestinalis cDNA clone cilv05e12 5', mRNA sequence.
ACCESSION AV962678
VERSION AV962678.1 GI:19450977
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 527)
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES Location/Qualifiers
source 1. .527
/organism="Ciona intestinalis"
/mol_type="mRNA"

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                     /db_xref="taxon:7719"
                     /clone="cilv05e12"
                     /tissue_type="whole animal"
                     /dev_stage="larva"
                     /clone_lib="Nori Satoh unpublished cDNA library, larva"
ORIGIN

  Query Match             4.2%;  Score 48.8;  DB 9;  Length 527;
  Best Local Similarity   45.8%;  Pred. No. 1.4;
  Matches  167;  Conservative    0;  Mismatches  198;  Indels    0;  Gaps    0;

Qy        242 TCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCG 301
              | ||  || |||  |   ||     |  ||   ||| || |  |    || |  ||
Db        476 TGGTGGTGATGTGTTNTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATT 417

Qy        302 ACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCT 361
              | |   ||| ||  ||||   |||   | |||||| | |  ||  | |  || | ||
Db        416 TCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCC 357

Qy        362 TTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTA 421
              | | || |    |  | | ||  |   |   ||     |  | ||| ||     |
Db        356 TGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGT 297

Qy        422 GGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAG 481
              |  |||  | |    ||| ||| ||| || |     || |     |||   || |||
Db        296 TGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGC 237

Qy        482 GGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGT 541
              || | ||| |  |     |      ||  |||      | ||| || |||| | ||
Db        236 TGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGTTGTTGT 177

Qy        542 GCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGT 601
              |    ||       ||  ||||| |  |  |  |  ||||| ||| | |    |   ||
Db        176 TGGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGTGCTTCTGTAGT 117

Qy        602 TCTCG 606
              |  ||
Db        116 TGCCG 112


RESULT 2
BW035294/c
LOCUS       BW035294                610 bp    mRNA    linear   EST 13-OCT-2002
DEFINITION  BW035294 Nori Satoh unpublished cDNA library, blood cells Ciona
            intestinalis cDNA clone cibd028f16 5', mRNA sequence.
ACCESSION   BW035294
VERSION     BW035294.1  GI:23951246
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 610)
  AUTHORS   Satou,Y., Satake,M., Azumi,K., Nonaka,M., Shin-i,T., Kohara,Y. and
            Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .610
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cibd028f16"
                     /tissue_type="blood cells"
                     /clone_lib="Nori Satoh unpublished cDNA library, blood
                     cells"
ORIGIN

  Query Match             4.2%;  Score 48.2;  DB 13;  Length 610;
  Best Local Similarity   45.8%;  Pred. No. 2;
  Matches  167;  Conservative    0;  Mismatches  198;  Indels    0;  Gaps    0;

Qy        242 TCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCG 301
              | ||  || |||  |   ||     |  ||   ||| || |  |    || |  ||
Db        475 TGGTGGTGATGTGTTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATT 416

Qy        302 ACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCT 361
              | |   ||| ||  ||||   |||   | |||||| | |  ||  | |  || | ||
Db        415 TCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCC 356

Qy        362 TTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTA 421
              | | || |    |  | | ||  |   |   ||     |  | ||| ||     |
Db        355 TGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGT 296

Qy        422 GGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAG 481
              |  |||  | |    ||| ||| ||| || |     || |     |||   || |||
Db        295 TGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGC 236

Qy        482 GGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGT 541
              || | ||| |  |     |      ||  |||      | ||| || |||| | ||
Db        235 TGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGTTGTTGT 176

Qy        542 GCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGT 601
              |    ||       ||  ||||| |  |  |  |  ||||| ||| | |    |   ||
Db        175 TGGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGTGCTTCTGTAGT 116

Qy        602 TCTCG 606
              |  ||
Db        115 TGCCG 111


RESULT 3
BW251013/c
LOCUS       BW251013                619 bp    mRNA    linear   EST 09-NOV-2002
DEFINITION  BW251013 Nori Satoh unpublished cDNA library, tailbud embryo Ciona
            intestinalis cDNA clone citb088l19 5', mRNA sequence.
ACCESSION   BW251013
VERSION     BW251013.1  GI:24830931
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 619)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .619
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="citb088l19"
                     /tissue_type="whole animal"
                     /dev_stage="tailbud embryo"
                     /clone_lib="Nori Satoh unpublished cDNA library, tailbud
                     embryo"
ORIGIN

  Query Match             4.1%;  Score 47.6;  DB 13;  Length 619;
  Best Local Similarity   46.0%;  Pred. No. 2.8;
  Matches  161;  Conservative    0;  Mismatches  189;  Indels    0;  Gaps    0;
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Qy        242 TCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCG 301
              | ||  || |||  |   ||      |  ||   ||| || |  |    || |  ||
Db        506 TGGTGGTGATGTGTTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATT 447

Qy        302 ACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCT 361
              | |   ||| ||  ||||   |||   |  |||||| | |  ||  | |  || | ||
Db        446 TCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCC 387

Qy        362 TTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTA 421
              | | || |    |   | || |    ||      |  | |||  ||    |
Db        386 TGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGT 327

Qy        422 GGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAG 481
              |  |||   | |    ||| ||| ||| || |    || |    |||   || |||
Db        326 TGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGC 267

Qy        482 GGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGT 541
              || | ||| |  |    |   || |||    |   | ||| || |||| | ||
Db        266 TGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGTTGTTGT 207

Qy        542 GCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAG 591
                |   ||      ||  ||||| | |  | |  ||||| ||| | |
Db        206 TGGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGTG 157
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RESULT 4
BW249566/c
LOCUS BW249566 546 bp mRNA linear EST 09-NOV-2002
DEFINITION BW249566 Nori Satoh unpublished cDNA library, tailbud embryo Ciona intestinalis cDNA clone citb082d19 5', mRNA sequence.
ACCESSION BW249566
VERSION BW249566.1 GI:24829484
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 546)
AUTHORS Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
TITLE Expressed genes in Ciona intestinalis (2002c)
JOURNAL Unpublished (2002)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES Location/Qualifiers
source 1. .546
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="citb082d19"
/tissue_type="whole animal"
/dev_stage="tailbud embryo"
/clone_lib="Nori Satoh unpublished cDNA library, tailbud embryo"
ORIGIN

Query Match 4.1%; Score 47; DB 13; Length 546;
Best Local Similarity 45.5%; Pred. No. 3.6;
Matches 167; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

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Qy        242 TCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCG 301
              | ||  || |||  |   ||      |  ||   ||| || |  |    || |  ||
Db        512 TGGTGGTGATGTGTTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATT 453

Qy        302 ACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCT 361
              | |   ||| ||  ||||   |||   |  |||||| | |  ||  | |  || | ||
Db        452 TCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCC 393

Qy        362 TTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTA 421
              | | || |    |   | || |    ||      |  | |||  ||    |
Db        392 TGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGT 333

Qy        422 GGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAG 481
              |  |||   | |    ||| ||| ||| || |    || |    |||   || |||
Db        332 TGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGC 273

Qy        482 GGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGT 541
              || | ||| |  |    |   || |||    |   | ||| || |||| | ||
Db        272 TGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGTTGT 213

Qy        542 GCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGT 601
                |   ||      ||  ||||| | |  | |  ||||| ||| | |  ||  ||||
Db        212 TGTTGGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGTGCTTCTGT 153

Qy        602 TCTCGTC 608
                | | |
Db        152 AGTTGCC 146
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RESULT 5
BW193819/c
LOCUS BW193819 660 bp mRNA linear EST 05-NOV-2002
DEFINITION BW193819 Nori Satoh unpublished cDNA library, cleaving embryo Ciona intestinalis cDNA clone cicl101p23 5', mRNA sequence.
ACCESSION BW193819
VERSION BW193819.1 GI:24608221
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 660)
AUTHORS Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
TITLE Expressed genes in Ciona intestinalis (2002c)
JOURNAL Unpublished (2002)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES Location/Qualifiers
source 1. .660
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cicl101p23"
/tissue_type="whole body"
/dev_stage="cleaving embryo"
/clone_lib="Nori Satoh unpublished cDNA library, cleaving embryo"
ORIGIN

Query Match 4.1%; Score 47; DB 13; Length 660;
Best Local Similarity 45.5%; Pred. No. 4;
Matches 167; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

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Qy        242 TCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCG 301
              | ||  || |||  |   ||      |  ||   ||| || |  |    || |  ||
Db        489 TGGTGGTGATGTGTTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATT 430

Qy        302 ACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCT 361
              | |   ||| ||  ||||   |||   |  |||||| | |  ||  | |  || | ||
Db        429 TCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCC 370

Qy        362 TTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTA 421
              | | || |    |   | || |    ||      |  | |||  ||    |
Db        369 TGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGT 310

Qy        422 GGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAG 481
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Db        309 TGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGC 250

Qy        482 GGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGT 541

Db        249 TGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGTTGGTGTTGTTGT 190

Qy        542 GCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGT 601

Db        189 TGTTGGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGTGCTTCTGT 130

Qy        602 TCTCGTC 608

Db        129 AGTTGCC 123


RESULT 6
BW192111/c
LOCUS       BW192111                602 bp    mRNA    linear   EST 05-NOV-2002
DEFINITION  BW192111 Nori Satoh unpublished cDNA library, young adult Ciona
            intestinalis cDNA clone ciad095m14 5', mRNA sequence.
ACCESSION   BW192111
VERSION     BW192111.1  GI:24606513
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 602)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .602
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="ciad095m14"
                     /tissue_type="whole animal"
                     /dev_stage="young adult"
                     /clone_lib="Nori Satoh unpublished cDNA library, young
                     adult"
ORIGIN

  Query Match             4.0%;  Score 45.8;  DB 13;  Length 602;
  Best Local Similarity   45.8%;  Pred. No. 7.2;
  Matches  158;  Conservative    0;  Mismatches  187;  Indels    0;  Gaps    0;

Qy        248 TGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTAC 307

Db        444 TGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGTTCC 385

Qy        308 CGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGT 367

Db        384 TGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGT 325

Qy        368 AGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCC 427

Db        324 TGTTCCTGTTGGTGCCGTTGTTGTCCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGA 265

Qy        428 TACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGC 487

Db        264 TGCTGTTGTTGTTGTTGATGATGCTGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGC 205

Qy        488 TGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAG 547

Db        204 TGTTGTTGTTGGTGTTGCTGTTGTTGGCGCTGCTGTTGTTGTTGTTGATGTTGTTGGTGC 145

Qy        548 GGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGT 592

Db        144 TTCTGTAGTTGCCGCTGTTGATATTGGCGGTGATTGCGCTTTTGT 100


RESULT 7
BW314712/c
LOCUS       BW314712                617 bp    mRNA    linear   EST 11-NOV-2002
DEFINITION  BW314712 Nori Satoh unpublished cDNA library, heart Ciona
            intestinalis cDNA clone ciht039h07 5', mRNA sequence.
ACCESSION   BW314712
VERSION     BW314712.1  GI:24895396
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 617)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .617
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="ciht039h07"
                     /tissue_type="heart"
                     /clone_lib="Nori Satoh unpublished cDNA library, heart"
ORIGIN

  Query Match             4.0%;  Score 45.8;  DB 13;  Length 617;
  Best Local Similarity   43.2%;  Pred. No. 7.3;
  Matches  212;  Conservative    0;  Mismatches  279;  Indels    0;  Gaps    0;

Qy        102 GTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTC 161

Db        602 GTTGCTGTTTCTGTGTTCGGTGTATTNTGTGTTGTTGTTGTGNGTAGTTGCTGCTGCT 543

Qy        162 GGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACG 221

Db        542 GCTGTTGTTGTTGCTGTAGTTGGTGGTGATGTGTTTTGTGTTGTTCTTGTATTAGGCGTT 483

Qy        222 GTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTG 281

Db        482 GTTGTTGATGTATTTCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGT 423

Qy        282 GCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCG 341

Db        422 GCTGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCT 363

Qy        342 GGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGT 401

Db        362 GTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTCCCTGTTGGT 303

Qy        402 CCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGAC 461

Db        302 GCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGTTGATGATGCTGTTGTTGTT 243

Qy        462 GGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGG 521

Db        242 GGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGCTGTTGTTGGCGCTGCT 183

Qy        522 CCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGAT 581
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Db        182 GTTGTTGTTGTTGATGTTGTTGGTGCTTCTGTAGTTGCCGCTGTTGATATTGGCGGTGAT 123

Qy        582 GTCGTTCGAGT 592
              || |   ||
Db        122 TGCGCTTTTGT 112
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RESULT 8
CA128348
LOCUS CA128348 1039 bp mRNA linear EST 24-SEP-2003
DEFINITION SCJLLR2006A05.g LR2 Saccharum officinarum cDNA clone SCJLLR2006A05 5', mRNA sequence.
ACCESSION CA128348
VERSION CA128348.1 GI:35009126
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE 1 (bases 1 to 1039)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 006 row: A column: 05
Seq primer: T7 Promoter Primer.
FEATURES Location/Qualifiers
source 1. .1039
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCJLLR2006A05"
/lab_host="DH10B"
/clone_lib="LR2"
/note="Organ: Leaf roll from field grown adult plants (small insert library); Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [Leaf roll from field grown adult plants (small insert library)]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
ORIGIN

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  Query Match             3.8%;  Score 43.6;  DB 13;  Length 1039;
  Best Local Similarity   45.6%;  Pred. No. 30;
  Matches  154;  Conservative    0;  Mismatches  184;  Indels    0;  Gaps    0;

Qy        442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501
              | |||  || || ||  ||   ||  ||   | | |   | || | | | || ||
Db        303 TCGGTGGAGACGTACAAGATCTACATCTTCAAGGTGCTGAAGCAGGTGCACCCGGACATC 362

Qy        502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561
              | ||||||    | |   | | |||  ||||    |   |    |  ||  | |
Db        363 TGCATCTCGTCCAAGGCCATGTCCATCATGAACTTCTTCATCAACGACATCTTCCATAAG 422

Qy        562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621
              |||  ||  | ||  ||  |    |      |   ||  |    | |||  |     || |
Db        423 CTGGCGGCGGAGGCGGCCAAACTGGCGCGCTACAACAAGAAGCCCACCATCACGTGCCGC 482

Qy        622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681
              |  ||| |     | |  ||| ||||  | || | | |  | |  || |||||
Db        483 GAGATCCAGACTTTCGTCCGCCTCGTCCTCCCCGGCGAGCTCGCCAAGCACGCCTTCTTC 542

Qy        682 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 741
              |||  | ||  |||||  |  || |   |     | | |  |  ||  |||     | |
Db        543 GAGGTGCACCAAGGCCGTTACCAAGTTCACCAGCTCCTATGCGAGCGATGGGACCTGCCT 602

Qy        742 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGT 779
              || ||| | |    | | |     || ||| ||  ||
Db        603 TAGTTTCGTTCATGAAGTACTAGTGTGTTGTCGTGTGT 640
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RESULT 9
AI869699/c
LOCUS AI869699 486 bp mRNA linear EST 07-MAR-2000
DEFINITION wm02f07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2433253 3' similar to gb:J05016 PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AI869699
VERSION AI869699.1 GI:5543667
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 486)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 751 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 282.
FEATURES Location/Qualifiers
source 1. .486
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2433253"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Brn25"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATAGGTTTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN

```
  Query Match             3.8%;  Score 43.2;  DB 9;  Length 486;
  Best Local Similarity   54.4%;  Pred. No. 26;
  Matches   87;  Conservative    0;  Mismatches   73;  Indels    0;  Gaps    0;

Qy        929 AGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGA 988
              | |||   |||||||  |||     | |    || |  || | |   ||   |   ||||
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Db        430 ACAGAGATCTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGA 371

Qy        989 CGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTC 1048

Db        370 CCAAGGAAGAGCTTTGAAGGCCTGAGGTCTGCGAAAGGTGGGAGGAGGCAGACGCCCTGC 311

Qy       1049 GTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1088

Db        310 GTGGCCCATGGTCGGGGCGTCCACGCCGAGGCCGGCAACA 271


RESULT 10
BW265514/c
LOCUS       BW265514                658 bp    mRNA    linear   EST 09-NOV-2002
DEFINITION  BW265514 Nori Satoh unpublished cDNA library, gastrula and neurula
            Ciona intestinalis cDNA clone cign040o10 5', mRNA sequence.
ACCESSION   BW265514
VERSION     BW265514.1  GI:24845432
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 658)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .658
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cign040o10"
                     /tissue_type="whole body"
                     /dev_stage="gastrula and neurula"
                     /clone_lib="Nori Satoh unpublished cDNA library, gastrula
                     and neurula"
ORIGIN

  Query Match             3.8%;  Score 43.2;  DB 13;  Length 658;
  Best Local Similarity   44.1%;  Pred. No. 30;
  Matches  180;  Conservative    0;  Mismatches  228;  Indels    0;  Gaps    0;

Qy        180 GTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCT 239

Db        566 GTTGTTGTTGTTGTAGTTGCTGCTGCTGCTGTTGTTGTTGCTGTAGTTGGTGGTGATGTG 507

Qy        240 CCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGAC 299

Db        506 TTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATTTCGTGTTGTTGCT 447

Qy        300 CGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCT 359

Db        446 GTTGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTT 387

Qy        360 CTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGG 419

Db        386 CCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTT 327

Qy        420 TAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGAT 479

Db        326 GGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGCTGTTGTTGTT 267

Qy        480 AGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTG 539

Db        266 GGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGTTGTTGTTGTTGTTGTT 207


Qy        540 GTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTT 587

Db        206 GGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGT 159


RESULT 11
BW259047/c
LOCUS       BW259047                663 bp    mRNA    linear   EST 09-NOV-2002
DEFINITION  BW259047 Nori Satoh unpublished cDNA library, gastrula and neurula
            Ciona intestinalis cDNA clone cign001j16 5', mRNA sequence.
ACCESSION   BW259047
VERSION     BW259047.1  GI:24838965
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 663)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .663
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cign001j16"
                     /tissue_type="whole body"
                     /dev_stage="gastrula and neurula"
                     /clone_lib="Nori Satoh unpublished cDNA library, gastrula
                     and neurula"
ORIGIN

  Query Match             3.8%;  Score 43.2;  DB 13;  Length 663;
  Best Local Similarity   44.1%;  Pred. No. 30;
  Matches  180;  Conservative    0;  Mismatches  228;  Indels    0;  Gaps    0;

Qy        180 GTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCT 239

Db        566 GTTGTTGTTGTTGTAGTTGCTGCTGCTGCTGTTGTTGTTGCTGTAGTTGGTGGTGATGTG 507

Qy        240 CCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGAC 299

Db        506 TTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATTTCGTGTTGTTGCT 447

Qy        300 CGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCT 359

Db        446 GTTGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTT 387

Qy        360 CTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGG 419

Db        386 CCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTT 327

Qy        420 TAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGAT 479

Db        326 GGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGCTGTTGTTGTT 267

Qy        480 AGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTG 539

Db        266 GGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGTTGTTGTTGTTGTTGTT 207

Qy        540 GTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTT 587

Db        206 GGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGT 159
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```
RESULT 12
CNS006ON
LOCUS       CNS006ON                910 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR14J21 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL065629
VERSION     AL065629.1  GI:4944698
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 910)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .910
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR14J21"
                     /clone_lib="RPCI-98"
                     /note="end : T7"
ORIGIN

  Query Match             3.8%;  Score 43.2;  DB 29;  Length 910;
  Best Local Similarity   19.2%;  Pred. No. 35;
  Matches   81;  Conservative  159;  Mismatches  180;  Indels    2;  Gaps    1;

Qy        330 GAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG 389
              | ||: |  : ||| ||| :|||||  | | |:|: |  : ||    |:  :::: |
Db        468 GGGGKGGGGKGGGGGGGGGHGGGGGSGGGTDTKTWTGGKSTGGGGGGGSSGGSSSKGGGC 527

Qy        390 GGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCA 449
              |:  :  || |:      : ||| :::| :  :::::  :  : ::| : :    | |:
Db        528 GSGSYGGGGGGYGGTGSGSGGGGSSSSGCSSSSSSSSSSSSCGSSSBGCBSSCGCGSCSY 587

Qy        450 GTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTC 509
              : ::  :||:   | :: :   ::      | :::|:||    : ::: :| : : : :|
Db        588 SSSSTGSTGSCGCGSSSSSSSSSSCSSTSTSSSSTSGCGYSSSGSBSSSCSSTBTSSSTT 647

Qy        510 GTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAG 569
              :|:  : :|:: ::|:|  ||: |:|::: ::|::: : :: ::  : : ::: ::  :
Db        648 BTBTKBTSTYSTSYTST--TTSTTSTBSBTSYGSBBKSTSSTSSSTSSSTSSSSSSSTSS 705

Qy        570 GAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAA 629
                : : :::::||:   |: : ::|  |:: ::   : :    : : :| : :
Db        706 CTSTKBYSTSTBSYSBTTBTBTTSTSTBBTTSTBYTBBTTBYTKSTTSMTSTYTTBBSTS 765

Qy        630 GAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGA 689
              : :|  : :::  |  :| :| :  : :: : |:    |: :::::: :|: :   : :
Db        766 KBSTBTSTBKSTGTKTBTSBTTSCTSSSSSBSTSYSYSTSCBSSBSBSSTSYSBCTSTST 825

Qy        690 CAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTG 749
              : : :::::    :   ::| ::|:||    :| |: :||:::: |  :  ||  || |
Db        826 STSSBBSSBSSSSSCGTSBTSSSTSTTSTCTSTTCKTSTGBSSYGTGTSTYTTBTTTATT 885

Qy        750 CT 751
              :|
Db        886 ST 887


RESULT 13
BF593096/c
LOCUS       BF593096                509 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  7o56e02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578187 3'
            similar to TR:Q29305 Q29305 DISULFIDE ISOMERASE-RELATED PROTEIN ;,
            mRNA sequence.
ACCESSION   BF593096
VERSION     BF593096.1  GI:11685420
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 509)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 405.
FEATURES             Location/Qualifiers
     source          1. .509
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3578187"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Kid11"
                     /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
                     prepared, and ss circles were made in vitro. Following HAP
                     purification, this DNA was used as tracer in a subtractive
                     hybridization reaction. The driver was PCR-amplified cDNAs
                     from a pool of 5,000 clones made from the same library
                     (cloneIDs 1322376-1323911, 1456007-1456775, and
                     1500552-1502855). Subtraction by Bento Soares and M.
                     Fatima Bonaldo.  "
ORIGIN

  Query Match             3.7%;  Score 42.8;  DB 10;  Length 509;
  Best Local Similarity   54.4%;  Pred. No. 33;
  Matches   86;  Conservative    0;  Mismatches   72;  Indels    0;  Gaps    0;

Qy        931 AGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACG 990
              |||   |||||||  |||     | |     || |  || | |   ||   |   |||||
Db        425 AGAAATCTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGACC 366

Qy        991 GTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGT 1050
                |||  |     |||| || ||  |||| |    | | ||   | |  | | |||  |||
Db        365 AAGGAAGAGCTTTGAAGGCCTGAGGTCTGCGGAAGGTGGGAGGAGGCAGACGCCCTGCGT 306

Qy       1051 AGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1088
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Db        305 GGCCCATGGTCGGGGCGTCCACACCGAGGCCGGCAACA 268


RESULT 14
CA686322/c
LOCUS       CA686322                552 bp    mRNA    linear   EST 25-NOV-2002
DEFINITION  wlm96.pk032.g24 wlm96 Triticum aestivum cDNA clone wlm96.pk032.g24
            5' end, mRNA sequence.
ACCESSION   CA686322
VERSION     CA686322.1  GI:25275677
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 552)
  AUTHORS   Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
            Miao,G., Caraher,N. and Hanafey,M.K.
  TITLE     DuPont Wheat cDNA Sequence
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Scott V. Tingey
            Crop Genetics
            E. I. DuPont de Nemours and Company
            1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
            Tel: 302-631-2602
            Fax: 302-631-2607
            Email: Scott.V.Tingey@USA.dupont.com
            Seq primer: M13.
FEATURES             Location/Qualifiers
     source          1. .552
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /cultivar="Stephens"
                     /db_xref="taxon:4565"
                     /clone="wlm96.pk032.g24"
                     /tissue_type="leaf"
                     /clone_lib="wlm96"
                     /note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
                     XhoI; Wheat (Triticum aestivum L.) seedlings 96 hr after
                     inoculation w/ E. graminis"
ORIGIN

  Query Match             3.7%;  Score 42.8;  DB 14;  Length 552;
  Best Local Similarity   48.0%;  Pred. No. 35;
  Matches  119;  Conservative    0;  Mismatches  129;  Indels    0;  Gaps    0;

Qy        417 GGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAA 476
Db        347 GGGTAGAGGCGTACGCGATGACCGAGAGGCCCAGCGGGGCGGGCCTGTTCAGTGGCCGCA 288

Qy        477 GATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTT 536
Db        287 GGTGCAGTTGGTGCAGGTGCAGCTGGCGCCGCACTTGCACTTGCCGTCGTTCTCCGCGGC 228

Qy        537 CTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCA 596
Db        227 CTCCTGCACCTCGAAGTGNCTCTTNTCGGTGTCGACCATGACGATGCCGTAGCCGTCGCC 168

Qy        597 CCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGA 656
Db        167 CTTCTTCACGCACTGGGTCTTGTCGGCGCAGTCGCAGTTGCCGCACTTGTCAGCCATGGC 108

Qy        657 CGTGTTGG 664
Db        107 GGTCTTGG 100


RESULT 15
CA012935/c
LOCUS       CA012935                642 bp    mRNA    linear   EST 23-OCT-2002
DEFINITION  HT06O08r HT Hordeum vulgare subsp. vulgare cDNA clone HT06O08
            5-PRIME, mRNA sequence.
ACCESSION   CA012935
VERSION     CA012935.1  GI:24290279
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. vulgare
  ORGANISM  Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 642)
  AUTHORS   Zhang,H., Potokina,E., Michalek,W., Weschke,W., Stein,N. and
            Graner,A.
  TITLE     Barley ESTs from germinating seeds
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Stein Nils
            Molecular Markers Group, Department Genbank
            Institute of Plant Genetics and Crop Plant Research (IPK)
            Corrensstr. 3, 06466, Gatersleben, Germany
            Tel: 039482-5522
            Fax: 039482-5595
            Email: stein@ipk-gatersleben.de
            Insert Length: 642   Std Error: 0.00
            Plate: 6  row: O  column: 8
            Seq primer: M13rev.
FEATURES             Location/Qualifiers
     source          1. .642
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                     /mol_type="mRNA"
                     /cultivar="barke"
                     /sub_species="vulgare"
                     /db_xref="GABI:261458"
                     /db_xref="taxon:112509"
                     /clone="HT06008"
                     /tissue_type="endosperm early"
                     /dev_stage="0-16 hours after imbibition"
                     /lab_host="XL10-Gold"
                     /clone_lib="HT"
                     /note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of
                     cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning
                     artefact caused by the kit, in most cases the EcoRI site
                     is NOT present, as well as the EcoRIadapter used for
                     cloning. To excise the insert, restriction sites upstream
                     EcoRI should be used (e.g. BamHI, SalI,PstI). NOTE: Also
                     due to the cloning system used Blue/white selection for
                     recombinats is not 100% reliable."
ORIGIN

  Query Match             3.7%;  Score 42.6;  DB 13;  Length 642;
  Best Local Similarity   44.3%;  Pred. No. 41;
  Matches  174;  Conservative    0;  Mismatches  219;  Indels    0;  Gaps    0;

Qy        288 CGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGG 347
Db        567 CTTCGTCTTGAGCCACGGCTCAATGGACTTGTACTGCTGGTAGAAGTTGGTGAGGTCGAC 508

Qy        348 TCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACAT 407
Db        507 GACGAGGTCCTTCACCACGTACATGTGCGGCAGCGGCGTGATCATGGTCGCCGTCGACGT 448

Qy        408 GTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCA 467
Db        447 GTCGGTGTCGATGGACTTCAGGCACGCCACCGTGTTCACCCCGTCGATGTTCATGGAGCA 388

Qy        468 GTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTT 527
Db        387 GGACCCGCAGATGCCCTCCCGGCAAGACCGGCGGAACGCCAGCGTCGAGTCGTGCTCCGA 328

Qy        528 GTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTT 587
Db        327 CTTGATCTTCTGGAGCACGTCCAGCACCATTGGGCCGCACGTGCCGAGGTCGACGAAGTA 268

Qy        588 CGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGT 647
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Db        267 GGACTGCAGGAACGGCCGGCCATGCGCGTCCGGGTTCCACCGGTATATCTGGAACTCCTT 208

Qy        648 ACTCCGAGACGTGTTGGTGATGTGCGTCTTCTC 680
                |   |  |  |||  | || || |||||||
Db        207 CACCGTCGTGGGCTTGCCGCTGCGCTTCTTCTC 175

Search completed: May  7, 2004, 12:50:58
Job time : 2223.5 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:37 ; Search time 3069 Seconds
(without alignments)
16029.437 Million cell updates/sec

Title: US-10-679-999-13
Perfect score: 1135
Sequence: 1 CATATGGACAAAACTCACAC.....TCCGGGTTGTTAATGGATCC 1135

Scoring table: IDENTITY_NUC
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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 5401154

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1109.4	97.7	1135	6	BD056523	BD056523 OB fusion
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6	684.8	60.3	757	6	AX304247	AX304247 Sequence
7	684.8	60.3	763	6	AR437969	AR437969 Sequence
8	684.8	60.3	763	6	AX304251	AX304251 Sequence
9	684.8	60.3	794	6	AR437913	AR437913 Sequence
10	684.8	60.3	794	6	AX303197	AX303197 Sequence
11	684.8	60.3	812	6	AR437917	AR437917 Sequence
12	684.8	60.3	812	6	AX303207	AX303207 Sequence
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ALIGNMENTS

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BD056521
LOCUS BD056521 1135 bp DNA linear PAT 27-AUG-2002
DEFINITION OB fusion protein compositions and methods.
ACCESSION BD056521
VERSION BD056521.1 GI:22602127
KEYWORDS JP 2001512417-A/9.
SOURCE Aequorea victoria
ORGANISM Aequorea victoria
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
REFERENCE 1 (bases 1 to 1135)
AUTHORS Mann,M.B. and Hecht,R.I.
TITLE OB fusion protein compositions and methods
JOURNAL Patent: JP 2001512417-A 9 21-AUG-2001;

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            AMGEN INC
COMMENT     PN   JP 2001512417-A/9
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
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            FH   Key             Location/Qualifiers.
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RESULT 2
BD056523
LOCUS       BD056523                1135 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056523
VERSION     BD056523.1  GI:22602129
KEYWORDS    JP 2001512417-A/11.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1135)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 11 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/11
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
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ORIGIN

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RESULT 3
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LOCUS       AR437973                748 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1067 from patent US 6660843.
ACCESSION   AR437973
VERSION     AR437973.1  GI:40203312
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 748)
  AUTHORS   Feige,U. and Liu,C.-F.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: US 6660843-A 1067 09-DEC-2003;
FEATURES             Location/Qualifiers
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ORIGIN

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RESULT 4
AX304259

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LOCUS       AX304259                748 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 1067 from Patent WO0183525.
ACCESSION   AX304259
VERSION     AX304259.1  GI:17383760
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Feige,U., Liu,C.F., Cheetham,J.C., Boone,T.C. and Gudas,J.M.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: WO 0183525-A 1067 08-NOV-2001;
            Amgen Inc., (US)
FEATURES             Location/Qualifiers
     source          1. .748
                     /organism="synthetic construct"
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     CDS             4. .735
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                     /transl_table=11
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                     /db_xref="GI:17383761"
                     /db_xref="REMTREMBL:CAD13122"
                     /translation="MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                     VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
                     KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
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ORIGIN

  Query Match             60.3%;  Score 684.8;  DB 6;  Length 748;
  Best Local Similarity   99.7%;  Pred. No. 2.9e-133;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
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Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
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Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
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Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
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Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
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Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
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Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

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Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 5
AR437967
LOCUS       AR437967                757 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1055 from patent US 6660843.
ACCESSION   AR437967
VERSION     AR437967.1  GI:40203306
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 757)
  AUTHORS   Feige,U. and Liu,C.-F.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: US 6660843-A 1055 09-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .757
                     /organism="unknown"
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ORIGIN

  Query Match             60.3%;  Score 684.8;  DB 6;  Length 757;
  Best Local Similarity   99.7%;  Pred. No. 2.9e-133;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
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Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
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Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
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Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
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Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
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Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 6
AX304247
LOCUS       AX304247                757 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 1055 from Patent WO0183525.
ACCESSION   AX304247
VERSION     AX304247.1  GI:17383748
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Feige,U., Liu,C.F., Cheetham,J.C., Boone,T.C. and Gudas,J.M.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: WO 0183525-A 1055 08-NOV-2001;
            Amgen Inc., (US)
FEATURES             Location/Qualifiers
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                     QKSLSLSPGKGGGGGDFLPHYKNTSLGHRP"
ORIGIN

  Query Match           60.3%;  Score 684.8;  DB 6;  Length 757;
  Best Local Similarity  99.7%;  Pred. No. 2.9e-133;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
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Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
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Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
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Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
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Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
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Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

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Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

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RESULT 7
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LOCUS       AR437969                763 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1059 from patent US 6660843.
ACCESSION   AR437969
VERSION     AR437969.1  GI:40203308
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 763)
  AUTHORS   Feige,U. and Liu,C.-F.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: US 6660843-A 1059 09-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .763
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           60.3%;  Score 684.8;  DB 6;  Length 763;
  Best Local Similarity  99.7%;  Pred. No. 2.9e-133;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
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Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
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Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

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Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688

Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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RESULT 8
AX304251
LOCUS       AX304251                763 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 1059 from Patent WO0183525.
ACCESSION   AX304251
VERSION     AX304251.1  GI:17383752
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Feige,U., Liu,C.F., Cheetham,J.C., Boone,T.C. and Gudas,J.M.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: WO 0183525-A 1059 08-NOV-2001;
            Amgen Inc., (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             60.3%;  Score 684.8;  DB 6;  Length 763;
  Best Local Similarity   99.7%;  Pred. No. 2.9e-133;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60

Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
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Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

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Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

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Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688

Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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RESULT 9
AR437913
LOCUS       AR437913                794 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 5 from patent US 6660843.
ACCESSION   AR437913
VERSION     AR437913.1  GI:40203252
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 794)
  AUTHORS   Feige,U. and Liu,C.-F.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: US 6660843-A 5 09-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .794
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             60.3%;  Score 684.8;  DB 6;  Length 794;
  Best Local Similarity   99.7%;  Pred. No. 2.9e-133;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60

Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
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Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
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Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
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Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
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Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
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Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
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Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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RESULT 10
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LOCUS       AX303197                794 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 5 from Patent WO0183525.
ACCESSION   AX303197
VERSION     AX303197.1  GI:17383677
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Feige,U., Liu,C.F., Cheetham,J.C., Boone,T.C. and Gudas,J.M.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: WO 0183525-A 5 08-NOV-2001;
            Amgen Inc., (US)
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                     KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
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ORIGIN

  Query Match           60.3%;  Score 684.8;  DB 6;  Length 794;
  Best Local Similarity  99.7%;  Pred. No. 2.9e-133;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
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Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
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Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
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Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
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Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
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Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

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Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
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Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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RESULT 11
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LOCUS       AR437917                812 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 15 from patent US 6660843.
ACCESSION   AR437917
VERSION     AR437917.1  GI:40203256
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 812)
  AUTHORS   Feige,U. and Liu,C.-F.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: US 6660843-A 15 09-DEC-2003;
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
ORIGIN

  Query Match             60.3%;  Score 684.8;  DB 6;  Length 812;
  Best Local Similarity   99.7%;  Pred. No. 2.9e-133;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
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Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
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Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
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Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
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Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
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Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 12
AX303207
LOCUS       AX303207                812 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 15 from Patent WO0183525.
ACCESSION   AX303207
VERSION     AX303207.1  GI:17383685
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Feige,U., Liu,C.F., Cheetham,J.C., Boone,T.C. and Gudas,J.M.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: WO 0183525-A 15 08-NOV-2001;
            Amgen Inc., (US)

FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             60.3%;  Score 684.8;  DB 6;  Length 812;
  Best Local Similarity   99.7%;  Pred. No. 2.9e-133;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
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Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

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Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
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Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
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RESULT 13
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LOCUS       AX327583                859 bp    DNA     linear   PAT 07-JAN-2002
DEFINITION  Sequence 108 from Patent WO0181377.
ACCESSION   AX327583
VERSION     AX327583.1  GI:18097963
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Feige,U., Kohno,T., Lacey,D.L. and Boone,T.C.
  TITLE     Integrin/adhesion antagonists
  JOURNAL   Patent: WO 0181377-A 108 01-NOV-2001;
            Amgen, Inc. (US)
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ORIGIN

  Query Match             60.3%;  Score 684.8;  DB 6;  Length 859;
  Best Local Similarity   99.7%;  Pred. No. 2.8e-133;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
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Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
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Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
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Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

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Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 14
BD263009
LOCUS       BD263009                861 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and
            having thrombopoietic activity.
ACCESSION   BD263009
VERSION     BD263009.1  GI:33072777
KEYWORDS    JP 2002536960-A/11.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 861)
  AUTHORS   Liu,C.F., Feige,U. and Cheetham,J.
  TITLE     Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and
            having thrombopoietic activity
  JOURNAL   Patent: JP 2002536960-A 11 05-NOV-2002;
            AMGEN INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002536960-A/11
            PD   05-NOV-2002
            PF   22-OCT-1999 JP 2000578340
            PR   23-OCT-1998 US    60/105348
            PI   CHUAN FA LIU,ULRICH FEIGE,JANET CHEETHAM
            PC   C12N15/09,A61K38/00,A61P7/00,C07K14/52,C07K19/00,C12N1/15, PC
             C12N1/19,
            PC   C12N1/21,C12N5/10,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC
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                 Location/Qualifiers
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FEATURES             Location/Qualifiers
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  Best Local Similarity   99.7%;  Pred. No. 2.8e-133;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
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AR437914
LOCUS       AR437914                 861 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 7 from patent US 6660843.
ACCESSION   AR437914
VERSION     AR437914.1  GI:40203253
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 861)
  AUTHORS   Feige,U. and Liu,C.-F.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: US 6660843-A 7 09-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .861
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ORIGIN

  Query Match           60.3%;  Score 684.8;  DB 6;  Length 861;
  Best Local Similarity   99.7%;  Pred. No. 2.8e-133;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
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Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
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Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
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Job time : 3072 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:35 ; Search time 333.5 Seconds
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Perfect score: 1135
Sequence: 1 CATATGGACAAAACTCACAC.....TCCGGGTTGTTAATGGATCC 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 5802412

Minimum DB seq length: 0
Maximum DB seq length: 1135

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: geneseqn2001bs:*
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8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1135	100.0	1135	2	AAV32902	Aav32902 Recombina
2	1135	100.0	1135	2	AAV69686	Aav69686 Recombina
3	1109.4	97.7	1135	2	AAV32903	Aav32903 Recombina
4	684.8	60.3	748	6	ABL35776	Abl35776 Fc-MMP in
5	684.8	60.3	757	3	AAA69501	Aaa69501 Fc-TNF-al
6	684.8	60.3	757	6	ABL35770	Abl35770 Fc-TNF-al
7	684.8	60.3	763	3	AAA69503	Aaa69503 Fc-IL-1 a
8	684.8	60.3	794	3	AAA69444	Aaa69444 Fc-TMP nu
9	684.8	60.3	794	6	ABL35761	Abl35761 Fc-TPO mi
10	684.8	60.3	812	3	AAA69448	Aaa69448 Fc-EMP nu
11	684.8	60.3	812	6	ABL35765	Abl35765 Fc-EPO mi
12	684.8	60.3	859	6	ABK24109	Abk24109 DNA encod
13	684.8	60.3	861	3	AAA29229	Aaa29229 Human IgG
14	684.8	60.3	861	3	AAA69445	Aaa69445 Fc-TMP-TM
15	684.8	60.3	861	6	ABL35762	Abl35762 Fc-TMP-TM
16	683.2	60.2	748	3	AAA69507	Aaa69507 Fc-MMP in
17	683.2	60.2	763	6	ABL35772	Abl35772 Fc-interl
18	680.8	60.0	684	3	AAA29220	Aaa29220 Human IgG
19	680.8	60.0	684	3	AAA69443	Aaa69443 Human IgG
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22	680.8	60.0	684	6	ABK24097	Abk24097 Human cDN
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29	676.8	59.6	773	3	AAA69505	Aaa69505 Fc-VEGF a
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33	676	59.6	757	3	AAA69504	Aaa69504 IL-1 anta
34	676	59.6	757	6	ABL35773	Abl35773 Interleuk
35	676	59.6	761	3	AAA69502	Aaa69502 TNF-alpha
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37	676	59.6	763	3	AAA69508	Aaa69508 MMP inhib
38	676	59.6	763	6	ABL35777	Abl35777 MMP inhib
39	676	59.6	784	9	ADD31406	Add31406 Ang-2 rel
40	676	59.6	789	3	AAA69447	Aaa69447 TMP-Fc nu
41	676	59.6	789	6	ABL35764	Abl35764 TMP-Fc nu
42	676	59.6	807	3	AAA69449	Aaa69449 EMP-Fc nu
43	676	59.6	807	6	ABL35766	Abl35766 EPO mimet
44	676	59.6	855	3	AAA69446	Aaa69446 TMP-TMP-F
45	676	59.6	855	6	ABL35763	Abl35763 TMP-TMP-F

ALIGNMENTS

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AAV32902
ID   AAV32902 standard; cDNA; 1135 BP.
XX
AC   AAV32902;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Recombinant human MetFc-OB variant 2 cDNA.
XX
KW   Recombinant human MetFc-OB variant 2 cDNA; chimeric; immunoglobulin;
KW   high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
KW   diabetes; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
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FT                   /note= "Encodes for the OB part of the fusion protein"
XX
PN   WO9828427-A1.
XX
PD   02-JUL-1998.
XX
PF   11-DEC-1997;   97WO-US023183.
XX
PR   20-DEC-1996;   96US-00770973.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Mann MB,  Hecht RI;
XX
DR   WPI; 1998-377658/32.
DR   P-PSDB; AAW49075.
XX
PT   New fusion proteins of OB and Fc - used for treating e.g. excess weight,
PT   diabetes, arterial sclerosis, arterial plaque, high blood lipid level,
PT   gall stones or stroke.
XX
```

```
PS   Disclosure; Fig 5A-5C; 107pp; English.
XX
CC   The present sequence represents a recombinant human MetFc-OB variant 2
CC   cDNA which encodes a recombinant human Fc-OB fusion variant 2 protein
CC   having a 5 residue deletion of residues 2-6 of the wild-type Fc-OB
CC   protein sequence shown in AAW49073. The invention provides Fc-OB fusion
CC   proteins whereby the Fc region of an immunoglobulin or its analogue is
CC   linked, either directly or indirectly using a linker, to the N-terminus
CC   of an OB protein or its analogue. The Fc-OB fusion proteins are claimed
CC   to demonstrate increased stability and clearance rate and decreased
CC   degradation as compared to OB protein or a fusion of Fc to the C-terminus
CC   of the OB protein. These Fc-OB fusion proteins are also claimed to be
CC   useful for treating excess weight in an individual or animal or for
CC   treating co-morbidities associated with excess fat such as diabetes, high
CC   blood lipid level, arterial sclerosis and stroke
XX
SQ   Sequence 1135 BP; 271 A; 361 C; 283 G; 220 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 1135;  DB 2;  Length 1135;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-248;
  Matches 1135;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
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Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

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Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
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Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
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Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
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Qy        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900
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Qy        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960
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Qy       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080
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Db       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080

Qy       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
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Db       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135


RESULT 2
AAV69686
ID   AAV69686 standard; DNA; 1135 BP.
XX
AC   AAV69686;
XX
DT   05-FEB-1999  (first entry)
XX
DE   Recombinant human metFc-OB protein variant encoding DNA.
XX
KW   Recombinant; metFc-OB protein; Fc region; immunoglobulin; Ig; OB;
KW   obesity; human; adiposity; blood lipid; diabetes type II; insulin;
KW   hypoglycaemic; antihypertensive; diuretic; appetite suppressant;
KW   suspension; variant; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             4. .1128
FT                   /*tag=  a
FT                   /product= "metFc-OB protein variant"
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PD   22-OCT-1998.
XX
PF   16-APR-1998;   98WO-US007828.
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PR   17-APR-1997;   97US-00843971.
PR   14-APR-1998;   98US-00059467.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Brems DN,  French DL,  Speed MA;
XX
DR   WPI; 1998-594525/50.
DR   P-PSDB; AAW83963.
XX
PT   Concentrated suspension of fusion of obesity protein with Fc
PT   immunoglobulin fragment - stable at physiological pH, used for e.g.
PT   reduction of weight and blood lipid levels, and for treatment of type II
PT   diabetes.
XX
PS   Disclosure; Fig 6A-C; 47pp; English.
XX
CC   This DNA encodes a recombinant metFc-OB protein variant which consists of
CC   an Fc region of human immunoglobulin (Ig) fused to a human OB (obesity)
```

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CC   protein. The invention provides a human OB protein suspension that
CC   contains at least 0.5 mg/ml of the human OB protein derivatised by
CC   attachment of the Fc region of an Ig to the N-terminus of OB, and has a
CC   pH 6-8. The suspensions are used to reduce weight, adiposity and blood
CC   lipid levels, to treat or prevent diabetes type II, and to increase lean
CC   mass and insulin sensitivity. They may be used in conjunction with
CC   insulin, hypoglycaemics, antihypertensives, diuretics, appetite
CC   suppressants etc. These suspensions are stable and active at
CC   physiological pH and are ready-for-use formulations that do not require
CC   freezing or freeze drying. As they are very concentrated, only small
CC   volumes are required and they provide a sustained-release effect, with
CC   increased potency and reduced frequency of injection
XX
SQ   Sequence 1135 BP; 271 A; 361 C; 283 G; 220 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1135;  DB 2;  Length 1135;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-248;
  Matches 1135;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720

Qy        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780

Qy        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840

Qy        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900

Qy        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960

Qy        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020

Qy       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080

Qy       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135


RESULT 3
AAV32903
ID   AAV32903 standard; cDNA; 1135 BP.
XX
AC   AAV32903;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Recombinant human MetFc-OB variant 3 cDNA.
XX
KW   Recombinant human MetFc-OB variant 3 cDNA; chimeric; immunoglobulin;
KW   high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
KW   diabetes; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             4. .1128
FT                   /*tag=  a
FT                   /product= "Recombinant human Fc-OB variant 3"
FT   mat_peptide     7. .1125
FT                   /*tag=  b
FT   misc_feature    685. .1125
FT                   /*tag=  c
FT                   /note= "Encodes for the OB part of the fusion protein"
XX
PN   WO9828427-A1.
XX
PD   02-JUL-1998.
XX
PF   11-DEC-1997;   97WO-US023183.
XX
PR   20-DEC-1996;   96US-00770973.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Mann MB,  Hecht RI;
XX
DR   WPI; 1998-377658/32.
DR   P-PSDB; AAW49076.
XX
PT   New fusion proteins of OB and Fc - used for treating e.g. excess weight,
PT   diabetes, arterial sclerosis, arterial plaque, high blood lipid level,
PT   gall stones or stroke.
XX
PS   Disclosure; Fig 6A-6C; 107pp; English.
XX
CC   The present sequence represents a recombinant human MetFc-OB variant 3
CC   cDNA which encodes a recombinant human Fc-OB fusion variant 3 protein
```

```
CC   having the L16E, E99A, K101A and K103A substitutions when compared with
CC   the template protein shown in AAW49075. The invention provides Fc-OB
CC   fusion proteins whereby the Fc region of an immunoglobulin or its
CC   analogue is linked, either directly or indirectly using a linker, to the
CC   N-terminus of an OB protein or its analogue. The Fc-OB fusion proteins
CC   are claimed to demonstrate increased stability and clearance rate and
CC   decreased degradation as compared to OB protein or a fusion of Fc to the
CC   C-terminus of the OB protein. These Fc-OB fusion proteins are also
CC   claimed to be useful for treating excess weight in an individual or
CC   animal or for treating co-morbidities associated with excess fat such as
CC   diabetes, high blood lipid level, arterial sclerosis and stroke
XX
SQ   Sequence 1135 BP; 270 A; 365 C; 283 G; 217 T; 0 U; 0 Other;

  Query Match           97.7%;  Score 1109.4;  DB 2;  Length 1135;
  Best Local Similarity  98.6%;  Pred. No. 1.2e-242;
  Matches 1119;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              ||||||||||||||||||||| ||||| || ||||||||||||||   || |||||
Db          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720

Qy        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780

Qy        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840

Qy        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900

Qy        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960

Qy        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020

Qy       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080

Qy       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135


RESULT 4
ABL35776
ID   ABL35776 standard; DNA; 748 BP.
XX
AC   ABL35776;
XX
DT   05-APR-2002  (first entry)
XX
DE   Fc-MMP inhibitor fusion amino acid SEQ ID NO:1068.
XX
KW   Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW   erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW   TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW   TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW   MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW   cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW   antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW   neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW   cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW   sleep disorder; neurological degenerative disease; anaemia;
KW   thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW   Fanconi's syndrome; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200183525-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US014310.
XX
PR   03-MAY-2000; 2000US-00563286.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C,  Cheetham JC,  Boone TC,  Gudas JM;
XX
DR   WPI; 2002-130313/17.
DR   P-PSDB; ABB73426.
XX
PT   Novel vehicle-peptide molecule or its multimers useful for treating
PT   inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT   diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS   Example 7; Fig 25A-B; 176pp; English.
XX
CC   The present invention describes a vehicle-peptide molecule (I) or its
CC   multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC   cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC   antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
```

CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 748 BP; 180 A; 240 C; 201 G; 127 T; 0 U; 0 Other;

Query Match 60.3%; Score 684.8; DB 6; Length 748;
Best Local Similarity 99.7%; Pred. No. 4.3e-146;
Matches 686; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

RESULT 5
AAA69501
ID AAA69501 standard; DNA; 757 BP.
XX
AC AAA69501;
XX
DT 31-OCT-2000 (first entry)
XX
DE Fc-TNF-alpha inhibitor fusion nucleotide sequence SEQ ID NO:1055.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical; ds.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
DR P-PSDB; AAB17951.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Example 4; Page 566-568; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 757 BP; 185 A; 244 C; 200 G; 128 T; 0 U; 0 Other;

Query Match 60.3%; Score 684.8; DB 3; Length 757;
Best Local Similarity 99.7%; Pred. No. 4.3e-146;
Matches 686; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy       121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy       181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy       241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy       301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy       361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy       421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy       481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy       541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy       601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy       661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
             |||||||||||||||||||||||||||
Db       661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

```
RESULT 6
ABL35770
ID   ABL35770 standard; DNA; 757 BP.
XX
AC   ABL35770;
XX
DT   05-APR-2002  (first entry)
XX
DE   Fc-TNF-alpha inhibitor fusion amino acid SEQ ID NO:1056.
XX
KW   Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW   erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW   TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW   TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW   MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW   cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW   antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW   neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW   cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW   sleep disorder; neurological degenerative disease; anaemia;
KW   thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW   Fanconi's syndrome; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200183525-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US014310.
XX
PR   03-MAY-2000; 2000US-00563286.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C,  Cheetham JC,  Boone TC,  Gudas JM;
XX
DR   WPI; 2002-130313/17.
DR   P-PSDB; ABB73420.
XX
PT   Novel vehicle-peptide molecule or its multimers useful for treating
PT   inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT   diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS   Example 4; Fig 19A-B; 176pp; English.
XX
CC   The present invention describes a vehicle-peptide molecule (I) or its
CC   multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC   cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC   antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC   neuroprotective activities. (I) can be used as a therapeutic or
CC   prophylactic agent as well as for screening purposes. (I) is useful for
CC   diagnosing diseases characterised by dysfunction of their associated
CC   protein of interest, for identifying normal or abnormal proteins of
CC   interest, as a part of diagnostic kit to detect the presence of their
CC   proteins of interest in a biological sample. Additionally, (I) is useful
CC   for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC   rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC   infertility, and neurological degenerative diseases. (I), comprising EPO-
CC   mimetic compounds are useful for treating disorders characterised by low
CC   red blood cell levels such as anaemia. The TPO-mimetic comprising
CC   compounds are useful for treating conditions that involve an existing
CC   megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC   deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC   tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC   and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC   represent amino acid and nucleic acid sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 757 BP; 185 A; 244 C; 200 G; 128 T; 0 U; 0 Other;

  Query Match            60.3%;  Score 684.8;  DB 6;  Length 757;
  Best Local Similarity  99.7%;  Pred. No. 4.3e-146;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db         1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy        61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy       121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy       181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy       241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy       301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy       361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
```

```
Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

RESULT 7
AAA69503
ID AAA69503 standard; DNA; 763 BP.
XX
AC AAA69503;
XX
DT 31-OCT-2000 (first entry)
XX
DE Fc-IL-1 antagonist fusion nucleotide sequence SEQ ID NO:1059.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical; ds.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
DR P-PSDB; AAB17953.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Example 5; Page 572-573; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 763 BP; 182 A; 243 C; 208 G; 130 T; 0 U; 0 Other;

```
  Query Match             60.3%;  Score 684.8;  DB 3;  Length 763;
  Best Local Similarity   99.7%;  Pred. No. 4.3e-146;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

RESULT 8
AAA69444
ID AAA69444 standard; DNA; 794 BP.
XX
AC AAA69444;
XX
DT 31-OCT-2000 (first entry)
XX
DE Fc-TMP nucleotide sequence SEQ ID NO:5.

```
XX
KW   Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW   autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW   immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW   inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW   cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW   vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW   thrombosis; pharmaceutical; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200024782-A2.
XX
PD   04-MAY-2000.
XX
PF   25-OCT-1999;   99WO-US025044.
XX
PR   23-OCT-1998;   98US-0105371P.
PR   22-OCT-1999;   99US-00428082.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C,  Cheetham J,  Boone TC;
XX
DR   WPI; 2000-350702/30.
DR   P-PSDB; AAB16958.
XX
PT   Novel composition of matter comprising an Fc domain and pharmacologically
PT   active peptides, useful for treating cancer and autoimmune diseases.
XX
PS   Example 2; Page 178-179; 608pp; English.
XX
CC   The present invention describes composition of matter (I) comprising an
CC   Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC   (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC   independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC   (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC   P3, and P4 = are each independently sequences of pharmacologically active
CC   peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC   c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC   of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC   thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC   cells from the present invention can be used for producing pharmaceutical
CC   compositions. The compositions are useful for treating cancer, asthma,
CC   thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC   a Fab domain) can provide a longer half-life or incorporate functions
CC   such as Fc receptor binding, protein A binding, complement fixation, and
CC   possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC   AAB18003 represent nucleotide and amino acid sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 794 BP; 195 A; 242 C; 213 G; 144 T; 0 U; 0 Other;

  Query Match             60.3%;  Score 684.8;  DB 3;  Length 794;
  Best Local Similarity   99.7%;  Pred. No. 4.4e-146;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 9
ABL35761
ID   ABL35761 standard; DNA; 794 BP.
XX
AC   ABL35761;
XX
DT   05-APR-2002  (first entry)
XX
DE   Fc-TPO mimetic peptide (Fc-TMP) nucleic acid SEQ ID NO:5.
XX
KW   Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW   erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW   TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW   TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW   MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW   cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW   antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW   neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW   cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW   sleep disorder; neurological degenerative disease; anaemia;
KW   thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW   Fanconi's syndrome; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200183525-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US014310.
XX
PR   03-MAY-2000; 2000US-00563286.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C,  Cheetham JC,  Boone TC,  Gudas JM;
XX
DR   WPI; 2002-130313/17.
```

```
DR   P-PSDB; ABB73411.
XX
PT   Novel vehicle-peptide molecule or its multimers useful for treating
PT   inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT   diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS   Example 2; Fig 7; 176pp; English.
XX
CC   The present invention describes a vehicle-peptide molecule (I) or its
CC   multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC   cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC   antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC   neuroprotective activities. (I) can be used as a therapeutic or
CC   prophylactic agent as well as for screening purposes. (I) is useful for
CC   diagnosing diseases characterised by dysfunction of their associated
CC   protein of interest, for identifying normal or abnormal proteins of
CC   interest, as a part of diagnostic kit to detect the presence of their
CC   proteins of interest in a biological sample. Additionally, (I) is useful
CC   for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC   rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC   infertility, and neurological degenerative diseases. (I), comprising EPO-
CC   mimetic compounds are useful for treating disorders characterised by low
CC   red blood cell levels such as anaemia. The TPO-mimetic comprising
CC   compounds are useful for treating conditions that involve an existing
CC   megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC   deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC   tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC   and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC   represent amino acid and nucleic acid sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 794 BP; 195 A; 242 C; 213 G; 144 T; 0 U; 0 Other;

  Query Match             60.3%;  Score 684.8;  DB 6;  Length 794;
  Best Local Similarity   99.7%;  Pred. No. 4.4e-146;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 10
AAA69448
ID   AAA69448 standard; DNA; 812 BP.
XX
AC   AAA69448;
XX
DT   31-OCT-2000  (first entry)
XX
DE   Fc-EMP nucleotide sequence SEQ ID NO:15.
XX
KW   Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW   autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW   immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW   inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW   cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW   vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW   thrombosis; pharmaceutical; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200024782-A2.
XX
PD   04-MAY-2000.
XX
PF   25-OCT-1999;   99WO-US025044.
XX
PR   23-OCT-1998;   98US-0105371P.
PR   22-OCT-1999;   99US-00428082.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C,  Cheetham J,  Boone TC;
XX
DR   WPI; 2000-350702/30.
DR   P-PSDB; AAB16964.
XX
PT   Novel composition of matter comprising an Fc domain and pharmacologically
PT   active peptides, useful for treating cancer and autoimmune diseases.
XX
PS   Example 3; Page 190-191; 608pp; English.
XX
CC   The present invention describes composition of matter (I) comprising an
CC   Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC   (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC   independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC   (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC   P3, and P4 = are each independently sequences of pharmacologically active
CC   peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC   c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC   of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC   thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC   cells from the present invention can be used for producing pharmaceutical
CC   compositions. The compositions are useful for treating cancer, asthma,
CC   thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC   a Fab domain) can provide a longer half-life or incorporate functions
CC   such as Fc receptor binding, protein A binding, complement fixation, and
CC   possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC   AAB18003 represent nucleotide and amino acid sequences used in the
CC   exemplification of the present invention
```

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XX
SQ   Sequence 812 BP; 198 A; 246 C; 218 G; 150 T; 0 U; 0 Other;

  Query Match            60.3%;  Score 684.8;  DB 3;  Length 812;
  Best Local Similarity  99.7%;  Pred. No. 4.4e-146;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 11
ABL35765
ID   ABL35765 standard; DNA; 812 BP.
XX
AC   ABL35765;
XX
DT   05-APR-2002  (first entry)
XX
DE   Fc-EPO mimetic peptide (Fc-EMP) nucleic acid SEQ ID NO:15.
XX
KW   Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW   erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW   TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW   TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW   MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW   cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW   antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW   neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW   cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW   sleep disorder; neurological degenerative disease; anaemia;
KW   thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW   Fanconi's syndrome; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200183525-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US014310.
XX
PR   03-MAY-2000; 2000US-00563286.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX
DR   WPI; 2002-130313/17.
DR   P-PSDB; ABB73415.
XX
PT   Novel vehicle-peptide molecule or its multimers useful for treating
PT   inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT   diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS   Example 3; Fig 13; 176pp; English.
XX
CC   The present invention describes a vehicle-peptide molecule (I) or its
CC   multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC   cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC   antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC   neuroprotective activities. (I) can be used as a therapeutic or
CC   prophylactic agent as well as for screening purposes. (I) is useful for
CC   diagnosing diseases characterised by dysfunction of their associated
CC   protein of interest, for identifying normal or abnormal proteins of
CC   interest, as a part of diagnostic kit to detect the presence of their
CC   proteins of interest in a biological sample. Additionally, (I) is useful
CC   for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC   rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC   infertility, and neurological degenerative diseases. (I), comprising EPO-
CC   mimetic compounds are useful for treating disorders characterised by low
CC   red blood cell levels such as anaemia. The TPO-mimetic comprising
CC   compounds are useful for treating conditions that involve an existing
CC   megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC   deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC   tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC   and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC   represent amino acid and nucleic acid sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 812 BP; 198 A; 246 C; 218 G; 150 T; 0 U; 0 Other;

  Query Match            60.3%;  Score 684.8;  DB 6;  Length 812;
  Best Local Similarity  99.7%;  Pred. No. 4.4e-146;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
```

RESULT 12
ABK24109
ID ABK24109 standard; DNA; 859 BP.
XX
AC ABK24109;
XX
DT 29-AUG-2003 (revised)
DT 09-APR-2002 (first entry)
XX
DE DNA encoding Echistatin/IgG Fc fusion protein.
XX
KW IgG Fc; ds; anticoagulant; thrombolytic; cytostatic; antiinflammatory;
KW immunosuppressive; osteopathic; antagonist; laminin; saw-scaled viper;
KW echistatin; integrin; selectin; vinculin; platelet aggregation;
KW angiogenesis; tumour; inflammation; autoimmune disease;
KW rheumatoid arthritis; osteoporosis.
XX
OS Echis carinatus.
OS Homo sapiens.
OS Chimeric.
XX
PN WO200181377-A2.
XX
PD 01-NOV-2001.
XX
PF 23-APR-2001; 2001WO-US013069.
XX
PR 21-APR-2000; 2000US-0198919P.
PR 03-MAY-2000; 2000US-0201394P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Kohno T, Lacey DL, Boone TC;
XX
DR WPI; 2002-062025/08.
DR P-PSDB; AAU81169.
XX
PT Composition comprising integrin or adhesion antagonistic peptide and
PT vehicle, useful for treating or preventing platelet aggregation, has a
PT longer half-life than free peptide.
XX
PS Example 1; Page 45-46; 68pp; English.
XX
CC The invention relates to a composition comprising an integrin/adhesion
CC antagonistic peptide (I) and a vehicle e.g. IgG Fc. The peptides are
CC based on laminin or saw-scaled viper echistatin and target integrin,
CC selectin or vinculin.Also included are compounds of formula (Ia) and
CC their multimers (X^1)_a-F^1-(X^2)_b where; F^1 = Fc domain; X^1 and X^2 =
CC -(L^1)_c-P^1, (L^1)_c-P^1-(L^2)_d-P^2, (L^1)_c-P^1-(L^2)_d-P^2-(L^3)_e-
CC P^3 or (L^1)_c-P^1-(L^2)_d-P^2-(L^3)_e-P^3-(L^4)_f-P^4; P^1-P^4 = same or
CC different (I); L^1-L^4 = same or different linkers; a-f = 0 or 1,
CC provided at least one of a and b = 1, a nucleic acid that encodes (Ia),
CC an expression vector containing the nucleic acid, host cells containing
CC the vector, producing a pharmaceutically active compound (B) by
CC covalently linking at least one Fc domain to at least one amino acid
CC sequence of a selected randomized (I) and any of six laminin-related
CC peptides (Ib). The compositions are used prophylactically and
CC therapeutically in the same way as (I), e.g. to inhibit platelet
CC aggregation or angiogenesis (tumours), or to treat inflammation and
CC autoimmune diseases (e.g. rheumatoid arthritis) and many different forms
CC of osteoporosis, also for diagnosis. Attaching the vehicle (especially Fc
CC domain) to (I) increases the half-life (free (I) are normally degraded
CC very quickly in vivo). The present sequence encodes all or part of an
CC antagonist peptide-IgG Fc fusion compound of the invention. (Updated on
CC 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 859 BP; 220 A; 258 C; 232 G; 149 T; 0 U; 0 Other;

```
  Query Match            60.3%;  Score 684.8;  DB 6;  Length 859;
  Best Local Similarity  99.7%;  Pred. No. 4.4e-146;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              ||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

RESULT 13
AAA29229
ID AAA29229 standard; DNA; 861 BP.
XX
AC AAA29229;
XX
DT 04-SEP-2000 (first entry)
XX
DE Human IgG1 Fc TMP fusion coding sequence.
XX
KW Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet;
KW megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV;
KW anti-anaemic; dermatological; immunosuppressive; anti-inflammatory; ds.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   39. .848
FT   /*tag= a
XX
PN WO200024770-A2.
XX
PD 04-MAY-2000.
XX
PF 22-OCT-1999; 99WO-US024834.
XX
PR 23-OCT-1998; 98US-0105348P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Liu C, Feige U, Cheetham J;
XX
DR WPI; 2000-365108/31.
DR P-PSDB; AAY96531.
XX
PT Thrombopoietic peptides which activate mpl receptors and increase the
PT production of platelets or platelet precursors, useful for treatment of
PT diseases which involve thombocytopenia.
XX
PS Example 2A; Page 49-50; 91pp; English.
XX
CC A compound which binds to an mpl receptor comprising a thrombopoietin
CC mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is
CC new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to
CC 14 residues in length comprising X_2-X_1_0, X_2-X_1_1, X_2-X_1_2, X_2-
CC X_1_3, X_2-X_1_4, X_1-X_1_0, X_1-X_1_1, X_1-X_1_2, X_1-X_1_3, and X_1-
CC X_1_4. X_1 = I, A, V, L, S or R; X_2 = E, D, K or V; X_3 = G or A; X_4 =
CC P; X_5 = T or S; X_6 = L, I, V, A or F; X_7 = R or K; X_8 = Q, N, or E;
CC X_9 = W, Y or F; X_1_0 = L, I, V, A, F, M, or K; X_1_1 = A, I, V, L, F,
CC S, T, K, H, or E; X_1_2 = A, I, V, L, F, G, S, or Q; X_1_3 = R, K, T, V,
CC N, Q or G; X_1_4 = A, I, V, L, F, T, R, E, or G; L_1 = linker comprising
CC 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and activate
CC the c-Mpl receptor which mediates the activity of endogenous
CC thrombopoietin. The TMPs are useful for increasing the production of
CC platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which
CC is useful for treatment of diseases which involve thombocytopenia, e.g.
CC aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency
CC virus associated ITP, and systemic lupus erythematosus
XX
SQ Sequence 861 BP; 206 A; 259 C; 241 G; 155 T; 0 U; 0 Other;

  Query Match   60.3%; Score 684.8; DB 3; Length 861;
  Best Local Similarity 99.7%; Pred. No. 4.4e-146;

  Matches 686; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

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Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              ||||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
```

RESULT 14
AAA69445
ID AAA69445 standard; DNA; 861 BP.
XX
AC AAA69445;
XX
DT 31-OCT-2000 (first entry)
XX
DE Fc-TMP-TMP nucleotide sequence SEQ ID NO:7.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200024782-A2.

XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
DR P-PSDB; AAB16959.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Example 2; Page 180-182; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 861 BP; 206 A; 259 C; 241 G; 155 T; 0 U; 0 Other;

Query Match 60.3%; Score 684.8; DB 3; Length 861;
Best Local Similarity 99.7%; Pred. No. 4.4e-146;
Matches 686; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
```

RESULT 15
ABL35762
ID ABL35762 standard; DNA; 861 BP.
XX
AC ABL35762;
XX
DT 05-APR-2002 (first entry)
XX
DE Fc-TMP-TMP nucleic acid SEQ ID NO:7.
XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome; gene; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200183525-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014310.
XX
PR 03-MAY-2000; 2000US-00563286.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX
DR WPI; 2002-130313/17.
DR P-PSDB; ABB73412.
XX
PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS Example 2; Fig 8; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or

CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 861 BP; 206 A; 259 C; 241 G; 155 T; 0 U; 0 Other;

Query Match 60.3%; Score 684.8; DB 6; Length 861;
Best Local Similarity 99.7%; Pred. No. 4.4e-146;
Matches 686; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
```

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Job time : 338.5 secs

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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:36 ; Search time 59.25 Seconds
(without alignments)
10630.705 Million cell updates/sec

Title: US-10-679-999-13
Perfect score: 1135
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1245136

Minimum DB seq length: 0
Maximum DB seq length: 1135

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	684.8	60.3	748	4	US-09-428-082B-1067	Sequence 1067, Ap
2	684.8	60.3	757	4	US-09-428-082B-1055	Sequence 1055, Ap
3	684.8	60.3	763	4	US-09-428-082B-1059	Sequence 1059, Ap
4	684.8	60.3	794	4	US-09-428-082B-5	Sequence 5, Appli
5	684.8	60.3	812	4	US-09-428-082B-15	Sequence 15, Appl
6	684.8	60.3	861	4	US-09-428-082B-7	Sequence 7, Appli
7	680.8	60.0	684	4	US-09-428-082B-1	Sequence 1, Appli
8	680.8	60.0	684	4	US-09-847-249A-1	Sequence 1, Appli
9	676.8	59.6	773	4	US-09-428-082B-1063	Sequence 1063, Ap
10	676.8	59.6	885	4	US-09-428-082B-21	Sequence 21, Appl
11	676	59.6	757	4	US-09-428-082B-1061	Sequence 1061, Ap
12	676	59.6	761	4	US-09-428-082B-1057	Sequence 1057, Ap
13	676	59.6	763	4	US-09-428-082B-1069	Sequence 1069, Ap
14	676	59.6	789	4	US-09-428-082B-11	Sequence 11, Appl
15	676	59.6	807	4	US-09-428-082B-17	Sequence 17, Appl
16	676	59.6	855	4	US-09-428-082B-9	Sequence 9, Appli
17	676	59.6	881	4	US-09-428-082B-19	Sequence 19, Appl
18	670.6	59.1	773	4	US-09-428-082B-1065	Sequence 1065, Ap
19	670	59.0	1050	1	US-07-940-861-42	Sequence 42, Appl
20	670	59.0	1050	1	US-08-459-512-42	Sequence 42, Appl
21	670	59.0	1050	2	US-08-459-657-42	Sequence 42, Appl
22	670	59.0	1050	2	US-08-460-132-42	Sequence 42, Appl
23	670	59.0	1050	3	US-08-466-465-7	Sequence 7, Appli
24	670	59.0	1050	5	PCT-US92-02050-42	Sequence 42, Appl
25	669.8	59.0	705	4	US-09-023-655-1223	Sequence 1223, Ap
26	669.8	59.0	1019	3	US-09-178-869-1	Sequence 1, Appli
27	669.8	59.0	1019	4	US-09-761-413-1	Sequence 1, Appli
28	669.8	59.0	1080	4	US-09-180-100-14	Sequence 14, Appl
29	668.6	58.9	706	4	US-09-122-144-1	Sequence 1, Appli
30	668.2	58.9	693	1	US-08-322-805-3	Sequence 3, Appli
31	668.2	58.9	693	2	US-08-429-499-3	Sequence 3, Appli
32	668.2	58.9	693	3	US-09-152-733-3	Sequence 3, Appli
33	668.2	58.9	699	2	US-08-595-043A-49	Sequence 49, Appl
34	666.6	58.7	1135	1	US-08-236-311-8	Sequence 8, Appli
35	666.6	58.7	1135	3	US-08-457-918-8	Sequence 8, Appli
36	665.2	58.6	768	2	US-08-284-391B-32	Sequence 32, Appl
37	665.2	58.6	768	3	US-09-218-950-32	Sequence 32, Appl
38	665	58.6	990	4	US-09-301-593-21	Sequence 21, Appl
39	661.8	58.3	705	3	US-09-131-247-5	Sequence 5, Appli
40	660.8	58.2	705	1	US-07-797-556-3	Sequence 3, Appli
41	660.8	58.2	705	1	US-08-308-881-3	Sequence 3, Appli
42	660.8	58.2	705	2	US-09-058-263-3	Sequence 3, Appli
43	660.8	58.2	705	2	US-09-059-099-3	Sequence 3, Appli
44	660.8	58.2	705	3	US-09-058-264-3	Sequence 3, Appli
45	660.8	58.2	705	4	US-09-455-962-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-428-082B-1067
; Sequence 1067, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1067
; LENGTH: 748
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc MMP INHIBITOR
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(732)
; OTHER INFORMATION:
US-09-428-082B-1067

Query Match 60.3%; Score 684.8; DB 4; Length 748;
Best Local Similarity 99.7%; Pred. No. 6.3e-168;
Matches 686; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
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Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
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Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
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Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
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Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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RESULT 2
US-09-428-082B-1055
; Sequence 1055, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1055
; LENGTH: 757
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-TNF-ALPA INHIBITORS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(747)
; OTHER INFORMATION:
US-09-428-082B-1055

Query Match 60.3%; Score 684.8; DB 4; Length 757;
Best Local Similarity 99.7%; Pred. No. 6.3e-168;
Matches 686; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
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Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
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Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
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Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
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Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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RESULT 3
US-09-428-082B-1059
; Sequence 1059, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1059
; LENGTH: 763
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-IL-1 ANTAGONIST
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(747)
; OTHER INFORMATION:
US-09-428-082B-1059

Query Match 60.3%; Score 684.8; DB 4; Length 763;
Best Local Similarity 99.7%; Pred. No. 6.4e-168;
Matches 686; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
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Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
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Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
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Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

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Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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RESULT 4
US-09-428-082B-5
; Sequence 5, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 794
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc-TMP

; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(779)
; OTHER INFORMATION:
US-09-428-082B-5

Query Match 60.3%; Score 684.8; DB 4; Length 794;
Best Local Similarity 99.7%; Pred. No. 6.4e-168;
Matches 686; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
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Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
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Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
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Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
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RESULT 5
US-09-428-082B-15
; Sequence 15, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371

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;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 812
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc-EMP
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (39)..(797)
;   OTHER INFORMATION:
US-09-428-082B-15

  Query Match             60.3%;  Score 684.8;  DB 4;  Length 812;
  Best Local Similarity   99.7%;  Pred. No. 6.5e-168;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
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Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
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Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              ||||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 6
US-09-428-082B-7
; Sequence 7, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/09/428,082B
;  CURRENT FILING DATE:  1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 861
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc-TMP-TMP
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (39)..(842)
;   OTHER INFORMATION:
US-09-428-082B-7

  Query Match             60.3%;  Score 684.8;  DB 4;  Length 861;
  Best Local Similarity   99.7%;  Pred. No. 6.6e-168;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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                    ||||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 7
US-09-428-082B-1
; Sequence 1, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/09/428,082B
;  CURRENT FILING DATE:  1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 684
;   TYPE: DNA
;   ORGANISM: HUMAN
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(684)
;   OTHER INFORMATION:
US-09-428-082B-1

  Query Match             60.0%;  Score 680.8;  DB 4;  Length 684;
  Best Local Similarity   99.7%;  Pred. No. 6.6e-167;
  Matches  682;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCA 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| || |||
Db          1 ATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCA 60

Qy         64 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 120

Qy        124 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG 180

Qy        184 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG 240

Qy        244 TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC 300

Qy        304 AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC 360

Qy        364 AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC 420

Qy        424 AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG 480

Qy        484 GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC 540

Qy        544 TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG 600

Qy        604 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG 660

Qy        664 AGCCTCTCCCTGTCTCCGGGTAAA 687
              |||||||||||||||||||||||||
Db        661 AGCCTCTCCCTGTCTCCGGGTAAA 684


RESULT 8
US-09-847-249A-1
; Sequence 1, Application US/09847249A
; Patent No. 6677136
; GENERAL INFORMATION:
;  APPLICANT: MARSHALL, WILLIAM S.
;  APPLICANT:  STARK, KEVIN LEE
;  TITLE OF INVENTION: GLUCAGON ANTAGONIST
;  FILE REFERENCE: A-693
;  CURRENT APPLICATION NUMBER: US/09/847,249A
;  CURRENT FILING DATE:  2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,436
;  PRIOR FILING DATE: 2000-05-03
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 684
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(684)
;   OTHER INFORMATION:
US-09-847-249A-1

  Query Match             60.0%;  Score 680.8;  DB 4;  Length 684;
  Best Local Similarity   99.7%;  Pred. No. 6.6e-167;
  Matches  682;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCA 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| || |||
Db          1 ATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCA 60

Qy         64 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 120

Qy        124 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG 180

Qy        184 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG 240

Qy        244 TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC 300

Qy        304 AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC 360

Qy        364 AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC 420

Qy        424 AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG 480

Qy        484 GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC 543
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC 540

Qy         544 TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG 603
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG 600

Qy         604 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG 663
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG 660

Qy         664 AGCCTCTCCCTGTCTCCGGGTAAA 687
               |||||||||||||||||||||||||
Db         661 AGCCTCTCCCTGTCTCCGGGTAAA 684


RESULT 9
US-09-428-082B-1063
; Sequence 1063, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/09/428,082B
;  CURRENT FILING DATE:  1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1063
;   LENGTH: 773
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc-VEGF ANTAGONIST
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(759)
;   OTHER INFORMATION:
US-09-428-082B-1063

  Query Match             59.6%;  Score 676.8;  DB 4;  Length 773;
  Best Local Similarity   99.0%;  Pred. No. 7.5e-166;
  Matches  681;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy           1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
               |||||||||||||||||||||||||||| || ||||| || ||||||||||||||| ||
Db           1 CATATGGACAAAACTCACACATGTCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCG 60

Qy          61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
               ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 TCAGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy         121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy         181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy         241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy         301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy         361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy         421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy         481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy         541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy         601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy         661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
               |||||||||||||||||||||||||||||
Db         661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 10
US-09-428-082B-21
; Sequence 21, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/09/428,082B
;  CURRENT FILING DATE:  1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
;   LENGTH: 885
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc-EMP-EMP
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (39)..(869)
;   OTHER INFORMATION:
US-09-428-082B-21

  Query Match             59.6%;  Score 676.8;  DB 4;  Length 885;
  Best Local Similarity   99.0%;  Pred. No. 7.9e-166;
  Matches  681;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy           1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
               |||||||||||||||||||||||||||| ||||| || ||||||||||||||| ||
Db          36 CATATGGACAAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCG 95

Qy          61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
               ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          96 TCAGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy         121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy         181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275
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Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCTCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              ||||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
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RESULT 11
US-09-428-082B-1061
; Sequence 1061, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1061
; LENGTH: 757
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST-FC
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(747)
; OTHER INFORMATION:
US-09-428-082B-1061

Query Match 59.6%; Score 676; DB 4; Length 757;
Best Local Similarity 98.6%; Pred. No. 1.2e-165;
Matches 682; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy          6 GGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGT 65
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Db         66 GGACAAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGT 125

Qy         66 CTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCAC 125
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Db        126 TTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCAC 185

Qy        126 ATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGA 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 ATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGA 245

Qy        186 CGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA 305

Qy        246 CCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAA 305
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Db        306 CCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAA 365

Qy        306 GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAA 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAA 425

Qy        366 AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAA 425
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Db        426 AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAA 485

Qy        426 GAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGA 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 GAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGA 545

Qy        486 GTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTC 545
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Db        546 GTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTC 605

Qy        546 CGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG 605
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG 665

Qy        606 GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAG 665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAG 725

Qy        666 CCTCTCCCTGTCTCCGGGTAAAGTACCGATCC 697
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Db        726 CCTCTCCCTGTCTCCGGGTAAATAATGGATCC 757
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RESULT 12
US-09-428-082B-1057
; Sequence 1057, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1057
; LENGTH: 761
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TNF-ALPHA INHIBITOR-Fc
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(747)
; OTHER INFORMATION:
US-09-428-082B-1057

Query Match 59.6%; Score 676; DB 4; Length 761;

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  Best Local Similarity   98.6%;  Pred. No. 1.2e-165;
  Matches  682;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          6 GGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGT 65
              ||||||||||||||||||||||||||||| ||||| || |||||||||||||| || |||||
Db         66 GGACAAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGT 125

Qy         66 CTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCAC 125
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Db        126 TTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCAC 185

Qy        126 ATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGA 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 ATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGA 245

Qy        186 CGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA 245
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Db        246 CGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA 305

Qy        246 CCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAA 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 CCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAA 365

Qy        306 GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAA 365
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Db        366 GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAA 425

Qy        366 AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAA 425
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Db        426 AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAA 485

Qy        426 GAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGA 485
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Db        486 GAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGA 545

Qy        486 GTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTC 545
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 GTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTC 605

Qy        546 CGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG 605
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Db        606 CGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG 665

Qy        606 GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAG 665
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Db        666 GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAG 725

Qy        666 CCTCTCCCTGTCTCCGGGTAAAGTACCGATCC 697
              |||||||||||||||||||  |  |||||
Db        726 CCTCTCCCTGTCTCCGGGTAAATAATGGATCC 757


RESULT 13
US-09-428-082B-1069
; Sequence 1069, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/09/428,082B
;  CURRENT FILING DATE:  1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1069
;   LENGTH: 763
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: MMP INHIBITOR-Fc
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(753)
;   OTHER INFORMATION:
US-09-428-082B-1069

  Query Match             59.6%;  Score 676;  DB 4;  Length 763;
  Best Local Similarity   98.6%;  Pred. No. 1.2e-165;
  Matches  682;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          6 GGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGT 65
              ||||||||||||||||||||||||||||| ||||| || |||||||||||||| || |||||
Db         72 GGACAAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGT 131

Qy         66 CTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCAC 125
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Db        132 TTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCAC 191

Qy        126 ATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGA 185
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Db        192 ATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGA 251

Qy        186 CGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA 245
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Db        252 CGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA 311

Qy        246 CCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAA 305
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Db        312 CCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAA 371

Qy        306 GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAA 365
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Db        372 GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAA 431

Qy        366 AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAA 425
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Db        432 AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAA 491

Qy        426 GAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGA 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        492 GAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGA 551

Qy        486 GTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTC 545
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Db        552 GTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTC 611

Qy        546 CGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG 605
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Qy        606 GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAG 665
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Db        672 GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAG 731

Qy        666 CCTCTCCCTGTCTCCGGGTAAAGTACCGATCC 697
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Db        732 CCTCTCCCTGTCTCCGGGTAAATAATGGATCC 763


RESULT 14
US-09-428-082B-11
; Sequence 11, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/09/428,082B
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;  CURRENT FILING DATE:  1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 789
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: TMP-Fc
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (39)..(779)
;   OTHER INFORMATION:
US-09-428-082B-11

  Query Match           59.6%;  Score 676;  DB 4;  Length 789;
  Best Local Similarity  98.6%;  Pred. No. 1.2e-165;
  Matches  682;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          6 GGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGT 65
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Db         98 GGACAAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGT 157

Qy         66 CTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCAC 125
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Db        158 TTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCAC 217

Qy        126 ATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGA 185
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Db        218 ATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGA 277

Qy        186 CGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA 245
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Db        278 CGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA 337

Qy        246 CCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAA 305
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Db        338 CCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAA 397

Qy        306 GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAA 365
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Qy        426 GAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGA 485
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Db        518 GAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGA 577

Qy        486 GTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTC 545
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Db        578 GTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTC 637

Qy        546 CGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG 605
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Db        638 CGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG 697

Qy        606 GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAG 665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        698 GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAG 757

Qy        666 CCTCTCCCTGTCTCCGGGTAAAGTACCGATCC 697
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Db        758 CCTCTCCCTGTCTCCGGGTAAATAATGGATCC 789


RESULT 15
US-09-428-082B-17
; Sequence 17, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/09/428,082B
;  CURRENT FILING DATE:  1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 807
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: EMP-Fc
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (39)..(797)
;   OTHER INFORMATION:
US-09-428-082B-17

  Query Match           59.6%;  Score 676;  DB 4;  Length 807;
  Best Local Similarity  98.6%;  Pred. No. 1.2e-165;
  Matches  682;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          6 GGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGT 65
              ||||||||||||||||||||||||||||| ||||| || ||||||||||||||| || |||||
Db        116 GGACAAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGT 175

Qy         66 CTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCAC 125
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Db        176 TTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCAC 235

Qy        126 ATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGA 185
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Db        236 ATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGA 295

Qy        186 CGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA 245
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Db        296 CGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA 355

Qy        246 CCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAA 305
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Db        356 CCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAA 415

Qy        306 GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAA 365
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Db        416 GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAA 475

Qy        366 AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAA 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAA 535

Qy        426 GAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGA 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 GAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGA 595

Qy        486 GTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTC 545
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 GTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTC 655

Qy        546 CGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG 605
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 CGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG 715

Qy        606 GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAG 665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAG 775
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Qy        666 CCTCTCCCTGTCTCCGGGTAAAGTACCGATCC 697
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Db        776 CCTCTCCCTGTCTCCGGGTAAATAATGGATCC 807
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Search completed: May 9, 2004, 22:17:13
Job time : 63.25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 10, 2004, 16:13:07 ; Search time 473.75 Seconds
(without alignments)
10852.855 Million cell updates/sec

Title: US-10-679-999-13
Perfect score: 1135
Sequence: 1 CATATGGACAAAACTCACAC.....TCCGGGTTGTTAATGGATCC 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 4861726

Minimum DB seq length: 0
Maximum DB seq length: 1135

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1135	100.0	1135	13	US-10-679-999-13	Sequence 13, Appl
2	1109.4	97.7	1135	13	US-10-679-999-16	Sequence 16, Appl
3	684.8	60.3	748	12	US-10-645-761-1067	Sequence 1067, Ap
4	684.8	60.3	748	13	US-10-609-217-1067	Sequence 1067, Ap
5	684.8	60.3	748	13	US-10-632-388-1067	Sequence 1067, Ap
6	684.8	60.3	748	13	US-10-651-723-1067	Sequence 1067, Ap
7	684.8	60.3	748	17	US-10-666-696-1067	Sequence 1067, Ap
8	684.8	60.3	757	12	US-10-645-761-1055	Sequence 1055, Ap
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28	684.8	60.3	837	15	US-10-269-806-151	Sequence 151, App
29	684.8	60.3	859	9	US-09-840-277-108	Sequence 108, App
30	684.8	60.3	861	12	US-10-645-761-7	Sequence 7, Appli
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ALIGNMENTS

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RESULT 1
US-10-679-999-13
; Sequence 13, Application US/10679999
; Publication No. US20040067520A1
;  GENERAL INFORMATION:
;       APPLICANT: Mann, Michael B.
;                  Hecht, Randy I.
;       TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                           METHODS
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Amgen Inc.
;            STREET: 1840 DeHavilland Drive
;            CITY: Thousand Oaks
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 91320-1789
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/679,999
;            FILING DATE: 06-Oct-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/568,528
;            FILING DATE: 09-May-2000
;            APPLICATION NUMBER: 09/267,517
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Knight, Matthew W.
;            REGISTRATION NUMBER: 36,846
;            REFERENCE/DOCKET NUMBER: A-416
;  INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
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;           LENGTH: 1135 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: double
;           TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;           NAME/KEY:  misc_feature
;           LOCATION:  4
;           OTHER INFORMATION:  /note= "Met = ATG"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-679-999-13

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  Matches 1135;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 2
US-10-679-999-16
; Sequence 16, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;       APPLICANT: Mann, Michael B.
;                  Hecht, Randy I.
;       TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                           METHODS
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Amgen Inc.
;           STREET: 1840 DeHavilland Drive
;           CITY: Thousand Oaks
;           STATE: CA
;           COUNTRY: USA
;           ZIP: 91320-1789
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/679,999
;           FILING DATE: 06-Oct-2003
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US/09/568,528
;           FILING DATE: 09-May-2000
;           APPLICATION NUMBER: 09/267,517
;           FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;           NAME: Knight, Matthew W.
;           REGISTRATION NUMBER: 36,846
;           REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 16:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 1135 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: double
;           TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;           NAME/KEY:  misc_feature
;           LOCATION:  4
;           OTHER INFORMATION:  /note= "Met = ATG"
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US-10-679-999-16

  Query Match            97.7%;  Score 1109.4;  DB 13;  Length 1135;
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RESULT 3
US-10-645-761-1067
; Sequence 1067, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1067
; LENGTH: 748
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc MMP INHIBITOR
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(732)
; OTHER INFORMATION:
US-10-645-761-1067

Query Match 60.3%; Score 684.8; DB 12; Length 748;
Best Local Similarity 99.7%; Pred. No. 8.7e-182;
Matches 686; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
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Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              ||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 4
US-10-609-217-1067
; Sequence 1067, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/609,217
;  CURRENT FILING DATE:  2003-06-27
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1067
;   LENGTH: 748
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc MMP INHIBITOR
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(732)
;   OTHER INFORMATION:
US-10-609-217-1067

  Query Match             60.3%;  Score 684.8;  DB 13;  Length 748;
  Best Local Similarity   99.7%;  Pred. No. 8.7e-182;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              ||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 5
US-10-632-388-1067
; Sequence 1067, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/632,388
;  CURRENT FILING DATE:  2003-07-31
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1067
;   LENGTH: 748
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc MMP INHIBITOR
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(732)
;   OTHER INFORMATION:
US-10-632-388-1067

  Query Match             60.3%;  Score 684.8;  DB 13;  Length 748;
  Best Local Similarity   99.7%;  Pred. No. 8.7e-182;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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RESULT 6
US-10-651-723-1067
; Sequence 1067, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1067
; LENGTH: 748
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc MMP INHIBITOR
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(732)
; OTHER INFORMATION:
US-10-651-723-1067

Query Match 60.3%; Score 684.8; DB 13; Length 748;
Best Local Similarity 99.7%; Pred. No. 8.7e-182;
Matches 686; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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RESULT 7
US-10-666-696-1067
; Sequence 1067, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1067
; LENGTH: 748
; TYPE: DNA

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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc-MMP INHIBITOR
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(732)
;   OTHER INFORMATION:
US-10-666-696-1067

  Query Match            60.3%;  Score 684.8;  DB 17;  Length 748;
  Best Local Similarity  99.7%;  Pred. No. 8.7e-182;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 8
US-10-645-761-1055
; Sequence 1055, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/645,761
;  CURRENT FILING DATE:  2003-08-18
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1055
;   LENGTH: 757
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: FC-TNF-ALPA INHIBITORS
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(747)
;   OTHER INFORMATION:
US-10-645-761-1055

  Query Match            60.3%;  Score 684.8;  DB 12;  Length 757;
  Best Local Similarity  99.7%;  Pred. No. 8.7e-182;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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RESULT 9
US-10-609-217-1055
; Sequence 1055, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/609,217
;  CURRENT FILING DATE:  2003-06-27
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1055
;   LENGTH: 757
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: FC-TNF-ALPA INHIBITORS
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(747)
;   OTHER INFORMATION:
US-10-609-217-1055

  Query Match           60.3%;  Score 684.8;  DB 13;  Length 757;
  Best Local Similarity  99.7%;  Pred. No. 8.7e-182;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 10
US-10-632-388-1055
; Sequence 1055, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/632,388
;  CURRENT FILING DATE:  2003-07-31
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1055
;   LENGTH: 757
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: FC-TNF-ALPA INHIBITORS
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(747)
;   OTHER INFORMATION:
US-10-632-388-1055

  Query Match           60.3%;  Score 684.8;  DB 13;  Length 757;
  Best Local Similarity  99.7%;  Pred. No. 8.7e-182;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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RESULT 11
US-10-651-723-1055
; Sequence 1055, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1055
; LENGTH: 757
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-TNF-ALPA INHIBITORS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(747)
; OTHER INFORMATION:
US-10-651-723-1055

Query Match 60.3%; Score 684.8; DB 13; Length 757;
Best Local Similarity 99.7%; Pred. No. 8.7e-182;
Matches 686; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              ||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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RESULT 12
US-10-666-696-1055
; Sequence 1055, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1055
; LENGTH: 757
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc-TNF-ALPHA INHIBITORS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(747)
; OTHER INFORMATION:
US-10-666-696-1055

Query Match 60.3%; Score 684.8; DB 17; Length 757;
Best Local Similarity 99.7%; Pred. No. 8.7e-182;
Matches 686; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
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Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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RESULT 13
US-10-645-761-1059
; Sequence 1059, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1059
; LENGTH: 763
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-IL-1 ANTAGONIST
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(747)
; OTHER INFORMATION:
US-10-645-761-1059

Query Match 60.3%; Score 684.8; DB 12; Length 763;
Best Local Similarity 99.7%; Pred. No. 8.7e-182;
Matches 686; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
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Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
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Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
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Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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RESULT 14
US-10-609-217-1059
; Sequence 1059, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22

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;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1059
;   LENGTH: 763
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: FC-IL-1 ANTAGONIST
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(747)
;   OTHER INFORMATION:
US-10-609-217-1059

  Query Match             60.3%;  Score 684.8;  DB 13;  Length 763;
  Best Local Similarity   99.7%;  Pred. No. 8.7e-182;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
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Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
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Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

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RESULT 15
US-10-632-388-1059
; Sequence 1059, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/632,388
;  CURRENT FILING DATE:  2003-07-31
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1059
;   LENGTH: 763
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: FC-IL-1 ANTAGONIST
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(747)
;   OTHER INFORMATION:
US-10-632-388-1059

  Query Match             60.3%;  Score 684.8;  DB 13;  Length 763;
  Best Local Similarity   99.7%;  Pred. No. 8.7e-182;
  Matches  686;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60
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Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
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Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
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Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
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Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

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Search completed: May 11, 2004, 09:06:40
Job time : 477.75 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 18:55:54 ; Search time 2223.5 Seconds
(without alignments)
15243.344 Million cell updates/sec

Title: US-10-679-999-13
Perfect score: 1135
Sequence: 1 CATATGGACAAAACTCACAC.....TCCGGGTTGTTAATGGATCC 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 54259654

Minimum DB seq length: 0
Maximum DB seq length: 1135

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
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26: em_gss_phg:*
27: em_gss_vrl:*
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	668.8	58.9	941	13	BQ712021	BQ712021 AGENCOURT
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6	667.4	58.8	973	13	BQ706204	BQ706204 AGENCOURT
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8	666.6	58.7	919	13	BQ709339	BQ709339 AGENCOURT
9	666	58.7	897	13	BQ709144	BQ709144 AGENCOURT
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14	662.4	58.4	914	13	BQ712363	BQ712363 AGENCOURT
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17	657.8	58.0	897	12	BM008412	BM008412 603617406
18	657.8	58.0	902	13	BU146962	BU146962 AGENCOURT
c 19	657	57.9	1015	13	BX367600	BX367600 BX367600
c 20	655.8	57.8	860	13	BX437583	BX437583 BX437583
c 21	655.4	57.7	954	12	BG746184	BG746184 602723696
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c 23	655.4	57.7	1034	13	BX337959	BX337959 BX337959
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c 27	653.4	57.6	898	13	BX415442	BX415442 BX415442
28	652.4	57.5	958	13	BQ706140	BQ706140 AGENCOURT
29	652.4	57.5	961	13	BQ710233	BQ710233 AGENCOURT
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33	649	57.2	926	12	BG755166	BG755166 602711488
34	648.4	57.1	857	13	BX429638	BX429638 BX429638
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41	643.6	56.7	925	13	BQ709853	BQ709853 AGENCOURT
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c 43	642.4	56.6	921	13	BX359858	BX359858 BX359858
c 44	642.2	56.6	980	13	BX325701	BX325701 BX325701
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ALIGNMENTS

RESULT 1
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LOCUS BG753979 871 bp mRNA linear EST 15-MAY-2001
DEFINITION 602709506F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4846201 5', mRNA sequence.
ACCESSION BG753979
VERSION BG753979.1 GI:14064632
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 871)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1686 row: k column: 02
High quality sequence stop: 848.

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FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             59.0%;  Score 669.8;  DB 12;  Length 871;
  Best Local Similarity   99.0%;  Pred. No. 4.7e-127;
  Matches  674;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 66
              ||||||||||||||||| ||||| || ||||| || ||||||||||||| || ||||||
Db         37 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 96

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         97 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 156

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        277 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 336

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RESULT 2
BQ708975
LOCUS       BQ708975                983 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8353514 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279683
            5', mRNA sequence.
ACCESSION   BQ708975
VERSION     BQ708975.1  GI:21847874
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 983)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2469  row: k  column: 12
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FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             59.0%;  Score 669.8;  DB 13;  Length 983;
  Best Local Similarity   99.0%;  Pred. No. 4.9e-127;
  Matches  674;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 66
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Db         24 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 83

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
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Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
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Db        144 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 203

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
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Db        204 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 263

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Qy        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
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Db        324 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 383
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Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
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Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
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Db        504 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 563

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Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
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RESULT 3
BM007897
LOCUS BM007897 843 bp mRNA linear EST 30-OCT-2001
DEFINITION 603617582F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450469 5', mRNA sequence.
ACCESSION BM007897
VERSION BM007897.1 GI:16522238
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 843)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1939 row: d column: 22
High quality sequence stop: 833.

FEATURES Location/Qualifiers
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/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 58.9%; Score 669; DB 12; Length 843;
Best Local Similarity 98.5%; Pred. No. 6.8e-127;
Matches 675; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Db        108 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 167

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
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Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
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Db        348 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 407

Qy        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
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Db        408 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 467

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
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RESULT 4
BQ712021
LOCUS BQ712021 941 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8418162 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281403 5', mRNA sequence.
ACCESSION BQ712021
VERSION BQ712021.1 GI:21850920
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 941)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2474 row: c column: 04
High quality sequence stop: 638.

FEATURES Location/Qualifiers
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/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 58.9%; Score 668.8; DB 13; Length 941;
Best Local Similarity 98.8%; Pred. No. 7.8e-127;
Matches 673; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db         50 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 109

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
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Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
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Db        290 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 349

Qy        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
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Db        350 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 409

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
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Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
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RESULT 5
BQ709152
LOCUS BQ709152 925 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8485151 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301245 5', mRNA sequence.
ACCESSION BQ709152
VERSION BQ709152.1 GI:21848051
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 925)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2516 row: m column: 22
High quality sequence stop: 739.

FEATURES Location/Qualifiers
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/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 58.9%; Score 668.2; DB 13; Length 925;
Best Local Similarity 98.8%; Pred. No. 1e-126;
Matches 673; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db         48 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 107

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
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Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
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Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306
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Qy        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
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Db        348 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 407

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
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RESULT 6
BQ706204
LOCUS       BQ706204                 973 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8352308 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277592
            5', mRNA sequence.
ACCESSION   BQ706204
VERSION     BQ706204.1  GI:21845103
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 973)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2464  row: d  column: 09
            High quality sequence stop: 640.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN
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Query Match 58.8%; Score 667.4; DB 13; Length 973;

Best Local Similarity 95.5%; Pred. No. 1.5e-126;
Matches 686; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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Qy          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 66
              |||||||||||||||| ||||| || ||||| || ||||||||||||| || ||||||
Db        108 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 167

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 227

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 287

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 347

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 407

Qy        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 467

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 527

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        528 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 587

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        588 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 647

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        648 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGNG 707

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        708 AACGTCTTCTCATGCTCCGTGATGCATGAAGCTCTGCACAACCACTACACGCAGAAGAGC 767

Qy        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAAACCT 724
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Db        768 CTCTCCCTGTCTCCGGGTAAATGAGTGCGACGGGCGGGAAAGCCCCCCTCCCCAGGCT 825
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RESULT 7
BX346946
LOCUS       BX346946                 858 bp    mRNA    linear   EST 05-MAY-2003
DEFINITION  BX346946 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI039YP09 5-PRIME, mRNA sequence.
ACCESSION   BX346946
VERSION     BX346946.1  GI:30377150
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 858)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
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          Invitrogen. This sequence belongs to sequence cluster 7198.r For
          more information about this cluster, see
          http://www.genoscope.cns.fr/
          cgi-bin/cluster.cgi?seq=CS0AT021ZE05_T01957_1&cluster=7198.r.
          Contact : Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
          Faraday Avenue Genoscope sequence ID : CS0AT021ZE05_T01957_1.
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     source          1. .858
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                     /clone="CS0DI039YP09"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             58.8%;  Score 667.2;  DB 13;  Length 858;
  Best Local Similarity   98.7%;  Pred. No. 1.6e-126;
  Matches  672;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 66
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Db         65 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 124

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 184

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 244

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 304

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 364

Qy        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 424

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 484

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 544

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
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Db        545 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 604

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
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Db        605 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 664

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        665 AACGTCTTCTCATGCTNCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 724

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
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Db        725 CTCTCCCTGTCTTCGGGTAAA 745
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RESULT 8
BQ709339
LOCUS       BQ709339                919 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_7976429 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214450
            5', mRNA sequence.
ACCESSION   BQ709339
VERSION     BQ709339.1  GI:21848238
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 919)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2381  row: m  column: 11
            High quality sequence stop: 576.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6214450"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             58.7%;  Score 666.6;  DB 13;  Length 919;
  Best Local Similarity   98.7%;  Pred. No. 2.2e-126;
  Matches  672;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 66
              ||||||||||||||||| ||||| || ||||| || ||||||||||||| || ||||||
Db         57 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 116

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 176

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        177 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 236

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 296

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 356

Qy        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 416
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Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
Db        417 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 476

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
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Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
Db        537 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 596

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
Db        597 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAAGTGGCAGCAGGGG 656

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
Db        657 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 716

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
Db        717 CTCTCCCTGTCTCCGGGTAAA 737
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RESULT 9
BQ709144
LOCUS BQ709144 897 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8474994 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301566 5', mRNA sequence.
ACCESSION BQ709144
VERSION BQ709144.1 GI:21848043
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 897)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2517 row: k column: 07
High quality sequence stop: 628.
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
ORIGIN

Query Match 58.7%; Score 666; DB 13; Length 897;
Best Local Similarity 98.5%; Pred. No. 2.9e-126;
Matches 672; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 66
Db         50 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 109

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
Db        110 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 169

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
Db        170 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 229

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
Db        230 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 289

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306
Db        290 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 349

Qy        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
Db        350 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 409

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
Db        410 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 469

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
Db        470 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 529

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
Db        530 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 589

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
Db        590 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 649

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
Db        650 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 709

Qy        667 CTCTCCCTGTCTCCGGGTAAAG 688
Db        710 CTCTCCCTGTCTCCGGTAAATG 731
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RESULT 10
BQ709771
LOCUS BQ709771 947 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8353965 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278583 5', mRNA sequence.
ACCESSION BQ709771
VERSION BQ709771.1 GI:21848670
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 947)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

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           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM2466  row: m  column: 16
           High quality sequence start: 3
           High quality sequence stop: 675.
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             58.6%;  Score 665;  DB 13;  Length 947;
  Best Local Similarity   98.5%;  Pred. No. 4.7e-126;
  Matches  671;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 66
              ||||||||||||||||| ||||| || ||||| || ||||||||||||| || ||||||
Db        197 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 256

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 316

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
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Db        317 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 376

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
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Db        377 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 436

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 496

Qy        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 556

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 616

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 676

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 736

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        737 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 796

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        797 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACCACCACTACACGCAGAAGAGC 856

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
              ||||||||||| ||||||||
Db        857 CTCTCCCTGTCCTCGGGTAAA 877


RESULT 11
BQ711291
LOCUS       BQ711291                881 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8347186 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279096
            5', mRNA sequence.
ACCESSION   BQ711291
VERSION     BQ711291.1  GI:21850190
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 881)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2468  row: c  column: 01
            High quality sequence stop: 721.
FEATURES             Location/Qualifiers
     source          1. .881
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6279096"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             58.6%;  Score 664.8;  DB 13;  Length 881;
  Best Local Similarity   99.0%;  Pred. No. 5e-126;
  Matches  669;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 66
              ||||||||||||||||| ||||| || ||||| || ||||||||||||| || ||||||
Db        137 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 196

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 256

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 316

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 376

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 436
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```
Qy        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 496

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 556

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 616

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 676

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 736

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        737 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 796

Qy        667 CTCTCCCTGTCTCCGG 682
              ||||||||||||||||
Db        797 CTCTCCCTGTCTCCGG 812
```

RESULT 12
BX360518/c
LOCUS BX360518 1013 bp mRNA linear EST 05-MAY-2003
DEFINITION BX360518 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI071YG21 3-PRIME, mRNA sequence.
ACCESSION BX360518
VERSION BX360518.1 GI:30372442
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1013)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7198.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI071AD11NP1&cluster=7198.r. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DI071AD11NP1.
FEATURES Location/Qualifiers
source 1. .1013
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI071YG21"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match 58.4%; Score 662.8; DB 13; Length 1013;
Best Local Similarity 97.7%; Pred. No. 1.4e-125;

Matches 665; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

```
Qy          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 66
              |||||||||||||||| ||||| || ||||| || |||||||||||||| || ||||||
Db        768 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 709

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        708 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 649

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        648 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 589

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              |||||||||||||||||||||||||||||||||||||||||||||||||||||  :|||||
Db        588 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACANGMCGTAC 529

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        528 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 469

Qy        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||||||||||||||||||||||:|:||||||||||||||||||||||||||||||||||||
Db        468 TGCAAGGTCTCCAACAAAGCCCTMCMAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 409

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 349

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTTTATCCCAGCGACATCGCCGTGGAG 289

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db        288 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCKTGCTGGACTCC 229

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 169

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 109

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
              |||||||::|||||||||||||
Db        108 CTCTCCCYBTCTCCGGGTAAA 88
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RESULT 13
BG674795
LOCUS BG674795 757 bp mRNA linear EST 01-MAY-2001
DEFINITION 602620925F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4746150 5', mRNA sequence.
ACCESSION BG674795
VERSION BG674795.1 GI:13906191
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 757)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.

```
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM10594  row: b  column: 07
          High quality sequence stop: 755.
FEATURES             Location/Qualifiers
     source          1. .757
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4746150"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Skn3"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             58.4%;  Score 662.4;  DB 12;  Length 757;
  Best Local Similarity   98.2%;  Pred. No. 1.5e-125;
  Matches  669;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 66
              ||||||||||||||||| ||||| || ||||| || ||||||||||||| || ||||||
Db         37 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 96

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         97 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 156

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 216

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 276

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        277 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 336

Qy        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        337 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 396

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              |||||||||||||||||||||||||||||||||||||||||||||||| ||| ||||||||
Db        397 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG 456

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        457 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 516

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        517 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 576

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        577 GACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 636

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        637 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAANCACTACACGCAGAAGAGC 696

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
              ||||||||||| |||||||||
Db        697 CTCTCCCTGTCCCCGGGTAAA 717


RESULT 14
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BQ712363
LOCUS       BQ712363                 914 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8475100 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301405
            5', mRNA sequence.
ACCESSION   BQ712363
VERSION     BQ712363.1  GI:21851262
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 914)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2517  row: d  column: 14
            High quality sequence stop: 585.
FEATURES             Location/Qualifiers
     source          1. .914
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6301405"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             58.4%;  Score 662.4;  DB 13;  Length 914;
  Best Local Similarity   98.2%;  Pred. No. 1.6e-125;
  Matches  669;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 66
              ||||||||||||||||| ||||| || ||||| || ||||||||||||| || ||||||
Db         69 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 128

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 188

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 248

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 308

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 368

Qy        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 428

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
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Db        429 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 488

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 548

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 608

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              |||||||||||||||||||||||||||||||||||||||||||||||||||||    |||
Db        609 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGNCAGGG 668

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        669 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAAAAGAGC 728

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
              |||||||||||||||||| |||
Db        729 CTCTCCCTGTCTCCGGGAAAA 749
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RESULT 15
BQ709859

LOCUS	BQ709859 856 bp mRNA linear EST 16-JUL-2002
DEFINITION	AGENCOURT_8349888 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6280560 5', mRNA sequence.
ACCESSION	BQ709859
VERSION	BQ709859.1 GI:21848758
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 856)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Mark Watson cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM2471 row: p column: 01 High quality sequence stop: 605.

FEATURES	Location/Qualifiers
source	1. .856 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6280560" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH_MGC_113" /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 58.2%; Score 660.6; DB 13; Length 856;
Best Local Similarity 98.0%; Pred. No. 3.6e-125;
Matches 669; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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Qy          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 66
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Db         24 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 83

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCCTGAGGTCACA 126
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Db         84 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 143

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
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Db        144 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 203

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
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Db        204 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 263

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306
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Db        264 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 323

Qy        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
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Db        384 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 443

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
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Db        444 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 503

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
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Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
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Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
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Search completed: May 10, 2004, 06:19:22
Job time : 2231 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:37 ; Search time 3069 Seconds
(without alignments)
16029.437 Million cell updates/sec

Title: US-10-679-999-14
Perfect score: 1135
Sequence: 1 GTATACCTGTTTTGAGTGTG.....AGGCCCAACAATTACCTAGG 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 5401154

Minimum DB seq length: 0
Maximum DB seq length: 1135

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		1135	100.0	1135	6	BD056522	BD056522 OB fusion
2		1109.4	97.7	1135	6	BD056524	BD056524 OB fusion
3		684.8	60.3	861	6	BD263010	BD263010 Dimeric t
4		680.8	60.0	684	6	BD263000	BD263000 Dimeric t
5		440.8	38.8	454	6	BD004077	BD004077 Methods o
6		440.8	38.8	454	6	BD056516	BD056516 OB fusion
7		378.4	33.3	491	6	BD004075	BD004075 Methods o
8		378.4	33.3	491	6	BD056514	BD056514 OB fusion
9		50.8	4.5	908	8	AB029092	AB029092 Cucumis s
10		50.8	4.5	1110	8	AB029147	AB029147 Cucumis s
11		43	3.8	468	6	I27620	I27620 Sequence 12
12		43	3.8	746	6	A51599	A51599 Sequence 9
13	c	40.4	3.6	1057	6	E02180	E02180 DNA sequenc
14	c	40.4	3.6	1057	6	E02181	E02181 DNA sequenc
15	c	40	3.5	533	6	AR365256	AR365256 Sequence
16		39.4	3.5	1011	6	AX616829	AX616829 Sequence
17	c	39	3.4	1046	3	AY058495	AY058495 Drosophil
18	c	38.6	3.4	462	10	AY300753	AY300753 Mesocrice
19	c	38.6	3.4	564	10	AY300754	AY300754 Mesocrice
20	c	37.8	3.3	451	10	MUSIR3E2	M10668 Mouse DNA w
21		37.8	3.3	789	6	AX756672	AX756672 Sequence
22		37.8	3.3	810	6	AX575331	AX575331 Sequence
23		37.8	3.3	813	6	AX467493	AX467493 Sequence
24		37.8	3.3	813	6	AX575327	AX575327 Sequence
25		37.8	3.3	815	6	AX527763	AX527763 Sequence
26		37.8	3.3	815	6	AX527765	AX527765 Sequence
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28	c	37.4	3.3	688	6	A86256	A86256 Sequence 91
29	c	37.4	3.3	688	6	AR155749	AR155749 Sequence
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35	c	36.6	3.2	1018	8	AF479764	AF479764 Triticum
36	c	36.4	3.2	744	6	BD180141	BD180141 Highly th
37	c	36.4	3.2	1029	4	TGU65923	U65923 Tupaia glis
38	c	36.2	3.2	393	8	AB101649	AB101649 Oryza sat
39		36.2	3.2	636	3	LTE494984	AJ494984 Liporrhop
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ALIGNMENTS

RESULT 1
BD056522
LOCUS BD056522 1135 bp DNA linear PAT 27-AUG-2002
DEFINITION OB fusion protein compositions and methods.
ACCESSION BD056522
VERSION BD056522.1 GI:22602128
KEYWORDS JP 2001512417-A/10.
SOURCE Aequorea victoria
ORGANISM Aequorea victoria
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
REFERENCE 1 (bases 1 to 1135)
AUTHORS Mann,M.B. and Hecht,R.I.
TITLE OB fusion protein compositions and methods
JOURNAL Patent: JP 2001512417-A 10 21-AUG-2001;

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            AMGEN INC
COMMENT     PN   JP 2001512417-A/10
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
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            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES            Location/Qualifiers
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ORIGIN

  Query Match           100.0%;  Score 1135;  DB 6;  Length 1135;
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  Matches 1135;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        841 AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA 900
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Qy        901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT 960
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Db       1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135


RESULT 2
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LOCUS       BD056524                1135 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056524
VERSION     BD056524.1  GI:22602130
KEYWORDS    JP 2001512417-A/12.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1135)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 12 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/12
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
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            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES            Location/Qualifiers
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ORIGIN

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  Matches 1119;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

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Qy         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120
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Qy       1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
Db       1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
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RESULT 3
BD263010
LOCUS BD263010 861 bp DNA linear PAT 17-JUL-2003
DEFINITION Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and having thrombopoietic activity.
ACCESSION BD263010
VERSION BD263010.1 GI:33072778
KEYWORDS JP 2002536960-A/12.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 861)
AUTHORS Liu,C.F., Feige,U. and Cheetham,J.
TITLE Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and having thrombopoietic activity
JOURNAL Patent: JP 2002536960-A 12 05-NOV-2002;
AMGEN INC
COMMENT OS Artificial Sequence
PN JP 2002536960-A/12
PD 05-NOV-2002
PF 22-OCT-1999 JP 2000578340
PR 23-OCT-1998 US 60/105348
PI CHUAN FA LIU,ULRICH FEIGE,JANET CHEETHAM
PC C12N15/09,A61K38/00,A61P7/00,C07K14/52,C07K19/00,C12N1/15, PC C12N1/19,
PC C12N1/21,C12N5/10,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC
Description of Artificial Sequence: oligonucleotide FH Key Location/Qualifiers
FT source 1. .861
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .861
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 60.3%; Score 684.8; DB 6; Length 861;
Best Local Similarity 99.7%; Pred. No. 4.2e-155;
Matches 686; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGA 60
Db         36 GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC 95

Qy         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120
Db         96 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 155

Qy        121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180
Db        156 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 215

Qy        181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240
Db        216 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 275

Qy        241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC 300
Db        276 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC 335

Qy        301 ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360
Db        336 ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 395

Qy        361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420
Db        396 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 455

Qy        421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480
Db        456 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 515

Qy        481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540
Db        516 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 575
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Qy        541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600
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Db        576 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 635

Qy        601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 695

Qy        661 TTCTCGGAGAGGGACAGAGGCCCATTTC 688
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Db        696 TTCTCGGAGAGGGACAGAGGCCCATTTC 723


RESULT 4
BD263000
LOCUS       BD263000                 684 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and
            having thrombopoietic activity.
ACCESSION   BD263000
VERSION     BD263000.1  GI:33072768
KEYWORDS    JP 2002536960-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 684)
  AUTHORS   Liu,C.F., Feige,U. and Cheetham,J.
  TITLE     Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and
            having thrombopoietic activity
  JOURNAL   Patent: JP 2002536960-A 2 05-NOV-2002;
            AMGEN INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002536960-A/2
            PD   05-NOV-2002
            PF   22-OCT-1999 JP 2000578340
            PR   23-OCT-1998 US    60/105348
            PI   CHUAN FA LIU,ULRICH FEIGE,JANET CHEETHAM
            PC   C12N15/09,A61K38/00,A61P7/00,C07K14/52,C07K19/00,C12N1/15, PC
             C12N1/19,
            PC   C12N1/21,C12N5/10,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC
            Description of Artificial Sequence: oligonucleotide FH   Key
                 Location/Qualifiers
            FT   source          1. .684
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .684
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             60.0%;  Score 680.8;  DB 6;  Length 684;
  Best Local Similarity   99.7%;  Pred. No. 3.9e-154;
  Matches  682;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGAAGT 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||| || |||
Db          1 TACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGT 60

Qy         64 CAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG 120

Qy        124 TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC 180

Qy        184 CTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGC 240

Qy        244 ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATG 300

Qy        304 TTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGG 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGG 360

Qy        364 TTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGG 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGG 420

Qy        424 TTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC 480

Qy        484 CTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTG 540

Qy        544 AGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC 600

Qy        604 CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTC 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTC 660

Qy        664 TCGGAGAGGGACAGAGGCCCATTT 687
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Db        661 TCGGAGAGGGACAGAGGCCCATTT 684


RESULT 5
BD004077
LOCUS       BD004077                 454 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Methods of increasing sensitivity of an individual to OB protein by
            up-regulating OB protein receptor.
ACCESSION   BD004077
VERSION     BD004077.1  GI:18632038
KEYWORDS    JP 2001501177-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 454)
  AUTHORS   Pelleymounter,M.A.
  TITLE     Methods of increasing sensitivity of an individual to OB protein by
            up-regulating OB protein receptor
  JOURNAL   Patent: JP 2001501177-A 4 30-JAN-2001;
            AMGEN INC
COMMENT     OS   Unidentified
            PN   JP 2001501177-A/4
            PD   30-JAN-2001
            PF   26-AUG-1997 JP 1998511882
            PR   30-AUG-1996 US    08/705981
            PI   MARY ANN PELLEYMOUNTER
            PC   A61K38/00,A61K31/425,A61P1/16,A61P3/04,A61P3/06,A61P3/10, PC
            A61P9/10,
            PC   A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .454
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .454
                     /organism="unidentified"
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                     /db_xref="taxon:32644"
ORIGIN

  Query Match             38.8%;  Score 440.8;  DB 6;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 5.5e-96;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
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Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
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Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
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Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              |||||||||||||||||||||||||||||||||||||| | ||||||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
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Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
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Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454
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RESULT 6
BD056516
LOCUS       BD056516                454 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056516
VERSION     BD056516.1  GI:22602122
KEYWORDS    JP 2001512417-A/4.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 454)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 4 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/4
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .454
                     /organism="Aequorea victoria"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:6100"
ORIGIN

  Query Match           38.8%;  Score 440.8;  DB 6;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 5.5e-96;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62
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Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              |||||||||||||||||||||||||||||||||||||| | ||||||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
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Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
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Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454
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RESULT 7
BD004075
LOCUS       BD004075                491 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Methods of increasing sensitivity of an individual to OB protein by
            up-regulating OB protein receptor.
ACCESSION   BD004075
VERSION     BD004075.1  GI:18632036
KEYWORDS    JP 2001501177-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 491)
  AUTHORS   Pelleymounter,M.A.
  TITLE     Methods of increasing sensitivity of an individual to OB protein by
            up-regulating OB protein receptor
  JOURNAL   Patent: JP 2001501177-A 2 30-JAN-2001;
            AMGEN INC
COMMENT     OS   Unidentified
            PN   JP 2001501177-A/2
            PD   30-JAN-2001
            PF   26-AUG-1997 JP 1998511882
            PR   30-AUG-1996 US    08/705981
            PI   MARY ANN PELLEYMOUNTER
            PC   A61K38/00,A61K31/425,A61P1/16,A61P3/04,A61P3/06,A61P3/10, PC
            A61P9/10,
            PC   A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .491
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match           33.3%;  Score 378.4;  DB 6;  Length 491;
  Best Local Similarity   89.8%;  Pred. No. 7.3e-81;
  Matches  406;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
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Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803

Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863

Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923

Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983

Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043

Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103

Db        400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135

Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491
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RESULT 8
BD056514
LOCUS       BD056514                491 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056514
VERSION     BD056514.1  GI:22602120
KEYWORDS    JP 2001512417-A/2.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 491)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 2 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/2
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .491
                        /organism="Aequorea victoria"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:6100"
ORIGIN

  Query Match           33.3%;  Score 378.4;  DB 6;  Length 491;
  Best Local Similarity  89.8%;  Pred. No. 7.3e-81;
  Matches  406;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743

Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99
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Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803

Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863

Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923

Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983

Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043

Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103

Db        400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135

Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491
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RESULT 9
AB029092
LOCUS       AB029092                908 bp    mRNA    linear   PLN 15-APR-2003
DEFINITION  Cucumis sativus mRNA for arabinogalactan protein, complete cds.
ACCESSION   AB029092
VERSION     AB029092.2  GI:29893813
KEYWORDS    .
SOURCE      Cucumis sativus (cucumber)
  ORGANISM  Cucumis sativus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
REFERENCE   1
  AUTHORS   Park,M.H., Suzuki,Y., Chono,M., Knox,J.P. and Yamaguchi,I.
  TITLE     CsAGP1, a Gibberellin-Responsive Gene from Cucumber Hypocotyls,
            Encodes a Classical Arabinogalactan Protein and Is Involved in Stem
            Elongation
  JOURNAL   Plant Physiol. 131 (3), 1450-1459 (2003)
  MEDLINE   22531811
   PUBMED   12644694
REFERENCE   2  (bases 1 to 908)
  AUTHORS   Chono,M., Suzuki,Y. and Yamaguchi,I.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-JUN-1999) Makiko Chono, University of Tokyo, Applied
            Biological Chemistry; Yayoi 1-1-1, Bunkyo-ku, Tokyo 113-8657, Japan
            (E-mail:mchono@pgr1.ch.a.u-tokyo.ac.jp, Tel:+81-3-5841-5160,
            Fax:+81-3-5841-8025)
COMMENT     On Apr 16, 2003 this sequence version replaced gi:5443647.
FEATURES             Location/Qualifiers
     source          1. .908
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                     /mol_type="mRNA"
                     /db_xref="taxon:3659"
                     /clone="203-1/5"
                     /note="obtained by differential display analysis"
     CDS             21. .752
                     /codon_start=1
                     /product="arabinogalactan protein"
                     /protein_id="BAC75541.1"
                     /db_xref="GI:29893814"
                     /translation="MGRQSVIALVLICAVVAGVGGQSPAAAPTTTPAATPPVAATYPP
                     PAASPVSTPTNPSPAAAPQKPATPAPVSTPPASAPPAVAPVASPPASTPPTASVPASS
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ORIGIN

Query Match 4.5%; Score 50.8; DB 8; Length 908;
Best Local Similarity 46.0%; Pred. No. 0.17;
Matches 172; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

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Qy      118 CTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACC 177
Db      283 CACCAGCCAGCACTCCTCCGACTGCTTCCGTTCCTGCCAGCTCTCCTCCGGCTGCTTCCG 342

Qy      178 ATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTG 237
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Qy      238 TCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTC 297
Db      403 CGGTTAGTTCTCCACCAGTTTCAGTACCGGTGAGCTCTCCTCCAGTACCAACTCCAACGG 462

Qy      298 CTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGG 357
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Qy      418 GACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAG 477
Db      583 CAGCGTTGCTTGGTCCACCTGCGCCTCCTTCTGAAGCTCCTGCAGGAAGCGAGGAAGGTC 642

Qy      478 CGGCACCTCACCCT 491
Db      643 CTGCGCCCAGCCCT 656
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RESULT 10
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LOCUS AB029147 1110 bp mRNA linear PLN 23-JUN-1999
DEFINITION Cucumis sativus mRNA expressed in cucumber hypocotyls, complete cds.
ACCESSION AB029147
VERSION AB029147.1 GI:5139694
KEYWORDS .
SOURCE Cucumis sativus (cucumber)
ORGANISM Cucumis sativus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
REFERENCE 1 (bases 1 to 1110)
AUTHORS Chono,M., Suzuki,Y. and Yamaguchi,I.
TITLE Molecular cloning of genes expressed in cucumber hypocotyls
JOURNAL Published Only in DataBase (1999)
REFERENCE 2 (bases 1 to 1110)
AUTHORS Chono,M., Suzuki,Y. and Yamaguchi,I.
TITLE Direct Submission
JOURNAL Submitted (18-JUN-1999) Makiko Chono, University of Tokyo, Applied Biological Chemistry; Yayoi 1-1-1, Bunkyo-ku, Tokyo 113-8657, Japan (E-mail:mchono@pgr1.ch.a.u-tokyo.ac.jp, Tel:+81-3-5841-5160, Fax:+81-3-5841-8025)
FEATURES Location/Qualifiers
source 1. .1110
/organism="Cucumis sativus"
/mol_type="mRNA"
/db_xref="taxon:3659"
CDS 21. .752
/note="expressed in cucumber hypocotyls"
/codon_start=1
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ORIGIN

Query Match 4.5%; Score 50.8; DB 8; Length 1110;
Best Local Similarity 46.0%; Pred. No. 0.18;
Matches 172; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

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Qy      238 TCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTC 297
Db      403 CGGTTAGTTCTCCACCAGTTTCAGTACCGGTGAGCTCTCCTCCAGTACCAACTCCAACGG 462

Qy      298 CTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGG 357
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Qy      358 TTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTC 417
Db      523 TTCCTGCCCCGGCACCTAGCAAGAAGAAGTCAAAGAAGCACAGAGCACCAGCTCCTTCTC 582

Qy      418 GACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAG 477
Db      583 CAGCGTTGCTTGGTCCACCTGCGCCTCCTTCTGAAGCTCCTGCAGGAAGCGAGGAAGGTC 642

Qy      478 CGGCACCTCACCCT 491
Db      643 CTGCGCCCAGCCCT 656
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RESULT 11
I27620
LOCUS I27620 468 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 12 from patent US 5565335.
ACCESSION I27620
VERSION I27620.1 GI:1818396
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 468)
AUTHORS Capon,D.J. and Gregory,T.J.
TITLE Adhesion variants
JOURNAL Patent: US 5565335-A 12 15-OCT-1996;
FEATURES Location/Qualifiers
source 1. .468
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 3.8%; Score 43; DB 6; Length 468;
Best Local Similarity 49.5%; Pred. No. 13;
Matches 143; Conservative 0; Mismatches 140; Indels 6; Gaps 1;

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Qy      379 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 438
Db      127 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 186

Qy      439 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 492
Db      187 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 246

Qy      493 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 552
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Qy        553 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 612
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Db        307 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 366

Qy        613 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 661
              | | | |||    ||  |  ||| |||  |||  |   | |  |||  |||
Db        367 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 415


RESULT 12
A51599
LOCUS       A51599                   746 bp    DNA     linear   PAT 10-MAR-1997
DEFINITION  Sequence 9 from Patent WO9616990.
ACCESSION   A51599
VERSION     A51599.1  GI:2304408
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 746)
  AUTHORS   Ellis,J.H. and Lewis,A.P.
  TITLE     HUMANIZED ANTIBODIES TO CD38
  JOURNAL   Patent: WO 9616990-A 9 06-JUN-1996;
            WELLCOME FOUND (GB)
COMMENT     Other publication AU 3933695 960619.
FEATURES             Location/Qualifiers
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ORIGIN

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Qy        379 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 438
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Db        429 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 488

Qy        439 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 492
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Db        489 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 548

Qy        493 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 552
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Db        549 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 608

Qy        553 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 612
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Db        609 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 668

Qy        613 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 661
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Db        669 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 717


RESULT 13
E02180/c
LOCUS       E02180                   1057 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  DNA sequence of fragment for which expression and secretion of
            xylanase.
ACCESSION   E02180
VERSION     E02180.1  GI:2170418
KEYWORDS    JP 1990002377-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 1057)
  AUTHORS   Nagashima,M., Okumoto,Y. and Okanishi,M.
  TITLE     DNA FRAGMENT FOR EXPRESSION AND SECRETION VECTOR FOR ACTINOMYCETE
  JOURNAL   Patent: JP 1990002377-A 1 08-JAN-1990;
            BANYU PHARMACEUT CO LTD
COMMENT     OS   Artificial gene
            OC   Artificial sequence; Genes.
            OS   Streptomyces sp.No.36a
            PN   JP 1990002377-A/1
            PD   08-JAN-1990
            PF   08-JUN-1988 JP 1988140990
            PI   NAGASHIMA MASAO, OKUMOTO YASUHIRO, OKANISHI MASANORI PC
            C12N15/76,C12N1/21,C12P21/00;
            CC   strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No.
FEATURES             Location/Qualifiers
     source          1. .1057
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Qy        255 GTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCA 314
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Db        784 GGCGTTGTACCGGGTCGTCTTGTAGATGTCGTAGGTGCCGCCGTCGCTGTGGACGGTGCC 725

Qy        315 GAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG 374
              |||  |  | || |||  |||  |  || |   | || || | |   ||   |     |
Db        724 CCGGTACTCGCCGGTGGGCCGGTAGCTGCCCCAGTTGTCGACGATGTAGTACTCGACGAG 665

Qy        375 GGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCA 434
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Db        664 CGGGTTGGAGGTCCAGCCGTAGAGGCAGCCGTAGCCGTTGCCCGACGGGTTGAACCAGCC 605

Qy        435 GTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTC 494
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Db        604 GGTGTACCGGACGGTCCGGCGCCCGCCGTTGGCCCAGCCCTTGCCGGCCACGAAGTTGCC 545

Qy        495 GTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAG 554
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Qy        555 GAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600
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Db        484 GCCGCCGTCGGTCCAGAACGAGTAGTACATGCCGTCGTACCCGGTC 439


RESULT 14
E02181/c
LOCUS       E02181                   1057 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  DNA sequence of fragment for which expression and secretion of
            xylanase.
ACCESSION   E02181
VERSION     E02181.1  GI:2170419
KEYWORDS    JP 1990002379-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 1057)
  AUTHORS   Nagashima,M., Okumoto,Y. and Okanishi,M.
  TITLE     DNA FRAGMENT FOR EXPRESSION AND SECRETION VECTOR FOR ACTINOMYCETE
  JOURNAL   Patent: JP 1990002379-A 1 08-JAN-1990;
            BANYU PHARMACEUT CO LTD
COMMENT     OS   Artificial gene
            OC   Artificial sequence; Genes.
            OS   Streptomyces sp.No.36a
            PN   JP 1990002379-A/1
            PD   08-JAN-1990
            PF   20-MAY-1988 JP 1988124658
            PI   NAGASHIMA MASAO, OKUMOTO YASUHIRO, OKANISHI MASANORI PC
            C12N15/80,C12N1/14,C12P21/00,(C12N15/80,C12R1:465),(C12N1/14, PC
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            C12R1:465),
            PC   (C12P21/00,C12R1:465);
            CC   strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No.
FEATURES             Location/Qualifiers
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  Best Local Similarity   44.8%;  Pred. No. 58;
  Matches  155;  Conservative    0;  Mismatches  191;  Indels    0;  Gaps    0;

Qy        255 GTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCA 314
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Db        784 GGCGTTGTACCGGGTCGTCTTGTAGATGTCGTAGGTGCCGCCGTCGCTGTGGACGGTGCC 725

Qy        315 GAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG 374
              |||  |  | || ||| |||  |  || |   | || || | |  ||   |      |
Db        724 CCGGTACTCGCCGGTGGGCCGGTAGCTGCCCCAGTTGTCGACGATGTAGTACTCGACGAG 665

Qy        375 GGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCA 434
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Db        664 CGGGTTGGAGGTCCAGCCGTAGAGGCAGCCGTAGCCGTTGCCCGACGGGTTGAACCAGCC 605

Qy        435 GTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTC 494
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Db        604 GGTGTACCGGACGGTCCGGCGCCCGCCGTTGGCCCAGCCCTTGCCGGCCACGAAGTTGCC 545

Qy        495 GTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAG 554
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Db        544 GCAGTTGGTCCACCGGGTGCTGTAGCTGCCGCCGCCGTTGAGCGTCATGGAGACGGACCC 485

Qy        555 GAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600
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Db        484 GCCGCCGTCGGTCCAGAACGAGTAGTACATGCCGTCGTACCCGGTC 439


RESULT 15
AR365256/c
LOCUS       AR365256                533 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 5 from patent US 5482709.
ACCESSION   AR365256
VERSION     AR365256.1  GI:34428778
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 533)
  AUTHORS   Jacobson,J.W., Strausberg,R.L., Wilson,S.D., Pope,S.H.,
            Strausberg,S.L., Ruff,M.D., Augustine,P.C. and Danforth,H.D.
  TITLE     Eimeria antigenic composition which elicits antibodies against
            avian coccidiosis
  JOURNAL   Patent: US 5482709-A 5 09-JAN-1996;
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches  121;  Conservative    0;  Mismatches  135;  Indels    0;  Gaps    0;

Qy         89 TCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGG 148
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Db        440 TCCCCCAGGCTTACCTGCTGCTGATGCTGCTGCTGCTCTTGCTGCAGCTGCTGTTGTTGC 381

Qy        149 TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT 208
              |||| ||  ||  |||  | |  | |||  |||| ||  ||||   |  | |
Db        380 TGCTGTTGCTGCTTGTGTTTTCGCTTTCTCTGCTTCTGCTGCTGCTCCTGCTGCTCCTTC 321

Qy        209 TCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGC 268
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Db        320 GGTTTCTGTTCGTGCTTCCGCTGCCTTTGCTGCTCCTGCTGCTCCTGCTGCGGCTGTCGC 261

Qy        269 AGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGG 328
              | |  |||| |||     |  | | ||| ||  || |   | | |||  | || | | |
Db        260 TGCAGCTGGTGCTGCTGCAGCTCCTGTTGCTGCTGCTGCTGCTGCAGCTGGTGCTGCTGC 201

Qy        329 AGGGTCGGGGGTAGCT 344
              ||    |  | ||||
Db        200 AGCTGGTGCTGCAGCT 185


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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	4	40.4	3.6	1057	2	AAQ03405	Aaq03405 Streptomy
	5	40.2	3.5	926	6	ABZ11846	Abz11846 Human pol
c	6	40	3.5	543	2	AAQ23092	Aaq23092 Antigen t
	7	39.4	3.5	1011	6	ABS78695	Abs78695 S. aeroco
c	8	39	3.4	922	4	ABL09597	Abl09597 Drosophil
	9	37.8	3.3	789	7	AAD56497	Aad56497 Human VLC
	10	37.8	3.3	810	6	ABZ22164	Abz22164 Human elo
	11	37.8	3.3	813	6	AAD42270	Aad42270 Human ELG
	12	37.8	3.3	813	6	ABZ22162	Abz22162 Human elo
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	14	37.8	3.3	815	6	ABN86919	Abn86919 Human NOV
	15	37.8	3.3	818	7	ABZ24216	Abz24216 Human LCE
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	23	35.4	3.1	1014	4	ABL15657	Abl15657 Drosophil
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c	33	34.6	3.0	422	9	ADE87899	Ade87899 Human lun
	34	34.6	3.0	950	6	ABK71707	Abk71707 Human dit
c	35	34.4	3.0	431	8	ACD25835	Acd25835 Maize EST
c	36	34.4	3.0	795	2	AAV55830	Aav55830 FLGA inse
	37	34.2	3.0	780	7	ACA37806	Aca37806 Prokaryot
c	38	34	3.0	621	3	AAF11323	Aaf11323 Aspergill
c	39	34	3.0	693	4	AAF87193	Aaf87193 Human ion
c	40	34	3.0	729	8	ADB10435	Adb10435 Alloiococ
c	41	34	3.0	729	8	ADB10437	Adb10437 Alloiococ
	42	33.8	3.0	355	4	AAL01952	Aal01952 Human rep
	43	33.8	3.0	355	4	ABL97245	Abl97245 Human tes
	44	33.8	3.0	436	4	AAL06169	Aal06169 Human rep
	45	33.8	3.0	436	4	ABL98734	Abl98734 Human tes

ALIGNMENTS

RESULT 1
AAL51057
ID AAL51057 standard; DNA; 138 BP.
XX
AC AAL51057;
XX
DT 20-FEB-2003 (first entry)
XX
DE Cyclic single-strand anti-tumour antibody-related coding sequence #6.
XX
KW Cyclic single-strand anti-tumour antibody; anti-tumour Fab; ds;
KW anti-human Cd3 Fab; anti-human CD28 Fab; immunotherapy; tumour;
KW ovarian cancer.
XX
OS Unidentified.
XX
PN WO200283738-A1.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-CN000252.
XX
PR 11-APR-2001; 2001CN-00110554.
XX
PA (GENE-) INST GENETICS CAS.
PA (BEIJ-) BEIJING ABT GENETIC ENG TECHNOLOGY CO LT.
XX
PI Huang H, Cheng J, Wang X, Song L, Zhang Z, Lin Q, Gu Y;
XX
DR WPI; 2003-075525/07.
DR P-PSDB; AAO16031.
XX
PT Cyclic single-strand tri-specific antibody made from antitumor Fab,
PT single-strand antibody and modified anti-human CD3 or CD28 Fab,
PT applicable in early-stage diagnosis, and prevention or treatment of
PT tumors e.g. ovarian cancer.
XX
PS Disclosure; Fig 4A; 49pp; Chinese.
XX
CC The invention comprises a cyclic single-strand anti-tumour antibody, the
CC antibody of the invention is obtained by combining anti-tumour Fab and
CC modified anti-human Cd3 or CD28 Fab. The antibody is useful in the
CC immunotherapy of tumours - particularly ovarian cancer, including the
CC sensitive early-stage diagnosis and post-operative eradication of
CC disease. The present DNA sequence encodes a peptide which was used in the
CC invention

```
XX
SQ   Sequence 138 BP; 35 A; 37 C; 39 G; 27 T; 0 U; 0 Other;

  Query Match             4.7%;  Score 53.6;  DB 7;  Length 138;
  Best Local Similarity   93.3%;  Pred. No. 4.7e-05;
  Matches   56;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        235 TTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCG 294
              ||||||||||||||  ||  || ||||||||||||||  ||||||||||||||||||||||
Db         61 TTGTCGTGCATGGCCCAACATTCGCAGGAGTGGCATGACGTGGTCCTGACCGACTTACCG 120


RESULT 2
AAT20112
ID   AAT20112 standard; cDNA to mRNA; 268 BP.
XX
AC   AAT20112;
XX
DT   29-JUL-1996  (first entry)
XX
DE   Human gene signature HUMGS01256.
XX
KW   Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW   human; cloning; mapping; non-biased library; diagnosis; detection;
KW   cell typing; abnormal cell function; ss.
XX
OS   Homo sapiens.
XX
PN   WO9514772-A1.
XX
PD   01-JUN-1995.
XX
PF   11-NOV-1994;   94WO-JP001916.
XX
PR   12-NOV-1993;   93JP-00355504.
XX
PA   (MATS/) MATSUBARA K.
PA   (OKUB/) OKUBO K.
XX
PI   Matsubara K,  Okubo K;
XX
DR   WPI; 1995-206931/27.
XX
PT   Single-stranded DNA for identifying gene signatures - isolated from 3'-
PT   directed human cDNA library that reflects relative abundance of corresp.
PT   mRNA in specific human tissues.
XX
PS   Claim 1; Page 563; 2245pp; Japanese.
XX
CC   A single-stranded DNA (or its complementary strand or the corresp. double
CC   -stranded DNA) which comprises one of the 7837 "GS" sequences given in
CC   AAT19001-T26837 and which is able to hybridise to part of human genomic
CC   DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were
CC   obtained from 3'-directed cDNA libraries prepared from various human
CC   tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using
CC   poly(T) as the sole primer. Since the 3'- untranslated sequence is unique
CC   to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise
CC   with specific mRNAs. Each library is constructed so as to reflect
CC   accurately the relative abundance of different mRNAs in the particular
CC   tissue from which it was derived. The appearance frequency of a given GS
CC   in a cDNA library can be determined (esp. using primers and probes
CC   derived from the GS sequences) as a means of diagnosing abnormal cell
CC   function or for recognising different cell types
XX
SQ   Sequence 268 BP; 68 A; 54 C; 70 G; 62 T; 0 U; 14 Other;

  Query Match             3.6%;  Score 40.6;  DB 2;  Length 268;
  Best Local Similarity   53.9%;  Pred. No. 0.31;
  Matches   82;  Conservative    0;  Mismatches   70;  Indels    0;  Gaps    0;

Qy        922 CTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGAC 981
              |||||||  |||      | |     || |  || | |    ||   |   |||||   |||
Db          4 CTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGACCAAGGAA 63

Qy        982 GGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCA 1041
              |      ||||  ||  ||  ||||  |     | |  ||    |  |  | | |||  ||| | |||
Db         64 GAGCTTTGAAGGCCTGAGGTCTGCGNAAGGTGGGAGGAGGCAGACGCCCTGCGTGGCCCA 123

Qy       1042 ATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1073
                ||||  |||  ||  ||  ||||  |  ||   | |
Db        124 TGGTCGGGGCGTCCACGCCGAGGCCGGCAACA 155


RESULT 3
AAF75507/c
ID   AAF75507 standard; DNA; 486 BP.
XX
AC   AAF75507;
XX
DT   09-MAY-2001  (first entry)
XX
DE   Polyglutamine tract coding sequence #2.
XX
KW   Animal model; polyglutamine tract; neurodegenerative disorder; HDJ1;
KW   heat shock protein 40; tetratricopeptide repeat protein 2; TPR2; stroke;
KW   myeloid leukaemia factor 1; MLF; human; fruit fly; Alzheimer's disease;
KW   Parkinson's disease; CJD; BSE; Huntington's disease; head trauma; cancer;
KW   ds.
XX
OS   Drosophila sp.
XX
PN   WO200112238-A1.
XX
PD   22-FEB-2001.
XX
PF   14-AUG-2000; 2000WO-US022496.
XX
PR   12-AUG-1999;   99US-0148933P.
PR   12-AUG-1999;   99US-0148934P.
PR   18-JAN-2000; 2000US-0177047P.
PR   19-MAY-2000; 2000US-0205720P.
XX
PA   (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
PI   Benzer S,  Kazemi-Esfarjani P;
XX
DR   WPI; 2001-147537/15.
XX
PT   Identifying genes or other compounds that modulate polyglutamine
PT   toxicity, useful for treating Alzheimer's disease, Parkinson's disease
PT   and Creutzfeldt-Jakob disease.
XX
PS   Disclosure; Fig 1A; 275pp; English.
XX
CC   The present invention describes a method of screening for genes which
CC   modulate polyglutamine toxicity using animal models with polyglutamine
CC   sequences that cause toxicity in the animal. The model is preferably
CC   Drosophila, and toxic polyglutamine sequences include the human and
CC   Drosophila heat shock protein 40/HDJ1, tetratricopeptide repeat protein 2
CC   (TPR2) and myeloid leukaemia factor 1 (MLF) genes. The model is useful
CC   for identifying treatments for neurodegenerative and proliferative
CC   disorders, including Alzheimer's disease, Parkinson's disease,
CC   Creutzfeldt-Jacob's disease (CJD), bovine spongiform encephalopathy
CC   (BSE), Huntington's disease, Machado-Joseph disease, spinocerebellar
CC   ataxias, dentatorubropallidoluysian atrophy, Kennedy's disease, stroke,
CC   head trauma and cancer
XX
SQ   Sequence 486 BP; 193 A; 164 C; 108 G; 21 T; 0 U; 0 Other;

  Query Match             3.6%;  Score 40.4;  DB 4;  Length 486;
  Best Local Similarity   45.2%;  Pred. No. 0.46;
  Matches  149;  Conservative    0;  Mismatches  181;  Indels    0;  Gaps    0;

Qy         82 TTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTG 141
              ||   | | |||| | |      | |   | |  || | ||     ||  |  |   ||
Db        375 TTGCTGCTGCTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTG 316
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```
Qy        142 CACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTA 201
              |  | | |||| |||    | | | |   ||||    |||  |||| |   || |   |
Db        315 CTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGCTGCTGCTG 256

Qy        202 TTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAG 261
              || | ||| |  ||        | ||  |  |||||  ||   ||   |    || || |
Db        255 TTGCTGTTGTTGTTGCTGTTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTGCTG 196

Qy        262 GAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTG 321
                | |  |     || | |||       | | | |  |  ||||   | | | |  ||||
Db        195 CTGCTGTTGCTGTTGCTGCTGCTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTG 136

Qy        322 TTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTT 381
              | | |  |  | |  | |||  | | ||  |  | | | |||  |   |   |  ||
Db        135 CTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTG 76

Qy        382 GGTGTCCACATGTGGGACGGGGGTAGGGCC 411
                | |  || |||  |  |  |||||
Db         75 TTGCTGCTGCTGGGGGGTTGACGGTGGGCC 46


RESULT 4
AAQ03405/c
ID   AAQ03405 standard; DNA; 1057 BP.
XX
AC   AAQ03405;
XX
DT   25-MAR-2003  (revised)
DT   10-MAR-2003  (revised)
DT   19-AUG-1990  (first entry)
XX
DE   Streptomyces gene encoding prepro xylanase.
XX
KW   Secretory expression vector; actinomycetes; Streptomyces; xylanase gene;
KW   endo-1,4-beta-D-xylanase; EC-3.2.1.8; endo-1,3-beta-D-xylanase;
KW   EC-3.2.1.32.
XX
OS   Streptomyces sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             416. .475
FT                   /*tag=  a
XX
PN   JP02002377-A.
XX
PD   08-JAN-1990.
XX
PF   08-JUN-1988;   88JP-00140990.
XX
PR   08-JUN-1988;   88JP-00140990.
XX
PA   (BANY ) BANYU PHARM CO LTD.
XX
DR   WPI; 1990-053427/08.
DR   P-PSDB; AAR03202.
XX
PT   DNA fragment for manifestation secretory vector for actinomycetes - using
PT   Streptomyces spp. as host.
XX
PS   Page 876; Fig 3; 17pp; Japanese.
XX
CC   Streptomyces or E. coli transformed with a secretory expression vector
CC   contg. the sequence efficiently secrete the protein into the culture
CC   medium. This sequence is identical to that of patent JO 2002-379-A.
CC   (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003
CC   to correct PR field.)
XX
SQ   Sequence 1057 BP; 186 A; 390 C; 336 G; 145 T; 0 U; 0 Other;

  Query Match             3.6%;  Score 40.4;  DB 2;  Length 1057;
  Best Local Similarity   44.8%;  Pred. No. 0.64;
  Matches  155;  Conservative    0;  Mismatches  191;  Indels    0;  Gaps    0;

Qy        255 GTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCA 314
              | ||  |  |  ||   | | ||    || |  |  |||        |||  ||| | ||
Db        784 GGCGTTGTACCGGGTCGTCTTGTAGATGTCGTAGGTGCCGCCGTCGCTGTGGACGGTGCC 725

Qy        315 GAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG 374
                |||  |  | || ||| |||  |  || |   | || || | |   ||  |      |
Db        724 CCGGTACTCGCCGGTGGGCCGGTAGCTGCCCCAGTTGTCGACGATGTAGTACTCGACGAG 665

Qy        375 GGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCA 434
                |  | |  |||||   || |     |     | |  | | |||| ||||       |
Db        664 CGGGTTGGAGGTCCAGCCGTAGAGGCAGCCGTAGCCGTTGCCCGACGGGTTGAACCAGCC 605

Qy        435 GTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTC 494
              |  | || |||||| ||  |   |||  | | |    ||  | || |  |   |  |  | |
Db        604 GGTGTACCGGACGGTCCGGCGCCCGCCGTTGGCCCAGCCCTTGCCGGCCACGAAGTTGCC 545

Qy        495 GTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAG 554
              |      |||  ||   || ||  | |    |          | || | ||  | |
Db        544 GCAGTTGGTCCACCGGGTGCTGTAGCTGCCGCCGCCGTTGAGCGTCATGGAGACGGACCC 485

Qy        555 GAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600
              |  |  | | |   | ||||| | || ||   |||| | |  |||
Db        484 GCCGCCGTCGGTCCAGAACGAGTAGTACATGCCGTCGTACCCGGTC 439


RESULT 5
ABZ11846
ID   ABZ11846 standard; cDNA; 926 BP.
XX
AC   ABZ11846;
XX
DT   20-JAN-2003  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 728.
XX
KW   Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW   cell-proliferative disorder; neurodegenerative disease; bacterial;
KW   Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW   multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW   arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW   antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW   haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
KW   antiarthritic; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200270539-A2.
XX
PD   12-SEP-2002.
XX
PF   05-MAR-2002; 2002WO-US005095.
XX
PR   05-MAR-2001; 2001US-00799451.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Zhou P,  Goodrich RW,  Asundi V,  Zhang J,  Zhao QA,  Ren F;
PI   Xue AJ,  Yang Y,  Ma Y,  Yamazaki V,  Chen R,  Wang Z,  Ghosh M;
PI   Wehrman T,  Wang J,  Wang D,  Drmanac RT;
XX
DR   WPI; 2002-759812/82.
DR   P-PSDB; ABP69629.
XX
PT   New polynucleotides comprising sequences assembled from expressed
PT   sequence tags (ESTs), useful for treating cell-proliferative,
PT   neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT   or coagulation disorders.
XX
PS   Claim 1; SEQ ID NO 728; 1012pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated polynucleotide (I) comprising a
CC   nucleotide sequence selected from any of 948 sequences (ABZ11119-
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CC   ABZ12066) or their mature protein coding portion, active domain coding
CC   protein or complementary sequences. The polynucleotides are useful for
CC   identifying expressed genes or for physical mapping of human genome. The
CC   encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
CC   markers, as a food supplement, for generating antibodies, in medical
CC   imaging, screening and diagnostic assays and for treating cell-
CC   proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC   or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC   diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC   platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC   or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC   arthritis, etc. Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic format
CC   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 926 BP; 159 A; 240 C; 307 G; 220 T; 0 U; 0 Other;

  Query Match             3.5%;  Score 40.2;  DB 6;  Length 926;
  Best Local Similarity   47.8%;  Pred. No. 0.69;
  Matches  117;  Conservative    0;  Mismatches  128;  Indels    0;  Gaps    0;

Qy         77 GGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACC 136
Db        510 GGGGGCTGTGGTTCCTGTGGGGGCTCCAAGGGGGGCTGTGGCTCCTGTGGGGGCTCCAAG 569

Qy        137 ACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCC 196
Db        570 GGGGGCTGTGGTTCTTGTGGGGGCTCCAAGGGGGGCTGTGGCTCCTGTGGGGGCTCCAAA 629

Qy        197 ACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGT 256
Db        630 GGTGGCTGTGGTTCCTGTGGGGGCTCCAAGGGGGGCTGTGGTTCTTGTGGCTGCTCCCAG 689

Qy        257 CGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGA 316
Db        690 TGCAATTGCTGTAAGCCCTGCTGCTGTCCCTCAGGCTGTGGATCCTGCTGCCAGTCCAGC 749

Qy        317 GGTTG 321
Db        750 TGCTG 754


RESULT 6
AAQ23092/c
ID   AAQ23092 standard; DNA; 543 BP.
XX
AC   AAQ23092;
XX
DT   25-MAR-2003  (revised)
DT   17-AUG-1992  (first entry)
XX
DE   Antigen tc-7a gene.
XX
KW   Oocysts; MAb 12-07; sporozoite; ss.
XX
OS   Eimeria tenella.
XX
PN   WO9204460-A.
XX
PD   19-MAR-1992.
XX
PF   05-SEP-1991;   91WO-US006430.
XX
PR   12-SEP-1990;   90US-00581693.
XX
PA   (GEMX ) GENEX CORP.
XX
PI   Jacobson JW,  Strausberg RL,  Wilson SD,  Pope SH,  Strausberg SL;
PI   Ruff MD,  Augustine PC,  Danforth HD;
XX
DR   WPI; 1992-114365/14.
DR   P-PSDB; AAR22392.
XX
PT   Vaccine against avian coccidiosis - comprising recombinant eimeria
PT   antigen ac-18 or ac-6b gene, or microorganisms expressing them.
XX
PS   Claim 5; Page 39 + Fig 5; 56pp; English.
XX
CC   To identify antigens of E. tenella, expression libraries were prepd. in
CC   lambda vector, lambda gt11, using cDNA prepd. from polyA mRNA isolated
CC   from E. tenella oocysts. The cDNA expression library was screened with
CC   monoclonal antibody (MAb) 12-07 which was raised against the sporozoite
CC   stage of E. tenella. The library to be screened was plated on a host that
CC   allows lysis and plaque formation. During induction of the antigens
CC   encoded by the phage, the plaques were identified by screening the
CC   filters with Mab 12-07. The cDNA inserts from the MAb 12-07 positive
CC   phage were cloned into bacteriophage M13 and subjected to sequence
CC   analysis. Following sequence analysis, E. tenella antigen tc-7a was
CC   identified. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 543 BP; 229 A; 135 C; 161 G; 18 T; 0 U; 0 Other;

  Query Match             3.5%;  Score 40;  DB 2;  Length 543;
  Best Local Similarity   47.3%;  Pred. No. 0.62;
  Matches  121;  Conservative    0;  Mismatches  135;  Indels    0;  Gaps    0;

Qy         89 TCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGG 148
Db        450 TCCCCCAGGCTTACCTGCTGCTGATGCTGCTGCTGCTCTTGCTGCAGCTGCTGTTGTTGC 391

Qy        149 TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT 208
Db        390 TGCTGTTGCTGCTTGTGTTTTCGCTTTCTCTGCTTCTGCTGCTGCTCCTGCTGCTCCTTC 331

Qy        209 TCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGC 268
Db        330 GGTTTCTGTTCGTGCTTCCGCTGCCTTTGCTGCTCCTGCTGCTCCTGCTGCGGCTGTCGC 271

Qy        269 AGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGG 328
Db        270 TGCAGCTGGTGCTGCTGCAGCTCCTGTTGCTGCTGCTGCTGCTGCAGCTGGTGCTGCTGC 211

Qy        329 AGGGTCGGGGGTAGCT 344
Db        210 AGCTGGTGCTGCAGCT 195


RESULT 7
ABS78695
ID   ABS78695 standard; DNA; 1011 BP.
XX
AC   ABS78695;
XX
DT   29-AUG-2003  (revised)
DT   16-DEC-2002  (first entry)
XX
DE   S. aerocolonigenes DNA encoding UNBU.
XX
KW   Enediyne; warhead structure; ds; cancer; cytostatic; PKSE; gene;
KW   polyketide synthase; TEBC; UNBL; UNBV; UNBU; genetic engineering;
KW   thioesterase unique to enediyne biosynthetic loci;
KW   unique to enediyne biosynthetic loci.
XX
OS   Lechevalieria aerocolonigenes.
XX
PN   CA2387401-A1.
XX
PD   04-SEP-2002.
XX
PF   21-MAY-2002; 2002CA-02387401.
XX
PR   21-MAY-2001; 2001US-0291959P.
PR   03-DEC-2001; 2001US-0334604P.
XX
PA   (ECOP-) ECOPIA BIOSCIENCES INC.
XX
```

PI Staffa A, Farnet CM, Zazopoulos E;
XX
DR WPI; 2002-692206/75.
DR P-PSDB; ABG97456.
XX
PT New enediyne polyketide synthase polypeptides involved in synthesis of
PT the warhead structure in enediyne compounds useful in design of new
PT enediyne compounds and identification of new enediyne biosynthetic loci.
XX
PS Claim 1; Page 247; 310pp; English.
XX
CC The invention relates to purified/isolated polypeptides involved in
CC synthesis of the warhead structure in enediyne compounds, or their
CC fragments or sequences 75% homologous to them. The polypeptides comprise
CC five families of proteins: PKSE (polyketide synthase), TEBC (thioesterase
CC unique to enediyne biosynthetic loci), UNBL, UNBV and UNBU (unique to
CC enediyne biosynthetic loci L, B and V). The proteins are isolated from 10
CC different micro-organisms. Also included are the nucleic acids encoding
CC the proteins, antibodies specifically binding the polypeptides, and a
CC computer system/computer readable medium comprising the sequences
CC referred to above. The polypeptides and polynucleotides are useful in
CC genetic engineering to design new enediyne compounds (which are potential
CC anti-cancer drugs) and identify new enediyne biosynthetic loci. They can
CC also be used to identify enediyne biosynthesis genes/gene fragments from
CC samples containing genomic DNA e.g. in biomass from an environmental
CC source (such as a mixed microbial culture/population of organisms), pure
CC cultures or genomic libraries obtained from a mixed population of
CC organisms or from pure culture. The present sequence encodes an enzyme of
CC the enediyne warhead structure biosynthetic pathway. (Updated on 29-AUG-
CC 2003 to standardise OS field)
XX
SQ Sequence 1011 BP; 138 A; 331 C; 348 G; 194 T; 0 U; 0 Other;

Query Match 3.5%; Score 39.4; DB 6; Length 1011;
Best Local Similarity 48.4%; Pred. No. 1.2;
Matches 109; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

```
Qy          96 GGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCT 155
               |||||     || | |   |    | |   |  | | || ||||| | |||
Db         507 GGAGTGGACCAGCGGCGTCGTCGACGCGCTGATCCCCGTCCTCCTGCTCGCGGCCGGCAC 566

Qy         156 GGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTT 215
               |  ||| |   ||| |||| | | |  | ||||  |||  |  |   |    | ||
Db         567 GATGCTCAACGCGAAGCTGACGAAGAAGATCCCGCTGATCCTGGGCTGGGTGGGTGGGTT 626

Qy         216 CGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGT 275
               ||  |   |   |||  ||  |||  | |  |  ||| ||||   |   |   || | |
Db         627 CGTCCTGCAGGCCGTGCTGCGTTCGGCCTTCACCGACCTGTCGATCGTCAGTGCGGTCCT 686

Qy         276 GGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTT 320
               |    | ||||    | ||||| || |||||||   | | | | |
Db         687 GCCGATCACCGGAACAGCGTTCATCCTGTTCACCAACTACATGAT 731
```

RESULT 8
ABL09597/c
ID ABL09597 standard; cDNA; 922 BP.
XX
AC ABL09597;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 23273.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB65494.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 23273; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 922 BP; 231 A; 257 C; 238 G; 196 T; 0 U; 0 Other;

Query Match 3.4%; Score 39; DB 4; Length 922;
Best Local Similarity 48.4%; Pred. No. 1.5;
Matches 108; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

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Qy         239 CGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCC 298
               ||| |||||  ||  | |||  | |  || |  | ||  |  | |  |  |  |||
Db         383 CGTCCATGGGGCAGAACTCGAGAGTGGCGCCGTCCTTGTGCTGTAACACCAGCCGATTCT 324

Qy         299 TCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT 358
               |   |  |||  |  | |  ||  |     |  ||| ||    |  ||| |||||||
Db         323 TGTGGAACACCATGTCGGGCAGGTGGGGCAGCTGCAGGGAGTGCTGGTAGTGGCAGAGGT 264

Qy         359 TTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCG 418
               | |    | | || | |  | ||    ||| ||  ||       || ||   || |||
Db         263 CGCAGCGGTCGGCCGAGTCCTTGGGACAGCACTTGGCGGTGCCCAGTTGGCAGCTGCTCT 204

Qy         419 ACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAA 461
               | || | |  | |   ||  ||| || || |||||    |||
Db         203 TCAGGATGTGCGACTTCTCATACTTGATGGCCCAGTCGTGGAA 161
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RESULT 9
AAD56497
ID AAD56497 standard; DNA; 789 BP.
XX
AC AAD56497;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human VLCFABE MOOSE00004 DNA from ctg13284.
XX
KW Human; very long chain fatty acid biosynthesis enzyme; VLFA; VLCFABE;
KW non-insulin dependent diabetes mellitus; NIDDM; adrenoleukodystrophy;
KW ALD; autosomal dominant macular dystrophy; adMD; Alzheimer's disease;
KW coronary heart disease; stroke; myocardial infarction; gene therapy;
KW gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .789
FT /*tag= a

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FT                   /product= "Human VLCFABE protein"
FT                   /note= "No start and stop codon"
FT                   /partial
XX
PN   WO2003040392-A2.
XX
PD   15-MAY-2003.
XX
PF   04-NOV-2002; 2002WO-IB004610.
XX
PR   06-NOV-2001; 2001US-0332864P.
XX
PA   (DECO-) DECODE GENETICS EHF.
XX
PI   Betts M,  Sigurdsson GT;
XX
DR   WPI; 2003-430674/40.
DR   P-PSDB; AAE37330.
XX
PT   New isolated nucleic acid molecule comprising a very long chain fatty
PT   acid biosynthesis enzyme nucleic acid, useful for treating a disease
PT   associated with the biosynthesis enzyme nucleic acid.
XX
PS   Claim 1; Page 86; 90pp; English.
XX
CC   The invention relates to very long chain fatty acid (VLFA) biosynthesis
CC   enzymes (VLCFABE) and polynucleotides encoding such proteins. Sequences
CC   of the invention are useful for treating VLCFABE diseases such as non-
CC   insulin dependent diabetes mellitus (NIDDM), adrenoleukodystrophy (ALD),
CC   autosomal dominant macular dystrophy (adMD), Alzheimer's disease and
CC   coronary heart diseases such as stroke and myocardial infarction. They
CC   are also used in gene therapy. The present sequence is human VLCFABE DNA
XX
SQ   Sequence 789 BP; 204 A; 215 C; 172 G; 198 T; 0 U; 0 Other;

  Query Match             3.3%;  Score 37.8;  DB 7;  Length 789;
  Best Local Similarity   47.3%;  Pred. No. 3.1;
  Matches  114;  Conservative    0;  Mismatches  127;  Indels    0;  Gaps    0;

Qy         65 AGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGT 124
Db        443 ACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCATCATGT 502

Qy        125 GTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACC 184
Db        503 ACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCATGCTCA 562

Qy        185 TGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCA 244
Db        563 TCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCACGTACA 622

Qy        245 TGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGT 304
Db        623 TCTGGAGGCAGGATCAGGGATGCCACACCACGATGGAACACTTATTCTGGTCCTTCATCT 682

Qy        305 T 305
Db        683 T 683


RESULT 10
ABZ22164
ID   ABZ22164 standard; cDNA; 810 BP.
XX
AC   ABZ22164;
XX
DT   12-MAR-2003  (first entry)
XX
DE   Human elongase HSELO1-like protein encoding cDNA SEQ ID NO:5.
XX
KW   Human; elongase; elongase HSELO1-like protein; enzyme; cytostatic;
KW   antidiabetic; antiasthmatic; anti-HIV; antiparkinsonian; nootropic;
KW   neuroprotective; tranquilliser; antimigraine; analgesic; neuroleptic;
KW   cerebroprotective; gene therapy; cancer; diabetes; CNS disorder; asthma;
KW   metabolic disease; central nervous system disorder; COPD; dementia;
KW   Parkinson's disease; multiple sclerosis; stroke; Alzheimer's disease;
KW   Huntington's disease; Creutzfeldt-Jakob disease; HIV; schizophrenia;
KW   psychosis; attention deficit disorder; headache pain; migraine; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .810
FT                   /*tag=  a
FT                   /partial
FT                   /product= "elongase HSELO1-like protein"
FT                   /note= "no stop codon given"
XX
PN   WO200262974-A2.
XX
PD   15-AUG-2002.
XX
PF   07-FEB-2002; 2002WO-EP001262.
XX
PR   08-FEB-2001; 2001US-0267135P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Zhu Z;
XX
DR   WPI; 2002-636596/68.
DR   P-PSDB; ABP56418.
XX
PT   New isolated human elongase HSELO1-like polynucleotide and encoded
PT   peptide, useful for treating, preventing and ameliorating diseases such
PT   as COPD, cancer, metabolic disease, diabetes, CNS disorders, or asthma.
XX
PS   Claim 1; Fig 5; 128pp; English.
XX
CC   The present sequence encodes a human elongase HSELO1-like protein (I).
CC   (I) has cytostatic, antidiabetic, antiasthmatic, anti-HIV, nootropic,
CC   antiparkinsonian, neuroprotective, tranquilliser, antimigraine,
CC   analgesic, neuroleptic and cerebroprotective activities, and can be used
CC   in gene therapy. (I) can be used in the treatment of a disease, such as
CC   cancer, diabetes, central nervous system (CNS) disorder, asthma,
CC   metabolic disease or COPD. The human elongase HSELO1-like protein is
CC   useful in preventing, treating or ameliorating the diseases cited above,
CC   including Parkinson's disease, dementia, multiple sclerosis, stroke, HIV,
CC   Alzheimer's disease, Huntington's disease, Creutzfeldt-Jakob disease,
CC   schizophrenia, psychosis, attention deficit disorders, pain associated
CC   with CNS disorders, with cancer, or headache pain, e.g. migraine. It can
CC   also be useful in identifying test compounds that may act as activators
CC   or inhibitors at the enzyme's active site, or in raising specific
CC   antibodies that can block and effectively reduce its activity
XX
SQ   Sequence 810 BP; 195 A; 231 C; 181 G; 203 T; 0 U; 0 Other;

  Query Match             3.3%;  Score 37.8;  DB 6;  Length 810;
  Best Local Similarity   47.3%;  Pred. No. 3.1;
  Matches  114;  Conservative    0;  Mismatches  127;  Indels    0;  Gaps    0;

Qy         65 AGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGT 124
Db        485 ACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCATCATGT 544

Qy        125 GTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACC 184
Db        545 ACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCATGCTCA 604

Qy        185 TGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCA 244
Db        605 TCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCACGTACA 664

Qy        245 TGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGT 304
Db        665 TCTGGAGGCAGGATCAGGGATGCCACACCACGATGGAACACTTATTCTGGTCCTTCATCT 724
```

```
Qy        305 T 305
              |
Db        725 T 725


RESULT 11
AAD42270
ID   AAD42270 standard; DNA; 813 BP.
XX
AC   AAD42270;
XX
DT   04-NOV-2002  (first entry)
XX
DE   Human ELG6 gene.
XX
KW   Human; elongase; therapy; enzyme; polyunsaturated fatty acid; sinusitis;
KW   PUFA disorder; cardiovascular disorder; articular cartilage degradation;
KW   peripheral vascular disease; atherosclerosis; coronary artery disease;
KW   inflammatory disorder; pancreatitis; asthma; gastrointestinal disorder;
KW   osteoarthritis; rheumatoid arthritis; congenital liver disease; cancer;
KW   acne; Sjogren's syndrome; body weight disorder; cerebrovascular disease;
KW   acute respiratory distress syndrome; hypercholesterolaemia; alcoholism;
KW   postviral fatigue; psychiatric disorder; pre-menstrual syndrome; eczema;
KW   Alzheimer's syndrome; hypertriglyceridaemia; cystic fibrosis; anorexia;
KW   autoimmune disorder; obesity; cachexia; viral disease; endometriosis;
KW   dyslipidaemia; atopic disorder; diabetes; ELG6; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .813
FT                   /*tag=  a
FT                   /product= "ELG6 protein"
XX
PN   WO200244320-A2.
XX
PD   06-JUN-2002.
XX
PF   29-NOV-2001; 2001WO-CA001705.
XX
PR   29-NOV-2000; 2000US-0253728P.
XX
PA   (XENO-) XENON GENETICS INC.
XX
PI   Winther MD,  Knickle LC,  Haardt M,  De Antueno RJ,  Jenkins DK;
PI   Nwaka SO,  Allen SJ,  Ponton A,  Goldberg YP;
XX
DR   WPI; 2002-547693/58.
DR   P-PSDB; AAE24550.
XX
PT   Novel elongase polypeptide, genes and their control regions useful in
PT   determining compositions for treating polyunsaturated fatty acid disorder
PT   e.g. cardiovascular, inflammation, gastrointestinal disorders and cancer.
XX
PS   Claim 1; Page 160; 173pp; English.
XX
CC   The invention relates to novel elongase polypeptides, genes and their
CC   control regions. Sequences of the invention are used in the diagnosis and
CC   treatment of polyunsaturated fatty acid (PUFA) disorders such as
CC   cardiovascular disorders (e.g. atherosclerosis, coronary artery disease),
CC   inflammatory disorders (e.g. sinusitis, pancreatitis, asthma,
CC   osteoarthritis, rheumatoid arthritis, acne), Sjogren's syndrome, body
CC   weight disorders (e.g. obesity, cachexia and anorexia), viral diseases
CC   and postviral fatigue, gastrointestinal disorders, eczema, psychiatric
CC   disorders, cancer, congenital liver disease, alcoholism, Alzheimer's
CC   syndrome, cystic fibrosis, endometriosis, pre-menstrual syndrome,
CC   hypercholesterolaemia, hypertriglyceridaemia, dyslipidaemia, peripheral
CC   vascular disease, cerebrovascular disease, autoimmune disorders, acute
CC   respiratory distress syndrome, atopic disorders, articular cartilage
CC   degradation, diabetes and diabetic complication. The present sequence is
CC   human elongase gene (ELG6)
XX

SQ   Sequence 813 BP; 196 A; 231 C; 182 G; 204 T; 0 U; 0 Other;

  Query Match             3.3%;  Score 37.8;  DB 6;  Length 813;
  Best Local Similarity   47.3%;  Pred. No. 3.1;
  Matches  114;  Conservative    0;  Mismatches  127;  Indels    0;  Gaps    0;

Qy         65 AGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGT 124
              | || | |   |  ||      ||||| |      | |||  | |     |   ||  ||
Db        485 ACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCATCATGT 544

Qy        125 GTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACC 184
                ||  || ||   ||| |  | |       ||   | ||     | | || ||||| |
Db        545 ACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCATGCTCA 604

Qy        185 TGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCA 244
              |  |  ||| ||  | || | | | | | | || ||| || ||  |||  |  ||| ||
Db        605 TCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCACGTACA 664

Qy        245 TGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGT 304
              |       |||  |||| || ||  |  | |      |  ||  || | |||| |
Db        665 TCTGGAGGCAGGATCAGGGATGCCACACCACGATGGAACACTTATTCTGGTCCTTCATCT 724

Qy        305 T 305
              |
Db        725 T 725


RESULT 12
ABZ22162
ID   ABZ22162 standard; cDNA; 813 BP.
XX
AC   ABZ22162;
XX
DT   12-MAR-2003  (first entry)
XX
DE   Human elongase HSELO1-like protein encoding cDNA SEQ ID NO:1.
XX
KW   Human; elongase; elongase HSELO1-like protein; enzyme; cytostatic;
KW   antidiabetic; antiasthmatic; anti-HIV; antiparkinsonian; nootropic;
KW   neuroprotective; tranquilliser; antimigraine; analgesic; neuroleptic;
KW   cerebroprotective; gene therapy; cancer; diabetes; CNS disorder; asthma;
KW   metabolic disease; central nervous system disorder; COPD; dementia;
KW   Parkinson's disease; multiple sclerosis; stroke; Alzheimer's disease;
KW   Huntington's disease; Creutzfeldt-Jakob disease; HIV; schizophrenia;
KW   psychosis; attention deficit disorder; headache pain; migraine; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .813
FT                   /*tag=  a
FT                   /product= "elongase HSELO1-like protein"
XX
PN   WO200262974-A2.
XX
PD   15-AUG-2002.
XX
PF   07-FEB-2002; 2002WO-EP001262.
XX
PR   08-FEB-2001; 2001US-0267135P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Zhu Z;
XX
DR   WPI; 2002-636596/68.
DR   P-PSDB; ABP56418.
XX
PT   New isolated human elongase HSELO1-like polynucleotide and encoded
PT   peptide, useful for treating, preventing and ameliorating diseases such
PT   as COPD, cancer, metabolic disease, diabetes, CNS disorders, or asthma.
XX
PS   Claim 1; Fig 1; 128pp; English.
```

```
XX
CC   The present sequence encodes a human elongase HSELO1-like protein (I).
CC   (I) has cytostatic, antidiabetic, antiasthmatic, anti-HIV, nootropic,
CC   antiparkinsonian, neuroprotective, tranquilliser, antimigraine,
CC   analgesic, neuroleptic and cerebroprotective activities, and can be used
CC   in gene therapy. (I) can be used in the treatment of a disease, such as
CC   cancer, diabetes, central nervous system (CNS) disorder, asthma,
CC   metabolic disease or COPD. The human elongase HSELO1-like protein is
CC   useful in preventing, treating or ameliorating the diseases cited above,
CC   including Parkinson's disease, dementia, multiple sclerosis, stroke, HIV,
CC   Alzheimer's disease, Huntington's disease, Creutzfeldt-Jakob disease,
CC   schizophrenia, psychosis, attention deficit disorders, pain associated
CC   with CNS disorders, with cancer, or headache pain, e.g. migraine. It can
CC   also be useful in identifying test compounds that may act as activators
CC   or inhibitors at the enzyme's active site, or in raising specific
CC   antibodies that can block and effectively reduce its activity
XX
SQ   Sequence 813 BP; 196 A; 231 C; 182 G; 204 T; 0 U; 0 Other;

  Query Match             3.3%;  Score 37.8;  DB 6;  Length 813;
  Best Local Similarity   47.3%;  Pred. No. 3.1;
  Matches  114;  Conservative    0;  Mismatches  127;  Indels    0;  Gaps    0;

Qy         65 AGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGT 124
              | || | |   |  ||     ||||| |      | |||   | |      |  ||  ||
Db        485 ACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCATCATGT 544

Qy        125 GTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACC 184
                ||  || ||   ||| |  | |      ||   | ||     | | || ||||||  |
Db        545 ACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCATGCTCA 604

Qy        185 TGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCA 244
              |  |   ||| ||  | || | | | | | | || ||| || ||  |||  |  ||| ||
Db        605 TCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCACGTACA 664

Qy        245 TGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGT 304
              |      |||   ||||  || ||   | | |      |   ||   || | |||| |
Db        665 TCTGGAGGCAGGATCAGGGATGCCACACCACGATGGAACACTTATTCTGGTCCTTCATCT 724

Qy        305 T 305
              |
Db        725 T 725


RESULT 13
ABN86918
ID   ABN86918 standard; cDNA; 815 BP.
XX
AC   ABN86918;
XX
DT   29-JUL-2002  (first entry)
XX
DE   Human NOV6a encoding cDNA sequence SEQ ID NO:17.
XX
KW   Human; NOVX; cytostatic; antiarteriosclerotic; cardiovascular; lymphoma;
KW   antidiabetic; immunosuppressive; neuroprotective; gene therapy; cancer;
KW   cardiomyopathy; atherosclerosis; cell signal processing; diabetes; AIDS;
KW   metabolic pathway modulation; neoplastic; neurological disorder; asthma;
KW   adenocarcinoma; prostate cancer; uterus cancer; immune response;
KW   Crohn's disease; multiple sclerosis; Graft versus host disease;
KW   chromosome 10; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .813
FT                   /*tag= a
FT                   /product= "NOV6a"
FT                   /note= "Cold inducible glycoprotein 30-like protein"
XX
PN   WO200230974-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US031922.
XX
PR   12-OCT-2000; 2000US-0240113P.
PR   16-OCT-2000; 2000US-0240625P.
PR   16-OCT-2000; 2000US-0240637P.
PR   16-OCT-2000; 2000US-0240648P.
PR   16-OCT-2000; 2000US-0240662P.
PR   16-OCT-2000; 2000US-0240669P.
PR   16-OCT-2000; 2000US-0240703P.
PR   16-OCT-2000; 2000US-0240732P.
PR   16-OCT-2000; 2000US-0241190P.
PR   18-JAN-2001; 2001US-0262455P.
XX
PA   (CURA-) CURAGEN CORP.
PA   (MILL/) MILLET I.
XX
PI   Grosse WM,  Alsobrook JP,  Lepley DM,  Burgess CE,  Mishra V;
PI   Kekuda R,  Li L,  Padigaru M,  Shimkets RA,  Zerhusen BD,  Spytek KA;
PI   Edinger S,  Gerlach V,  Macdougall J,  Stone D,  Gunther E,  Ellerman K;
XX
DR   WPI; 2002-444172/47.
DR   P-PSDB; ABB78812.
XX
PT   New NOVX polypeptides and polynucleotides, useful for treating or
PT   preventing a NOVX-associated disorder or a pathological state in a
PT   subject, particularly a human, e.g. cardiomyopathy, atherosclerosis,
PT   cancer or diabetes.
XX
PS   Claim 9; Page 51; 227pp; English.
XX
CC   The present invention describes novel human proteins designated NOVX
CC   (where X is 1, 2a, 2b, 2c, 2d, 3, 4, 5, 6a, 6b, 7, 8, or 9). NOV1 is a
CC   tyrosine-protein kinase 6-like protein; NOV2a-d are keratin 4-like
CC   proteins; NOV3 is a collagen-like protein; NOV4 is a cystatin B-like
CC   protein; NOV5 is a serotonin receptor-like protein; NOV6a and NOV65v are
CC   cold inducible glycoprotein 30-like proteins; NOV7 is a matrilin-2-like
CC   protein; NOV8 is a leukocyte surface antigen (CD53)-like protein; and
CC   NOV9 is a tyrosine kinase-like protein. NOVX sequences have cytostatic,
CC   antiarteriosclerotic, cardiovascular, antidiabetic, immunosuppressive and
CC   neuroprotective activities, and can be used in gene therapy. The NOVX
CC   sequences can be used in therapeutics, particularly for treating,
CC   preventing or alleviating a NOVX-associated disorder or a pathological
CC   state in a subject, particularly a human. These disorders include
CC   cardiomyopathy, atherosclerosis, a disorder related to cell signal
CC   processing and metabolic pathway modulation or diabetes. The NOVX
CC   sequences are also useful for determining the presence of or
CC   predisposition to a disease associated with altered levels of NOVX
CC   polypeptide or nucleic acid, particularly cancer. The NOVX sequences are
CC   especially useful in therapeutic or prophylactic applications for
CC   neoplastic or neurological disorders, and in the treatment of
CC   adenocarcinoma, lymphoma, prostate cancer, uterus cancer, immune
CC   response, AIDS, asthma, Crohn's disease, multiple sclerosis or Graft
CC   versus host disease. The present sequence encodes the human NOV6a protein
CC   from the present invention. NOV6a is located to chromosome 10
XX
SQ   Sequence 815 BP; 196 A; 231 C; 183 G; 205 T; 0 U; 0 Other;

  Query Match             3.3%;  Score 37.8;  DB 6;  Length 815;
  Best Local Similarity   47.3%;  Pred. No. 3.1;
  Matches  114;  Conservative    0;  Mismatches  127;  Indels    0;  Gaps    0;

Qy         65 AGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGT 124
              | || | |   |  ||     ||||| |      | |||   | |      |  ||  ||
Db        485 ACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCATCATGT 544

Qy        125 GTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACC 184
                ||  || ||   ||| |  | |      ||   | ||     | | || ||||||  |
Db        545 ACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCATGCTCA 604

Qy        185 TGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCA 244
              |  |   ||| ||  | || | | | | | | || ||| || ||  |||  |  ||| ||
Db        605 TCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCACGTACA 664
```

```
Qy        245 TGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGT 304
              |     |||   ||||  || ||   |  | |       |   ||   || | |||| |
Db        665 TCTGGAGGCAGGATCAGGGATGCCACACCACGATGGAACACTTATTCTGGTCCTTCATCT 724

Qy        305 T 305
              |
Db        725 T 725
```

RESULT 14
ABN86919
ID ABN86919 standard; cDNA; 815 BP.
XX
AC ABN86919;
XX
DT 29-JUL-2002 (first entry)
XX
DE Human NOV6b encoding cDNA sequence SEQ ID NO:19.
XX
KW Human; NOVX; cytostatic; antiarteriosclerotic; cardiovascular; lymphoma;
KW antidiabetic; immunosuppressive; neuroprotective; gene therapy; cancer;
KW cardiomyopathy; atherosclerosis; cell signal processing; diabetes; AIDS;
KW metabolic pathway modulation; neoplastic; neurological disorder; asthma;
KW adenocarcinoma; prostate cancer; uterus cancer; immune response;
KW Crohn's disease; multiple sclerosis; Graft versus host disease;
KW chromosome 10; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1. .813
FT   /*tag= a
FT   /product= "NOV6b"
FT   /note= "Cold inducible glycoprotein 30-like protein"
XX
PN WO200230974-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US031922.
XX
PR 12-OCT-2000; 2000US-0240113P.
PR 16-OCT-2000; 2000US-0240625P.
PR 16-OCT-2000; 2000US-0240637P.
PR 16-OCT-2000; 2000US-0240648P.
PR 16-OCT-2000; 2000US-0240662P.
PR 16-OCT-2000; 2000US-0240669P.
PR 16-OCT-2000; 2000US-0240703P.
PR 16-OCT-2000; 2000US-0240732P.
PR 16-OCT-2000; 2000US-0241190P.
PR 18-JAN-2001; 2001US-0262455P.
XX
PA (CURA-) CURAGEN CORP.
PA (MILL/) MILLET I.
XX
PI Grosse WM, Alsobrook JP, Lepley DM, Burgess CE, Mishra V;
PI Kekuda R, Li L, Padigaru M, Shimkets RA, Zerhusen BD, Spytek KA;
PI Edinger S, Gerlach V, Macdougall J, Stone D, Gunther E, Ellerman K;
XX
DR WPI; 2002-444172/47.
DR P-PSDB; ABB78813.
XX
PT New NOVX polypeptides and polynucleotides, useful for treating or
PT preventing a NOVX-associated disorder or a pathological state in a
PT subject, particularly a human, e.g. cardiomyopathy, atherosclerosis,
PT cancer or diabetes.
XX
PS Claim 9; Page 53; 227pp; English.
XX
CC The present invention describes novel human proteins designated NOVX
CC (where X is 1, 2a, 2b, 2c, 2d, 3, 4, 5, 6a, 6b, 7, 8, or 9). NOV1 is a
CC tyrosine-protein kinase 6-like protein; NOV2a-d are keratin 4-like
CC proteins; NOV3 is a collagen-like protein; NOV4 is a cystatin B-like
CC protein; NOV5 is a serotonin receptor-like protein; NOV6a and NOV65v are
CC cold inducible glycoprotein 30-like proteins; NOV7 is a matrilin-2-like
CC protein; NOV8 is a leukocyte surface antigen (CD53)-like protein; and
CC NOV9 is a tyrosine kinase-like protein. NOVX sequences have cytostatic,
CC antiarteriosclerotic, cardiovascular, antidiabetic, immunosuppressive and
CC neuroprotective activities, and can be used in gene therapy. The NOVX
CC sequences can be used in therapeutics, particularly for treating,
CC preventing or alleviating a NOVX-associated disorder or a pathological
CC state in a subject, particularly a human. These disorders include
CC cardiomyopathy, atherosclerosis, a disorder related to cell signal
CC processing and metabolic pathway modulation or diabetes. The NOVX
CC sequences are also useful for determining the presence of or
CC predisposition to a disease associated with altered levels of NOVX
CC polypeptide or nucleic acid, particularly cancer. The NOVX sequences are
CC especially useful in therapeutic or prophylactic applications for
CC neoplastic or neurological disorders, and in the treatment of
CC adenocarcinoma, lymphoma, prostate cancer, uterus cancer, immune
CC response, AIDS, asthma, Crohn's disease, multiple sclerosis or Graft
CC versus host disease. The present sequence encodes the human NOV6b protein
CC from the present invention. NOV6b is located to chromosome 10
XX
SQ Sequence 815 BP; 196 A; 231 C; 183 G; 205 T; 0 U; 0 Other;

  Query Match   3.3%; Score 37.8; DB 6; Length 815;
  Best Local Similarity   47.3%; Pred. No. 3.1;
  Matches 114; Conservative   0; Mismatches 127; Indels   0; Gaps   0;

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Qy        125 GTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACC 184
                ||  || ||   ||| | | |       ||   | ||     | | || ||||| |
Db        545 ACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCATGCTCA 604

Qy        185 TGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCA 244
              |  |   ||| ||  | || | | | | | | || ||| || ||  |||  |  ||| ||
Db        605 TCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCACGTACA 664

Qy        245 TGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGT 304
              |     |||   ||||  || ||   |  | |       |   ||   || | |||| |
Db        665 TCTGGAGGCAGGATCAGGGATGCCACACCACGATGGAACACTTATTCTGGTCCTTCATCT 724

Qy        305 T 305
              |
Db        725 T 725
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RESULT 15
ABZ24216
ID ABZ24216 standard; DNA; 818 BP.
XX
AC ABZ24216;
XX
DT 14-APR-2003 (first entry)
XX
DE Human LCE gene related DNA (sequence Id No. 2).
XX
KW LCE; long chain fatty acyl elongase; p53; cytostatic; gene therapy;
KW cancer; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200299068-A2.
XX
PD 12-DEC-2002.
XX
PF 03-JUN-2002; 2002WO-US017739.
XX
PR 05-JUN-2001; 2001US-0296076P.
PR 10-OCT-2001; 2001US-0328605P.
PR 15-FEB-2002; 2002US-0357253P.

PR 01-MAR-2002; 2002US-0361196P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
PI Karim FD, Keyes LN, Koblizek TI;
XX
DR WPI; 2003-167338/16.
XX
PT Identifying a candidate p53 pathway modulating agent for
PT diagnosing/treating cancer comprises detecting a test agent-biased
PT activity of an assay system comprising a purified long chain fatty acyl
PT elongase (LCE) polypeptide or nucleic acid.
XX
PS Disclosure; Page 50; 69pp; English.
XX
CC The invention relates to identifying a candidate p53 pathway modulating
CC agent that involves assaying a purified LCE (long chain fatty acyl
CC elongase) polypeptide or nucleic acid or its functionally active fragment
CC or derivative, with a test agent. The methods are useful for identifying
CC a candidate p53 pathway modulating agent, modulating a p53 pathway of a
CC cell, or a mammalian cell, diagnosing a disease in a patient, identifying
CC a candidate branching morphogenesis modulating agent, and modulating
CC branching morphogenesis in a mammalian cell. The diseases that can be
CC diagnosed are breast, colon, lung or ovary cancer having greater than 25%
CC expression level. The method is useful for manufacturing a medicament for
CC diagnosing or treating breast, colon, lung or ovary cancer. Sequences
CC ABZ24215-222 represent DNA sequences related to human LCE gene
XX
SQ Sequence 818 BP; 198 A; 232 C; 183 G; 205 T; 0 U; 0 Other;

Query Match 3.3%; Score 37.8; DB 7; Length 818;
Best Local Similarity 47.3%; Pred. No. 3.1;
Matches 114; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

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Qy         65 AGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGT 124
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Db        489 ACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCATCATGT 548

Qy        125 GTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACC 184
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Db        549 ACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCATGCTCA 608

Qy        185 TGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCA 244
              |  |   ||| ||  | || | | | | | | || ||| || ||  |||  |  ||| ||
Db        609 TCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCACGTACA 668

Qy        245 TGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGT 304
              |      |||   ||||  || ||   |  | |      |   ||   || | |||| |
Db        669 TCTGGAGGCAGGATCAGGGATGCCACACCACGATGGAACACTTATTCTGGTCCTTCATCT 728

Qy        305 T 305
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Db        729 T 729
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Search completed: May 8, 2004, 19:18:25
Job time : 337.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:36 ; Search time 59.25 Seconds
(without alignments)
10630.705 Million cell updates/sec

Title: US-10-679-999-14
Perfect score: 1135
Sequence: 1 GTATACCTGTTTTGAGTGTG.....AGGCCCAACAATTACCTAGG 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1245136

Minimum DB seq length: 0
Maximum DB seq length: 1135

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	43	3.8	468	1	US-08-236-311-12	Sequence 12, Appl
	2	43	3.8	468	3	US-08-457-918-12	Sequence 12, Appl
c	3	40	3.5	533	6	5482709-5	Patent No. 5482709
c	4	40	3.5	543	6	5273901-6	Patent No. 5273901
c	5	37.4	3.3	688	3	US-08-998-416-915	Sequence 915, App
	6	37	3.3	505	4	US-09-621-976-15639	Sequence 15639, A
	7	36.4	3.2	1125	4	US-09-252-991A-16469	Sequence 16469, A
c	8	36.2	3.2	615	4	US-09-252-991A-242	Sequence 242, App
	9	36.2	3.2	1041	4	US-09-252-991A-296	Sequence 296, App
c	10	36	3.2	909	4	US-09-252-991A-7481	Sequence 7481, Ap
	11	35.2	3.1	675	4	US-09-252-991A-7278	Sequence 7278, Ap
	12	35	3.1	627	4	US-09-252-991A-3035	Sequence 3035, Ap
	13	35	3.1	630	4	US-09-252-991A-953	Sequence 953, App
	14	35	3.1	720	4	US-09-252-991A-3133	Sequence 3133, Ap
c	15	35	3.1	777	4	US-09-252-991A-1127	Sequence 1127, Ap
	16	34.8	3.1	695	4	US-09-221-017B-767	Sequence 767, App
	17	34.6	3.0	822	4	US-09-252-991A-9029	Sequence 9029, Ap
c	18	34.4	3.0	431	4	US-09-433-241A-1	Sequence 1, Appli
	19	34.4	3.0	1011	4	US-09-252-991A-3833	Sequence 3833, Ap
	20	34.2	3.0	846	4	US-09-252-991A-6073	Sequence 6073, Ap
	21	34.2	3.0	882	4	US-09-252-991A-16446	Sequence 16446, A
c	22	34.2	3.0	927	4	US-09-252-991A-15945	Sequence 15945, A
c	23	34.2	3.0	1080	4	US-09-252-991A-6480	Sequence 6480, Ap
	24	33.8	3.0	1053	4	US-09-252-991A-15787	Sequence 15787, A
	25	33.8	3.0	1134	4	US-09-252-991A-15842	Sequence 15842, A
c	26	33.6	3.0	839	3	US-08-998-416-519	Sequence 519, App
c	27	33	2.9	684	4	US-09-252-991A-230	Sequence 230, App
c	28	32.8	2.9	753	4	US-09-252-991A-10372	Sequence 10372, A
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c	34	32.6	2.9	872	1	US-08-381-280-19	Sequence 19, Appl
c	35	32.6	2.9	872	2	US-08-445-533-19	Sequence 19, Appl
c	36	32.6	2.9	872	3	US-09-052-085-19	Sequence 19, Appl
c	37	32.6	2.9	1116	3	US-09-104-308-2	Sequence 2, Appli
c	38	32.6	2.9	1116	3	US-09-321-981-2	Sequence 2, Appli
c	39	32.6	2.9	1116	4	US-09-739-861A-2	Sequence 2, Appli
c	40	32.6	2.9	1116	4	US-09-795-583-2	Sequence 2, Appli
	41	32.4	2.9	718	4	US-09-659-845A-25	Sequence 25, Appl
c	42	32.4	2.9	756	4	US-09-252-991A-2763	Sequence 2763, Ap
	43	32.4	2.9	889	4	US-09-464-535-27	Sequence 27, Appl
	44	32.2	2.8	503	4	US-09-297-269-40	Sequence 40, Appl
	45	32.2	2.8	822	4	US-09-252-991A-876	Sequence 876, App

ALIGNMENTS

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RESULT 1
US-08-236-311-12
; Sequence 12, Application US/08236311
; Patent No. 5565335
;  GENERAL INFORMATION:
;    APPLICANT:  Capon, Daniel J.
;    APPLICANT:  Gregory, Timothy J.
;    TITLE OF INVENTION:  Adheson Variants
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/236,311
;      FILING DATE:  02-MAY-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/936190
;      FILING DATE:  26-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/842777
;      FILING DATE:  18-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/250785
;      FILING DATE:  28-SEP-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/104329
;      FILING DATE:  02-OCT-1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  444P1C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  468 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
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;      TOPOLOGY:  linear
US-08-236-311-12

  Query Match             3.8%;  Score 43;  DB 1;  Length 468;
  Best Local Similarity   49.5%;  Pred. No. 0.022;
  Matches  143;  Conservative    0;  Mismatches  140;  Indels    6;  Gaps    1;

Qy        379 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 438
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Qy        439 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 492
                |    |||||| | ||   |||||||||||| ||   |   ||  ||||      |||
Db        187 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 246

Qy        493 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 552
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Qy        553 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 612
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RESULT 2
US-08-457-918-12
; Sequence 12, Application US/08457918
; Patent No. 6117655
;  GENERAL INFORMATION:
;    APPLICANT:  Capon, Daniel J.
;    APPLICANT:  Gregory, Timothy J.
;    TITLE OF INVENTION:  Adheson Variants
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/457,918
;      FILING DATE:  1-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/236311
;      FILING DATE:  02-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/936190
;      FILING DATE:  26-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/842777
;      FILING DATE:  18-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/250785
;      FILING DATE:  28-SEP-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/104329
;      FILING DATE:  02-OCT-1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kubinec, Jeffrey S.
;      REGISTRATION NUMBER:  36,575
;      REFERENCE/DOCKET NUMBER:  P0444P1C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-8228
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  468 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-457-918-12

  Query Match             3.8%;  Score 43;  DB 3;  Length 468;
  Best Local Similarity   49.5%;  Pred. No. 0.022;
  Matches  143;  Conservative    0;  Mismatches  140;  Indels    6;  Gaps    1;

Qy        379 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 438
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Db        127 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 186

Qy        439 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 492
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Qy        493 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 552
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Qy        553 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 612
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Db        307 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 366

Qy        613 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 661
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Db        367 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 415


RESULT 3
5482709-5/c
;Patent No. 5482709
;    APPLICANT: JACOBSON, JAMES W.;STRAUSBERG, ROBERT L.;WILSON,
;SUSAN D.;POPE, SHARON H.;STRAUSBERG, SUSAN L.;RUFF, MICHAEL D.;
; AUGUSTINE, PATRICIA C.;DANFORTH, HARRY D.
;    TITLE OF INVENTION: EIMERIA ANTIGENIC COMPOSITION WHICH
;ELICITS ANTIBODIES AGAINST AVIAN COCCIDIOSIS
;    NUMBER OF SEQUENCES: 10
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/148,432
;      FILING DATE: 08-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 581,693
;      FILING DATE: 12-SEP-1990
;      APPLICATION NUMBER: 215,162
;      FILING DATE: 05-JUL-1989
;      APPLICATION NUMBER: 746,520
;      FILING DATE: 19-JUN-1985
;      APPLICATION NUMBER: 627,811
;      FILING DATE: 05-JUL-1984
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;      LENGTH: 533
5482709-5

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  Best Local Similarity   47.3%;  Pred. No. 0.15;
  Matches  121;  Conservative    0;  Mismatches  135;  Indels    0;  Gaps    0;

Qy         89 TCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGG 148
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Db        260 TGCAGCTGGTGCTGCTGCAGCTCCTGTTGCTGCTGCTGCTGCTGCAGCTGGTGCTGCTGC 201

Qy        329 AGGGTCGGGGGTAGCT 344
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Db        200 AGCTGGTGCTGCAGCT 185


RESULT 4
5273901-6/c
;Patent No. 5273901
;    APPLICANT: JACOBSON, JAMES W.;STRAUSBERG, ROBERT L.;WILSON,
;SUSAN D.;POPE, SHARON H.;STRAUSBERG, SUSAN L.;RUFF,MICHAEL D.;
;AUGUSTINE, PATRICIA C.;DANFORTH, HARRY D.
;    TITLE OF INVENTION: GENETICALLY ENGINEERED COCCIDIOSIS
;SPOROZOITE 21.5 KB ANTIGEN, AC-6B
;    NUMBER OF SEQUENCES: 11
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/581,693
;      FILING DATE: 12-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 215,162
;      FILING DATE: 05-JUL-1988
;      APPLICATION NUMBER: 746,520
;      FILING DATE: 19-JUN-1985
;      APPLICATION NUMBER: 627,811
;      FILING DATE: 05-JUL-1984
;SEQ ID NO:6:
;      LENGTH:543
5273901-6

  Query Match             3.5%;  Score 40;  DB 6;  Length 543;
  Best Local Similarity   47.3%;  Pred. No. 0.15;
  Matches  121;  Conservative    0;  Mismatches  135;  Indels    0;  Gaps    0;

Qy         89 TCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGG 148
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Qy        149 TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT 208
              ||||  ||   ||   |||  | |  |  ||| |||| ||  ||||   |  | |
Db        390 TGCTGTTGCTGCTTGTGTTTTCGCTTTCTCTGCTTCTGCTGCTGCTCCTGCTGCTCCTTC 331

Qy        209 TCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGC 268
              | | |    ||  || |    |    ||| |  | ||   | || |  || |  || ||
Db        330 GGTTTCTGTTCGTGCTTCCGCTGCCTTTGCTGCTCCTGCTGCTCCTGCTGCGGCTGTCGC 271

Qy        269 AGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGG 328
              | |  |||| |||    |  | | ||| ||  || |   | | |||  | || | | |
Db        270 TGCAGCTGGTGCTGCTGCAGCTCCTGTTGCTGCTGCTGCTGCTGCAGCTGGTGCTGCTGC 211

Qy        329 AGGGTCGGGGGTAGCT 344
              ||    |  | ||||
Db        210 AGCTGGTGCTGCAGCT 195


RESULT 5
US-08-998-416-915/c
; Sequence 915, Application US/08998416
; Patent No. 6239264
;  GENERAL INFORMATION:
;    APPLICANT:  Philippsen, Peter
;    APPLICANT:  Pohlmann, Rainer
;    APPLICANT:  Steiner, Sabine
;    APPLICANT:  Mohr, Christine
;    APPLICANT:  Wendland, Jurgen
;    APPLICANT:  Knechtle, Philipp
;    APPLICANT:  Rebischung, Corinne
;    TITLE OF INVENTION:  GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
;    TITLE OF INVENTION:  AND USES THEREOF
;    NUMBER OF SEQUENCES:  1152
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6239264artis Corporation
;      STREET:  3054 Cornwallis Road
;      CITY:  Research Triangle Park
;      STATE:  No. 6239264th Carolina
;      COUNTRY:  USA
;      ZIP:  27709
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/998,416
;      FILING DATE:  24-DEC-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  CH 0016/97
;      FILING DATE:  31-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meigs, J. Timothy
;      REGISTRATION NUMBER:  38,241
;      REFERENCE/DOCKET NUMBER:  PF/5-30306/A/CGC1976
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-541-8587
;      TELEFAX:  919-541-8689
;  INFORMATION FOR SEQ ID NO:  915:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  688 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  PAG1570RP
US-08-998-416-915

  Query Match             3.3%;  Score 37.4;  DB 3;  Length 688;
  Best Local Similarity   45.0%;  Pred. No. 0.87;
  Matches  140;  Conservative    0;  Mismatches  171;  Indels    0;  Gaps    0;

Qy         48 GGACCCCCCAGGAAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAG 107
              ||||   |  | | | |  |  | |  | | | ||  |||| |  | |  ||  | |
Db        547 GGACTTGCTGTGGAACCGGTTGTGGTTGCTGTGATTGTGGTTTCAATTGTGGTTGTGGTT 488

Qy        108 GGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTT 167
              ||  | | | || | |       |  |  |  ||||    | |||| |||   || | | |
Db        487 GGTGTTGTGTCTGCTGCTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 428

Qy        168 CAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCT 227
              |       |||  |  | ||  ||  |   | |    |||  |  |  ||    | ||
Db        427 GCTGCGTCTGCTGCTGCGTCTGCTGCTGCGGTTGTGGTTGTTGCGCCTGCGCCTGCGCCA 368

Qy        228 CGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGA 287
              |   | ||  | |  ||  |  | ||  |  |  || |  | |  ||    |||
Db        367 GTTGTGGCTGATGAGGCTGTAAACCAAGCTGTTGTTGTTGTTGTAGTTGCGGTTGAGGTT 308

Qy        288 CTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTT 347
              | | | ||  ||||   |||   | |||||||  |   |   | | |||  |   |
Db        307 GGGGCTGCTGCTGCTGTTGTGGTTGTTGTGGTTGTTGTGTTTGTTGCTGTGGTTGTGGTG 248

Qy        348 TTGGTAGAGGT 358
              ||||  | |||
Db        247 GTGGTGGTGGT 237


RESULT 6
US-09-621-976-15639
; Sequence 15639, Application US/09621976
; Patent No. 6639063
```

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; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 15639
;   LENGTH: 505
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-15639

  Query Match             3.3%;  Score 37;  DB 4;  Length 505;
  Best Local Similarity   14.0%;  Pred. No. 0.99;
  Matches   34;  Conservative  107;  Mismatches  102;  Indels    0;  Gaps    0;

Qy          3 ATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGAAG 62
              ::: : : : :| :::     :: :  |: :|::   || |  ::| :|:   :: : :|
Db          8 RYRTSSKSKRYGGKYSMYSSRWSMKYYAWGRGKYGTSGGRCGGSRGWMCSKWGYRYSYWG 67

Qy         63 TCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCA 122
              : :: ::: :|: || :  ::: :|:: ::   :  :: :   ::: ::::: 
Db         68 YKWKSWSKKMKKYSGKMGTSKSTRKYRTYTSKCRKTTCKYRGWWSWKWRMWKRRKMYYYR 127

Qy        123 GTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCA 182
               : : | : :: : :| :   :| | :||::   ::   :: ::|  :: ||||: : : 
Db        128 MKCYSCASYSYSYRRCRKYTGMTRGWYGCKKRMCKSSTRYMTRYTRYWKMTGACYGSKGM 187

Qy        183 CCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTG 242
              :|:|: :  :    ::   :|:| :::  ::  ::::::|:|:: | :  :  | |:::: 
Db        188 SCKGSRSKYYGSWKWYYGKYTMCTSKYKSSKMSYKKSSMCYTYMMCYYTYWWCTCTYKKS 247

Qy        243 CAT 245
              : |
Db        248 YYT 250


RESULT 7
US-09-252-991A-16469
; Sequence 16469, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 16469
;   LENGTH: 1125
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16469

  Query Match             3.2%;  Score 36.4;  DB 4;  Length 1125;
  Best Local Similarity   49.5%;  Pred. No. 2;
  Matches   94;  Conservative    0;  Mismatches   96;  Indels    0;  Gaps    0;

Qy        412 CTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCG 471
              || || | | |       | || |  || |  ||  || |  | |    ||| |  |||
Db        791 CTGCTGGCCGGCAAGGAAGGCCCGCTGGGCAAGAACTACAACATGCGCTGGATCGCCTCG 850

Qy        472 CTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGA 531
               ||       || ||  || |    |  ||   |||  | | || |||| |  | |||
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Db        851 ATGGTCGCCGACGTCCACCGCATCCTGACCCGTGGCGGCGTCTTCATGTACCCGCGCGAC 910

Qy        532 GGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCG 591
              |  | ||| | |  |  |||  | |||  |    ||  || |||     ||| | | |||
Db        911 GCCCGCGAGCCGGAGAAGCCCGGCAAGCTGCGCCTGATGTACGAAGCCAACCCGATGTCG 970

Qy        592 TCCACCGTCG 601
              | || | |||
Db        971 TTCATCATCG 980


RESULT 8
US-09-252-991A-242/c
; Sequence 242, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 242
;   LENGTH: 615
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-242

  Query Match             3.2%;  Score 36.2;  DB 4;  Length 615;
  Best Local Similarity   49.2%;  Pred. No. 1.8;
  Matches   95;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy        418 GACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAG 477
              |||  |  |   | || | ||   ||| |||| | |   ||   ||  | | | |||  |
Db        359 GACATGCGCCGCGCCCTGGCGCTATGGCCGGAACTGGCGCCTTGGAGCGAGGCCCTGCTG 300

Qy        478 CGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCAC 537
              | ||  |     |  |   || | |  ||      ||  ||||  | ||||| ||  |
Db        299 GGCCAGTACCTTGCCGTGCACCCGGGCTTCCAGCGCCTGGCGTTCGCGGGCGGAAGGGTC 240

Qy        538 GACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACC 597
              | |||||  |||| |  |    | |  |||  || |  |  ||| ||   | ||     |
Db        239 GGCCTGACCCTGCTGCTGGGCGATGCCATGGAGTGCCTGCCGCAGCTCGACGCGCGGGTC 180

Qy        598 GTCGTCCCCTTGC 610
              | ||| |   || |
Db        179 GACGCCTGGTTCC 167


RESULT 9
US-09-252-991A-296
; Sequence 296, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 296
;   LENGTH: 1041
;   TYPE: DNA
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;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-296

  Query Match             3.2%;  Score 36.2;  DB 4;  Length 1041;
  Best Local Similarity   49.2%;  Pred. No. 2.2;
  Matches   95;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy        418 GACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAG 477
              |||  |  |   | || | ||   ||| |||| | |   ||  ||  | | | |||  |
Db        338 GACATGCGCCGCGCCCTGGCGCTATGGCCGGAACTGGCGCCTTGGAGCGAGGCCCTGCTG 397

Qy        478 CGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCAC 537
              | ||   |    |  |   || | |  ||      ||  ||||  | ||||| ||  |
Db        398 GGCCAGTACCTTGCCGTGCACCCGGGCTTCCAGCGCCTGGCGTTCGCGGGCGGAAGGGTC 457

Qy        538 GACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACC 597
              | ||||| ||||  |  |    | |  |||  || |  |  ||| ||   | ||      |
Db        458 GGCCTGACCCTGCTGCTGGGCGATGCCATGGAGTGCCTGCCGCAGCTCGACGCGCGGGTC 517

Qy        598 GTCGTCCCCTTGC 610
              | ||  |   || |
Db        518 GACGCCTGGTTCC 530


RESULT 10
US-09-252-991A-7481/c
; Sequence 7481, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7481
;   LENGTH: 909
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7481

  Query Match             3.2%;  Score 36;  DB 4;  Length 909;
  Best Local Similarity   45.4%;  Pred. No. 2.3;
  Matches  129;  Conservative    0;  Mismatches  155;  Indels    0;  Gaps    0;

Qy        794 AATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGG 853
              ||    | || |  | | | |      | ||  | ||| |      ||   ||  || ||
Db        350 AAACACTGGCCAGGGAAAACGCCTTGATCTTGCACGAGGGCCCCGCCACCCTTGGCCGGG 291

Qy        854 TCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCT 913
              ||  |  || |||| | |   | | |  || | |     | | | | ||||    ||| |
Db        290 TCGGCAACGGACAGAGGTGGGACATGCGTTTGCGCAGAAGGACGACGTTGCTGCTGGTAT 231

Qy        914 AGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGA 973
                | |||||  |||  |||          |||  |  |||  | | |    ||  |   |
Db        230 TTGCAGTGCTGTTGCTGCTGGCGTTCGGCTACGGCTGGCATGCCTGGCGCAGCCTGTTGC 171

Qy        974 CGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTC 1033
                | | | |||   |    | |  ||      || |||| |     |  || | | | |
Db        170 GCGAGCAGGGTGTCGAGCGCCTGGAGTGGCAAGGCCTGGGCCTGTCCGCCGAAGGCATCG 111

Qy       1034 GTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTC 1077
              |   || |  |  |  |||  | |  || | |  ||  | ||| |
Db        110 GGCTGCGACGGCTGGCGCTGGAGCGGCGCGGCGCGGATGGCGCC 67


RESULT 11
US-09-252-991A-7278
; Sequence 7278, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7278
;   LENGTH: 675
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7278

  Query Match             3.1%;  Score 35.2;  DB 4;  Length 675;
  Best Local Similarity   46.1%;  Pred. No. 3.4;
  Matches  118;  Conservative    0;  Mismatches  138;  Indels    0;  Gaps    0;

Qy        822 CGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAA 881
              | ||  | ||| |      ||   ||  || |||| |  || |||| | |   | | |
Db          2 CTTGCACGAGGGCCCCGCCACCCTTGGCCGGGTCGGCAACGGACAGAGGTGGGACATGCG 61

Qy        882 TTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCT 941
              || | |     | | | | ||||    ||| |    | |||||  |||  |||
Db         62 TTTGCGCAGAAGGACGACGTTGCTGCTGGTATTTGCAGTGCTGTTGCTGCTGGCGTTCGG 121

Qy        942 GGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACT 1001
                |||  | |||  | | |      ||  |   |   | | | |||  |    | |  ||
Db        122 CTACGGCTGGCATGCCTGGCGCAGCCTGTTGCGCGAGCAGGGTGTCGAGCGCCTGGAGTG 181

Qy       1002 CTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACG 1061
                || |||| |      |  || | | | |   || |  |  |  |||  | |  ||
Db        182 GCAAGGCCTGGGCCTGTCCGCCGAAGGCATCGGGCTGCGACGGCTGGCGCTGGAGCGGCG 241

Qy       1062 AGACAGGGCAGACGTC 1077
                | |  ||  | || |
Db        242 CGGCGCGGATGGCGCC 257


RESULT 12
US-09-252-991A-3035
; Sequence 3035, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 3035
;   LENGTH: 627
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3035

  Query Match             3.1%;  Score 35;  DB 4;  Length 627;
  Best Local Similarity   51.6%;  Pred. No. 3.8;
  Matches   80;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy        151 CTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTC 210
                ||||     |||   | |  | |  |  ||  |||| |||  |||  | |    | |||
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Db          8 CTTCCCATGCTCGCTTACGTGATCCCGCTGTGCCTGGCGCTGCTCGGCCTGGCCCTGTTG 67

Qy        211 TGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAG 270

Db         68 CTGACCCTGGCGCGCCTGGTCAAGGGGCCGTGCCTGCCGGACCGGGCGCTGGCGCTGGAC 127

Qy        271 GACGTGGTCCTGACCGACTTACCGTTCCTCATGTT 305

Db        128 ACCCTCTACGTGAACGCCATCGCCCTGCTGGTGCT 162


RESULT 13
US-09-252-991A-953
; Sequence 953, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 953
;   LENGTH: 630
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-953

  Query Match             3.1%;  Score 35;  DB 4;  Length 630;
  Best Local Similarity   49.7%;  Pred. No. 3.8;
  Matches   89;  Conservative    0;  Mismatches   90;  Indels    0;  Gaps    0;

Qy        470 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 529

Db         59 CCCTGATCCTGGTCAGCGCCATCCTGGTCAACAACTTTGTCCTGGTGCAGTTCCTCGGCC 118

Qy        530 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 589

Db        119 TGTGCCCGTTCATGGGCGTGTCGCGGAAGATCGAGACGGCCATCGGCCTGTCCCTCGCCA 178

Qy        590 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG 648

Db        179 CCACCTTCGTCCTGACCCTGGCGGCGATGTGCAGCCATATCCTGCAACGCTACGTGCTG 237


RESULT 14
US-09-252-991A-3133
; Sequence 3133, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 3133
;   LENGTH: 720
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3133

  Query Match             3.1%;  Score 35;  DB 4;  Length 720;
  Best Local Similarity   51.6%;  Pred. No. 4;
  Matches   80;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy        151 CTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTC 210

Db        445 CTTCCCATGCTCGCTTACGTGATCCCGCTGTGCCTGGCGCTGCTCGGCCTGGCCCTGTTG 504

Qy        211 TGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAG 270

Db        505 CTGACCCTGGCGCGCCTGGTCAAGGGGCCGTGCCTGCCGGACCGGGCGCTGGCGCTGGAC 564

Qy        271 GACGTGGTCCTGACCGACTTACCGTTCCTCATGTT 305

Db        565 ACCCTCTACGTGAACGCCATCGCCCTGCTGGTGCT 599


RESULT 15
US-09-252-991A-1127/c
; Sequence 1127, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 1127
;   LENGTH: 777
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1127

  Query Match             3.1%;  Score 35;  DB 4;  Length 777;
  Best Local Similarity   49.7%;  Pred. No. 4.1;
  Matches   89;  Conservative    0;  Mismatches   90;  Indels    0;  Gaps    0;

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Job time : 60.25 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 10, 2004, 16:13:07 ; Search time 473.75 Seconds
(without alignments)
10852.855 Million cell updates/sec

Title: US-10-679-999-14
Perfect score: 1135
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 4861726

Minimum DB seq length: 0
Maximum DB seq length: 1135

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1135	100.0	1135	13	US-10-679-999-14	Sequence 14, Appl
	2	1109.4	97.7	1135	13	US-10-679-999-17	Sequence 17, Appl
	3	440.8	38.8	454	9	US-09-366-133-5	Sequence 5, Appli
	4	440.8	38.8	454	13	US-10-679-999-5	Sequence 5, Appli
	5	440.8	38.8	454	15	US-10-214-037-5	Sequence 5, Appli
	6	378.4	33.3	491	9	US-09-366-133-2	Sequence 2, Appli
	7	378.4	33.3	491	13	US-10-679-999-2	Sequence 2, Appli
	8	378.4	33.3	491	15	US-10-214-037-2	Sequence 2, Appli
	9	43	3.8	468	15	US-10-097-044A-12	Sequence 12, Appl
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c	11	40.4	3.6	486	13	US-10-465-217-13	Sequence 13, Appl
	12	40.4	3.6	754	9	US-09-229-200A-13	Sequence 13, Appl
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	14	39.4	3.5	1011	13	US-10-152-886-82	Sequence 82, Appl
c	15	38.6	3.4	711	15	US-10-156-761-2558	Sequence 2558, Ap
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	42	36.6	3.2	957	15	US-10-156-761-867	Sequence 867, App
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	44	36.2	3.2	816	15	US-10-156-761-5917	Sequence 5917, Ap
c	45	36	3.2	705	9	US-09-974-300-858	Sequence 858, App

ALIGNMENTS

RESULT 1
US-10-679-999-14
; Sequence 14, Application US/10679999
; Publication No. US20040067520A1
; GENERAL INFORMATION:
; APPLICANT: Mann, Michael B.
; Hecht, Randy I.
; TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
; METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/679,999
; FILING DATE: 06-Oct-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/568,528
; FILING DATE: 09-May-2000
; APPLICATION NUMBER: 09/267,517
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Knight, Matthew W.
; REGISTRATION NUMBER: 36,846
; REFERENCE/DOCKET NUMBER: A-416
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:

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;             LENGTH: 1135 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;          MOLECULE TYPE: cDNA
;          SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-679-999-14

  Query Match             100.0%;  Score 1135;  DB 13;  Length 1135;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1135;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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; Sequence 17, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1135 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-679-999-17

  Query Match             97.7%;  Score 1109.4;  DB 13;  Length 1135;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches 1119;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

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Db        781 AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC 840

Qy        841 AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA 900
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Qy        901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT 960
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RESULT 3
US-09-366-133-5
; Sequence 5, Application US/09366133
; Patent No. US20020009798A1
;  GENERAL INFORMATION:
;    APPLICANT:  Pelleymounter, Mary Ann
;    APPLICANT:  Hecht, Randy I
;    APPLICANT:  Mann, Michael B
;    TITLE OF INVENTION:  OB PROTEIN COMPOSITIONS AND METHODS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  91230-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/366,133
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/920,608
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pessin, Karol M.
;      REFERENCE/DOCKET NUMBER:  A-345
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  454 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-366-133-5

  Query Match             38.8%;  Score 440.8;  DB 9;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 2.5e-129;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              |||||||||||||||||||||||||||||||||||||||| | ||||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              ||||||||||||||||||||||||||||||
Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454
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RESULT 4
US-10-679-999-5
; Sequence 5, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 454 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-679-999-5

  Query Match             38.8%;  Score 440.8;  DB 13;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 2.5e-129;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              |||||||||||||||||||||||||||||||||||||| | ||||||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              ||||||||||||||||||||||||||||||
Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 5
US-10-214-037-5
; Sequence 5, Application US/10214037
; Publication No. US20030054997A1
;   GENERAL INFORMATION:
;        APPLICANT: Pelleymounter, Mary Ann
;                   Hecht, Randy I
;                   Mann, Michael B
;        TITLE OF INVENTION: OB PROTEIN COMPOSITIONS AND METHODS
;        NUMBER OF SEQUENCES: 6
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 Dehavilland Drive
;             CITY: Thousand Oaks
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 91230-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/214,037
;             FILING DATE: 05-Aug-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/920,608
;             FILING DATE: 07-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Pessin, Karol M.
;             REFERENCE/DOCKET NUMBER: A-345
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 454 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-214-037-5

  Query Match             38.8%;  Score 440.8;  DB 15;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 2.5e-129;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              |||||||||||||||||||||||||||||||||||||| | ||||||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
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Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
                 |||||||||||||||||||||||||||||||
Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 6
US-09-366-133-2
; Sequence 2, Application US/09366133
; Patent No. US20020009798A1
;  GENERAL INFORMATION:
;    APPLICANT:  Pelleymounter, Mary Ann
;    APPLICANT:  Hecht, Randy I
;    APPLICANT:  Mann, Michael B
;    TITLE OF INVENTION:  OB PROTEIN COMPOSITIONS AND METHODS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  91230-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/366,133
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/920,608
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pessin, Karol M.
;      REFERENCE/DOCKET NUMBER:  A-345
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-366-133-2

  Query Match           33.3%;  Score 378.4;  DB 9;  Length 491;
  Best Local Similarity  89.8%;  Pred. No. 1.7e-109;
  Matches  406;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
                 ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
                 ||||||||||||||||||||||||||||||||    | ||||||||    ||||| || ||
Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
                 |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
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Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
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Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
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Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
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Db        400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
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Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491


RESULT 7
US-10-679-999-2
; Sequence 2, Application US/10679999
; Publication No. US20040067520A1
;  GENERAL INFORMATION:
;       APPLICANT: Mann, Michael B.
;                  Hecht, Randy I.
;       TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                           METHODS
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Amgen Inc.
;            STREET: 1840 DeHavilland Drive
;            CITY: Thousand Oaks
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 91320-1789
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/679,999
;            FILING DATE: 06-Oct-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/568,528
;            FILING DATE: 09-May-2000
;            APPLICATION NUMBER: 09/267,517
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Knight, Matthew W.
;            REGISTRATION NUMBER: 36,846
;            REFERENCE/DOCKET NUMBER: A-416
;  INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 491 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-679-999-2

  Query Match           33.3%;  Score 378.4;  DB 13;  Length 491;
  Best Local Similarity  89.8%;  Pred. No. 1.7e-109;
  Matches  406;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
                 ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99
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Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||    | ||||||||   ||||| || ||
Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              ||||||||||| | |||||||||| |||||||| | |||||| |||||||
Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
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Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
                | | |||||||||| |||  | ||| || |||| ||||||||||||||||||   ||
Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
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Db        400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              ||||||| | |||||||  ||||||||||||
Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491
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RESULT 8
US-10-214-037-2
; Sequence 2, Application US/10214037
; Publication No. US20030054997A1
; GENERAL INFORMATION:
; APPLICANT: Pelleymounter, Mary Ann
; Hecht, Randy I
; Mann, Michael B
; TITLE OF INVENTION: OB PROTEIN COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 91230-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/214,037
; FILING DATE: 05-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,608
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REFERENCE/DOCKET NUMBER: A-345
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-214-037-2

Query Match 33.3%; Score 378.4; DB 15; Length 491;

Best Local Similarity 89.8%; Pred. No. 1.7e-109;
Matches 406; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

```
Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
              ||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||    | ||||||||   ||||| || ||
Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              ||||||||||| | |||||||||| |||||||| | |||||| |||||||
Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
              |||||||||||||||||||||||||||| ||||||||||||||||||||||  ||||||
Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
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Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
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Db        400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              ||||||| | |||||||  ||||||||||||
Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491
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RESULT 9
US-10-097-044A-12
; Sequence 12, Application US/10097044A
; Publication No. US20030143220A1
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/097,044A
; FILING DATE: 28-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; APPLICATION NUMBER: 07/104329

```
;             FILING DATE: 02-OCT-1987
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kubinec, Jeffrey S.
;             REGISTRATION NUMBER: 36,575
;             REFERENCE/DOCKET NUMBER: P0444P1C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415/225-8228
;             TELEFAX: 415/952-9881
;             TELEX: 910/371-7168
;    INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 468 bases
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-097-044A-12

  Query Match             3.8%;  Score 43;  DB 15;  Length 468;
  Best Local Similarity   49.5%;  Pred. No. 0.0064;
  Matches  143;  Conservative    0;  Mismatches  140;  Indels    6;  Gaps    1;

Qy        379 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 438
              | |||||   || | || | | | || |||||     ||  || |||          | |
Db        127 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 186

Qy        439 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 492
              |    ||||||  | ||   ||||||||||||  ||   |  ||  ||||      |||
Db        187 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 246

Qy        493 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 552
              | |      ||  |||  |||  | |  |||       |       |    ||| ||
Db        247 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 306

Qy        553 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 612
              |||  |  ||||  |||||  ||  ||  ||  |||       |   ||  |    || |||
Db        307 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 366

Qy        613 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 661
              | | | |||   || |  ||| |||  |||  |   | |  |||  |||
Db        367 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 415


RESULT 10
US-10-156-761-6640/c
; Sequence 6640, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
;  APPLICANT: OMURA, SATOSHI
;  APPLICANT:  IKEDA, HARUO
;  APPLICANT:  ISHIKAWA, JUN
;  APPLICANT:  HORIKAWA, HIROSHI
;  APPLICANT:  SHIBA, TADAYOSHI
;  APPLICANT:  SAKAKI, YOSHIYUKI
;  APPLICANT:  HATTORI, MASAHIRA
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-262
;  CURRENT APPLICATION NUMBER: US/10/156,761
;  CURRENT FILING DATE:  2002-05-29
;  PRIOR APPLICATION NUMBER: JP 2001-204089
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-272697
;  PRIOR FILING DATE: 2001-08-02
;  NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 6640
;   LENGTH: 1116
;   TYPE: DNA
;   ORGANISM: Streptomyces avermitilis
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1116)
US-10-156-761-6640

  Query Match             3.7%;  Score 42.4;  DB 15;  Length 1116;
  Best Local Similarity   51.0%;  Pred. No. 0.014;
  Matches  100;  Conservative    0;  Mismatches   96;  Indels    0;  Gaps    0;

Qy        434 AGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCT 493
              ||  | |||  |   |    ||   | ||  ||  ||| |||  || |||    | ||||  |
Db        706 AGGAGAACTCGGGGTCGAAGACCCGGACGACCGGGGCGCCGTCGCGCTCGCCCACCATGA 647

Qy        494 CGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGA 553
              || | |||||  |    |   |  | | ||  | | | ||  || | ||| |  |  |
Db        646 CGCTGCCCGTGTGGAGGTCACCGTGGAGCGGGGCCTGCGCGCTCGTCATGAAGACGTGGC 587

Qy        554 GGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGA 613
              |||  |  || ||  ||| |     ||| |  ||   ||   | ||  | | ||  |  |
Db        586 GGAGGTCGGCGACCTCGGTGCGCAGGCGCGGGTCGGCGCGGAACGCGGCCGCCAGGTCGT 527

Qy        614 AGAGTACGAGGCACTA 629
              |||| || ||  | |
Db        526 CGAGTCCGGGGTGCCA 511


RESULT 11
US-10-465-217-13/c
; Sequence 13, Application US/10465217
; Publication No. US20030204859A1
; GENERAL INFORMATION:
;  APPLICANT: Kazemi-Esfarjani, Parsa
;  APPLICANT:  Benzer, Seymour
;  TITLE OF INVENTION: AN ANIMAL MODEL OF POLYGLUTAMINE
;  TITLE OF INVENTION:  TOXICITY, METHODS OF USE, AND MODULATORS OF POLYGLUTAMINE
;  TITLE OF INVENTION:  TOXICITY
;  FILE REFERENCE: 06618-686001
;  CURRENT APPLICATION NUMBER: US/10/465,217
;  CURRENT FILING DATE:  2003-06-18
;  PRIOR APPLICATION NUMBER: US/09/639,207
;  PRIOR FILING DATE: 2000-08-14
;  PRIOR APPLICATION NUMBER: US 60/148,934
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: US 60/148,933
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: US 60/177,047
;  PRIOR FILING DATE: 2000-01-18
;  PRIOR APPLICATION NUMBER: US 60/205,720
;  PRIOR FILING DATE: 2000-05-19
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 486
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-10-465-217-13

  Query Match             3.6%;  Score 40.4;  DB 13;  Length 486;
  Best Local Similarity   45.2%;  Pred. No. 0.044;
  Matches  149;  Conservative    0;  Mismatches  181;  Indels    0;  Gaps    0;

Qy         82 TTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTG 141
              ||   | | |||| |  |    |  |   | |   || | ||    ||  |  |   ||
Db        375 TTGCTGCTGCTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTG 316

Qy        142 CACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTA 201
              | | | |||| |||    | | | |  ||||    |||  |||| |   || |   |
Db        315 CTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGCTGCTGCTG 256

Qy        202 TTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAG 261
              || | ||| |  ||         | ||  |  |||||  ||    ||    || || |
Db        255 TTGCTGTTGTTGTTGCTGTTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTGCTG 196

Qy        262 GAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTG 321
              |  | |   || | |||       | | | |  |||   | | | |  ||||
Db        195 CTGCTGTTGCTGTTGCTGCTGCTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTG 136
```

```
Qy        322 TTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTT 381
              | | |  |   | |  |  |||  | | || |  | | | ||| |   |   |   ||
Db        135 CTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTG 76

Qy        382 GGTGTCCACATGTGGGACGGGGGTAGGGCC 411
                | |   || |||   |  |  |||||
Db         75 TTGCTGCTGCTGGGGGGTTGACGGTGGGCC 46


RESULT 12
US-09-229-200A-13
; Sequence 13, Application US/09229200A
; Patent No. US20020099179A1
;   GENERAL INFORMATION:
;        APPLICANT: Jolliffe et al.
;        TITLE OF INVENTION: CD4 Specific Recombinant Antibody
;        NUMBER OF SEQUENCES: 28
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Johnson & Johnson
;             STREET: One Johnson & Johnson Plaza
;             CITY: New Brunswick
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08933-7003
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: <Unknown>
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/229,200A
;             FILING DATE: 13-Jan-1999
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: John W. Wallen, III
;             REGISTRATION NUMBER: 35,403
;             REFERENCE/DOCKET NUMBER: ORT-948
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (858) 784-3239
;             TELEFAX: (908) 524-2808
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 754
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        ANTI-SENSE: no
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-229-200A-13

  Query Match             3.6%;  Score 40.4;  DB 9;  Length 754;
  Best Local Similarity   49.3%;  Pred. No. 0.052;
  Matches  138;  Conservative    0;  Mismatches  136;  Indels    6;  Gaps    1;

Qy        388 CACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACG 447
              || | || | | || |||||     ||  || |||           | |     |    |||
Db        411 CAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGACAACACACG 470

Qy        448 GACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTCTCGTTACCC 501
              ||| | ||   ||||||||||||| ||    |   ||  ||||      ||| | ||
Db        471 GACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTATTGCGGGAG 530

Qy        502 GTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAG 561
              ||  |||  |||  | |  |||     |      |    |  ||| || ||| | |
Db        531 GTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCGTGGATGTCG 590

Qy        562 GAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACG 621
              |||  ||||| || ||  ||  |||       |   || |    || |||| | | |||
Db        591 GAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAGATGCGGACG 650

Qy        622 AGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 661
                || |  ||| |||  |||  |   | |  |||  |||
Db        651 CTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 690


RESULT 13
US-10-156-761-2371
; Sequence 2371, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
;  APPLICANT: OMURA, SATOSHI
;  APPLICANT:  IKEDA, HARUO
;  APPLICANT:  ISHIKAWA, JUN
;  APPLICANT:  HORIKAWA, HIROSHI
;  APPLICANT:  SHIBA, TADAYOSHI
;  APPLICANT:  SAKAKI, YOSHIYUKI
;  APPLICANT:  HATTORI, MASAHIRA
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-262
;  CURRENT APPLICATION NUMBER: US/10/156,761
;  CURRENT FILING DATE:  2002-05-29
;  PRIOR APPLICATION NUMBER: JP 2001-204089
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-272697
;  PRIOR FILING DATE: 2001-08-02
;  NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2371
;   LENGTH: 675
;   TYPE: DNA
;   ORGANISM: Streptomyces avermitilis
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(675)
US-10-156-761-2371

  Query Match             3.5%;  Score 39.4;  DB 15;  Length 675;
  Best Local Similarity   49.3%;  Pred. No. 0.1;
  Matches  103;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;

Qy        422 GGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGC 481
              || | || |   |||||||  ||| |||      | ||||||  ||  |||||   || |
Db        410 GGCTGTTCGCGGAGTCGGACGCGACCGACATCCCGCAGAAGATGGGCACGCTGCGCCGCC 469

Qy        482 ACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACC 541
              |  ||   || | |     | ||  |||     |   |  ||    || ||   ||  |
Db        470 AGATCTATCTGTGGCGCGGCATCTACCTGCACATCCAGGACTTCGCCGTAGCCAACAGCA 529

Qy        542 TGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCG 601
              ||  |  |   ||  ||  |  || |      |||    | | |  ||  |  |  || ||
Db        530 TGGAGGCGATCAGCGAGGTGTGGACGGAAGGCGATCCCCGCTTCCTCCAGCTCGTCGACG 589

Qy        602 TCCCCTTGCAGAAGAGTACGAGGCACTAC 630
                || |  | |||  | | ||  | || ||
Db        590 ACCTCACGGAGATCATTCCGCCGTACGAC 618


RESULT 14
US-10-152-886-82
; Sequence 82, Application US/10152886
; Publication No. US20030064491A1
; GENERAL INFORMATION:
;  APPLICANT: ECOPIA BIOSCIENCES INC.
;  APPLICANT:  Farnet, Chris
;  APPLICANT:  Staffa, Alfredo
;  APPLICANT:  Zazopoulos, Emmanuel
;  TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF ENEDIYNE RING
;  TITLE OF INVENTION:  STRUCTURES
;  FILE REFERENCE: 3011-3US
;  CURRENT APPLICATION NUMBER: US/10/152,886
;  CURRENT FILING DATE:  2002-05-21
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 82
;   LENGTH: 1011
;   TYPE: DNA
```

; ORGANISM: Saccharothrix aerocolonigenes
US-10-152-886-82

Query Match 3.5%; Score 39.4; DB 13; Length 1011;
Best Local Similarity 48.4%; Pred. No. 0.12;
Matches 109; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

```
Qy          96 GGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCT 155
               |||||     || | |   |   |  |   |  | |  || ||||| | |||
Db         507 GGAGTGGACCAGCGGCGTCGTCGACGCGCTGATCCCCGTCCTCCTGCTCGCGGCCGGCAC 566

Qy         156 GGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTT 215
               |   ||| |    ||| |||| | | |  | ||||  |||  |  |    |    | ||
Db         567 GATGCTCAACGCGAAGCTGACGAAGAAGATCCCGCTGATCCTGGGCTGGGTGGGTGGGTT 626

Qy         216 CGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGT 275
               || |   |    |||  ||   |||  | |  |  ||| ||||   |   |   || | |
Db         627 CGTCCTGCAGGCCGTGCTGCGTTCGGCCTTCACCGACCTGTCGATCGTCAGTGCGGTCCT 686

Qy         276 GGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTT 320
               |    | ||||    | ||||| || |||||||   | | | | |
Db         687 GCCGATCACCGGAACAGCGTTCATCCTGTTCACCAACTACATGAT 731
```

RESULT 15
US-10-156-761-2558/c
; Sequence 2558, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2558
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(711)
US-10-156-761-2558

Query Match 3.4%; Score 38.6; DB 15; Length 711;
Best Local Similarity 52.1%; Pred. No. 0.19;
Matches 86; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

```
Qy         436 TCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCG 495
               |||  |   ||     |  ||  |||| | |    | || | | | || | |       || |
Db         650 TCGAAGCCGAACTGCACGTCACCGATGGTCACATTGCCGAACCAGCCCTTGGTGTCCTTG 591

Qy         496 TTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGG 555
                | | | || |  ||  |  || ||||  |       | | ||||       | |||  |||
Db         590 ATCCACTTCAGGATCGGGAGGACGTTCACGGTGCCGGAGGACGAGTCCGAGGTGCGCAGG 531

Qy         556 AAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600
               ||  || ||| ||||||||||  |    ||  || ||  || |||
Db         530 AACGAGAAGACGTCGTTCGAGCCGTTGTTGCCCTTGTAGACGGTC 486
```

Search completed: May 11, 2004, 09:06:42
Job time : 475.75 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 18:55:54 ; Search time 2223.5 Seconds
(without alignments)
15243.344 Million cell updates/sec

Title: US-10-679-999-14
Perfect score: 1135
Sequence: 1 GTATACCTGTTTTGAGTGTG.....AGGCCCAACAATTACCTAGG 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 54259654

Minimum DB seq length: 0
Maximum DB seq length: 1135

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	48.8	4.3	527	9	AV962678	AV962678 AV962678
c	2	48.2	4.2	610	13	BW035294	BW035294 BW035294
c	3	47.6	4.2	619	13	BW251013	BW251013 BW251013
c	4	47	4.1	546	13	BW249566	BW249566 BW249566
c	5	47	4.1	660	13	BW193819	BW193819 BW193819
c	6	45.8	4.0	602	13	BW192111	BW192111 BW192111
c	7	45.8	4.0	617	13	BW314712	BW314712 BW314712
	8	43.6	3.8	1039	13	CA128348	CA128348 SCJLLR200
c	9	43.2	3.8	486	9	AI869699	AI869699 wm02f07.x
c	10	43.2	3.8	658	13	BW265514	BW265514 BW265514
c	11	43.2	3.8	663	13	BW259047	BW259047 BW259047
	12	43.2	3.8	910	29	CNS006ON	AL065629 Drosophil
c	13	42.8	3.8	509	10	BF593096	BF593096 7o56e02.x
c	14	42.8	3.8	552	14	CA686322	CA686322 wlm96.pk0
c	15	42.6	3.8	642	13	CA012935	CA012935 HT06O08r
c	16	42.6	3.8	649	14	CD907542	CD907542 G468.107E
c	17	42.6	3.8	673	13	CA014102	CA014102 HT10G06r
c	18	42.6	3.8	725	14	CD910343	CD910343 G550.001A
c	19	42.6	3.8	763	14	CD906072	CD906072 G468.103N
c	20	42.6	3.8	838	12	BI948448	BI948448 HVSME1000
c	21	42.2	3.7	512	9	AI289506	AI289506 qw28e11.x
c	22	42.2	3.7	586	9	AI687271	AI687271 tp94e04.x
c	23	42.2	3.7	659	13	CA014547	CA014547 HT11K11r
	24	41.8	3.7	343	9	AA330793	AA330793 EST34531
	25	41.8	3.7	1101	29	CNS00LXJ	AL078875 Drosophil
	26	41.6	3.7	337	14	CB047414	CB047414 NISC_gg02
	27	41.6	3.7	340	9	AA302570	AA302570 EST15740
c	28	41.6	3.7	408	14	CA720412	CA720412 wkm2n.pk0
c	29	41.6	3.7	414	12	BJ248630	BJ248630 BJ248630
c	30	41.6	3.7	439	10	BE488609	BE488609 WHE1051_G
c	31	41.6	3.7	442	14	CA719617	CA719617 wkm2n.pk0
c	32	41.6	3.7	443	9	AI582641	AI582641 tn47h04.x
c	33	41.6	3.7	443	14	CA656554	CA656554 wlm0.pk00
c	34	41.6	3.7	447	14	CA687517	CA687517 wlm96.pk0
c	35	41.6	3.7	448	14	CA692819	CA692819 wlm96.pk0
c	36	41.6	3.7	451	9	AI083954	AI083954 oz53b09.x
c	37	41.6	3.7	451	10	AW276084	AW276084 xq45c08.x
c	38	41.6	3.7	455	10	AW590575	AW590575 hg46c10.x
c	39	41.6	3.7	458	9	AW088852	AW088852 xd31e06.x
c	40	41.6	3.7	463	10	BF056551	BF056551 7k06g10.x
	41	41.6	3.7	466	10	AW673691	AW673691 ba56g10.y
c	42	41.6	3.7	467	9	AI752976	AI752976 cr03b09.x
c	43	41.6	3.7	467	9	AI879509	AI879509 au53d05.x
c	44	41.6	3.7	469	9	AI088760	AI088760 qa16h11.x
c	45	41.6	3.7	472	14	CA448944	CA448944 UI-H-EI1-

ALIGNMENTS

RESULT 1
AV962678/c
LOCUS AV962678 527 bp mRNA linear EST 14-MAR-2002
DEFINITION AV962678 Nori Satoh unpublished cDNA library, larva Ciona intestinalis cDNA clone cilv05e12 5', mRNA sequence.
ACCESSION AV962678
VERSION AV962678.1 GI:19450977
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 527)
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES Location/Qualifiers
source 1. .527
/organism="Ciona intestinalis"
/mol_type="mRNA"

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                     /db_xref="taxon:7719"
                     /clone="cilv05e12"
                     /tissue_type="whole animal"
                     /dev_stage="larva"
                     /clone_lib="Nori Satoh unpublished cDNA library, larva"
ORIGIN

  Query Match             4.3%;  Score 48.8;  DB 9;  Length 527;
  Best Local Similarity   45.8%;  Pred. No. 1.4;
  Matches  167;  Conservative    0;  Mismatches  198;  Indels    0;  Gaps    0;

Qy        227 TCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCG 286
              | ||  || |||  |   ||     |  ||   ||| || |  |    || |  ||
Db        476 TGGTGGTGATGTGTTNTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATT 417

Qy        287 ACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCT 346
              | |   ||| ||  ||||   |||   | |||||| | |  ||  | |  || | ||
Db        416 TCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCC 357

Qy        347 TTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTA 406
              | | ||  |    |  | | ||  |   |   ||      |   | |||  ||    |
Db        356 TGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGT 297

Qy        407 GGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAG 466
              |  |||  | |    ||| ||| ||| || |     ||  |    |||   || |||
Db        296 TGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGC 237

Qy        467 GGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGT 526
              || | |||  |  |    |   ||  |||      |  ||| || |||| | ||
Db        236 TGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGTTGTTGT 177

Qy        527 GCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGT 586
              |    ||      ||  ||||| |  |  |  |  ||||| ||| | |   |    ||
Db        176 TGGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGTGCTTCTGTAGT 117

Qy        587 TCTCG 591
              |  ||
Db        116 TGCCG 112


RESULT 2
BW035294/c
LOCUS       BW035294                 610 bp    mRNA    linear   EST 13-OCT-2002
DEFINITION  BW035294 Nori Satoh unpublished cDNA library, blood cells Ciona
            intestinalis cDNA clone cibd028f16 5', mRNA sequence.
ACCESSION   BW035294
VERSION     BW035294.1  GI:23951246
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 610)
  AUTHORS   Satou,Y., Satake,M., Azumi,K., Nonaka,M., Shin-i,T., Kohara,Y. and
            Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .610
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cibd028f16"
                     /tissue_type="blood cells"
                     /clone_lib="Nori Satoh unpublished cDNA library, blood
                     cells"
ORIGIN

  Query Match             4.2%;  Score 48.2;  DB 13;  Length 610;
  Best Local Similarity   45.8%;  Pred. No. 2;
  Matches  167;  Conservative    0;  Mismatches  198;  Indels    0;  Gaps    0;

Qy        227 TCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCG 286
              | ||  || |||  |   ||     |  ||   ||| || |  |    || |  ||
Db        475 TGGTGGTGATGTGTTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATT 416

Qy        287 ACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCT 346
              | |   ||| ||  ||||   |||   | |||||| | |  ||  | |  || | ||
Db        415 TCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCC 356

Qy        347 TTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTA 406
              | | ||  |    |  | | ||  |   |   ||      |   | |||  ||    |
Db        355 TGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGT 296

Qy        407 GGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAG 466
              |  |||  | |    ||| ||| ||| || |     ||  |    |||   || |||
Db        295 TGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGC 236

Qy        467 GGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGT 526
              || | |||  |  |    |   ||  |||      |  ||| || |||| | ||
Db        235 TGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGTTGTTGT 176

Qy        527 GCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGT 586
              |    ||      ||  ||||| |  |  |  |  ||||| ||| | |   |    ||
Db        175 TGGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGTGCTTCTGTAGT 116

Qy        587 TCTCG 591
              |  ||
Db        115 TGCCG 111


RESULT 3
BW251013/c
LOCUS       BW251013                 619 bp    mRNA    linear   EST 09-NOV-2002
DEFINITION  BW251013 Nori Satoh unpublished cDNA library, tailbud embryo Ciona
            intestinalis cDNA clone citb088119 5', mRNA sequence.
ACCESSION   BW251013
VERSION     BW251013.1  GI:24830931
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 619)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .619
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="citb088119"
                     /tissue_type="whole animal"
                     /dev_stage="tailbud embryo"
                     /clone_lib="Nori Satoh unpublished cDNA library, tailbud
                     embryo"
ORIGIN

  Query Match             4.2%;  Score 47.6;  DB 13;  Length 619;
  Best Local Similarity   46.0%;  Pred. No. 2.8;
  Matches  161;  Conservative    0;  Mismatches  189;  Indels    0;  Gaps    0;
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Qy        227 TCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCG 286
              | ||  || |||  |   ||     | ||   ||| || | |    || |  ||
Db        506 TGGTGGTGATGTGTTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATT 447

Qy        287 ACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCT 346
              | |   ||| ||  |||| |||   |  |||||| | |  ||  | |  || | ||
Db        446 TCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCC 387

Qy        347 TTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTA 406
              | | || |   |  | | ||  |   |  ||     |  | ||| ||    |
Db        386 TGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGT 327

Qy        407 GGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAG 466
              |  |||  | |   ||| ||| ||| || |     || |     |||   || |||
Db        326 TGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGC 267

Qy        467 GGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGT 526
              || | ||| |  |     |     ||  |||     |     | ||| || |||| | ||
Db        266 TGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGTTGTTGT 207

Qy        527 GCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAG 576
              |    ||      ||  ||||| | |  |  |  ||||| ||| | |
Db        206 TGGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGTG 157
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RESULT 4
BW249566/c
LOCUS BW249566 546 bp mRNA linear EST 09-NOV-2002
DEFINITION BW249566 Nori Satoh unpublished cDNA library, tailbud embryo Ciona intestinalis cDNA clone citb082d19 5', mRNA sequence.
ACCESSION BW249566
VERSION BW249566.1 GI:24829484
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 546)
AUTHORS Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
TITLE Expressed genes in Ciona intestinalis (2002c)
JOURNAL Unpublished (2002)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES Location/Qualifiers
source 1. .546
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="citb082d19"
/tissue_type="whole animal"
/dev_stage="tailbud embryo"
/clone_lib="Nori Satoh unpublished cDNA library, tailbud embryo"
ORIGIN

Query Match 4.1%; Score 47; DB 13; Length 546;
Best Local Similarity 45.5%; Pred. No. 3.6;
Matches 167; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

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Qy        227 TCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCG 286
              | ||  || |||  |   ||     | ||   ||| || | |    || |  ||
Db        512 TGGTGGTGATGTGTTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATT 453

Qy        287 ACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCT 346
              | |   ||| ||  |||| |||   |  |||||| | |  ||  | |  || | ||
Db        452 TCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCC 393

Qy        347 TTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTA 406
              | | || |   |  | | ||  |   |  ||     |  | ||| ||    |
Db        392 TGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGT 333

Qy        407 GGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAG 466
              |  |||  | |   ||| ||| ||| || |     || |     |||   || |||
Db        332 TGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGC 273

Qy        467 GGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGT 526
              || | ||| |  |     |     ||  |||     |     | |||||  |||| | ||
Db        272 TGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGTTGGTGTTGTTGT 213

Qy        527 GCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGT 586
                | |         ||  || || | |  |  |  |||| |||   |  ||  ||||
Db        212 TGTTGGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGTGCTTCTGT 153

Qy        587 TCTCGTC 593
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Db        152 AGTTGCC 146
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RESULT 5
BW193819/c
LOCUS BW193819 660 bp mRNA linear EST 05-NOV-2002
DEFINITION BW193819 Nori Satoh unpublished cDNA library, cleaving embryo Ciona intestinalis cDNA clone cicl101p23 5', mRNA sequence.
ACCESSION BW193819
VERSION BW193819.1 GI:24608221
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 660)
AUTHORS Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
TITLE Expressed genes in Ciona intestinalis (2002c)
JOURNAL Unpublished (2002)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES Location/Qualifiers
source 1. .660
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cicl101p23"
/tissue_type="whole body"
/dev_stage="cleaving embryo"
/clone_lib="Nori Satoh unpublished cDNA library, cleaving embryo"
ORIGIN

Query Match 4.1%; Score 47; DB 13; Length 660;
Best Local Similarity 45.5%; Pred. No. 4;
Matches 167; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

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Qy        227 TCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCG 286
              | ||  || |||  |   ||     | ||   ||| || | |    || |  ||
Db        489 TGGTGGTGATGTGTTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATT 430

Qy        287 ACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCT 346
              | |   ||| ||  |||| |||   |  |||||| | |  ||  | |  || | ||
Db        429 TCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCC 370

Qy        347 TTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTA 406
              | | || |   |  | | ||  |   |  ||     |  | ||| ||    |
Db        369 TGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGT 310

Qy        407 GGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAG 466
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Db        309 TGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGC 250

Qy        467 GGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGT 526

Db        249 TGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGTTGGTGTTGTTGT 190

Qy        527 GCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGT 586

Db        189 TGTTGGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGTGCTTCTGT 130

Qy        587 TCTCGTC 593

Db        129 AGTTGCC 123


RESULT 6
BW192111/c
LOCUS       BW192111                602 bp    mRNA    linear   EST 05-NOV-2002
DEFINITION  BW192111 Nori Satoh unpublished cDNA library, young adult Ciona
            intestinalis cDNA clone ciad095m14 5', mRNA sequence.
ACCESSION   BW192111
VERSION     BW192111.1  GI:24606513
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 602)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .602
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="ciad095m14"
                     /tissue_type="whole animal"
                     /dev_stage="young adult"
                     /clone_lib="Nori Satoh unpublished cDNA library, young
                     adult"
ORIGIN

  Query Match             4.0%;  Score 45.8;  DB 13;  Length 602;
  Best Local Similarity   45.8%;  Pred. No. 7.3;
  Matches  158;  Conservative    0;  Mismatches  187;  Indels    0;  Gaps    0;

Qy        233 TGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTAC 292

Db        444 TGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGTTCC 385

Qy        293 CGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGT 352

Db        384 TGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGT 325

Qy        353 AGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCC 412

Db        324 TGTTCCTGTTGGTGCCGTTGTTGTCCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGA 265

Qy        413 TACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGC 472

Db        264 TGCTGTTGTTGTTGTTGATGATGCTGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGC 205

Qy        473 TGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAG 532

Db        204 TGTTGTTGTTGGTGTTGCTGTTGTTGGCGCTGCTGTTGTTGTTGATGTTGTTGGTGC 145

Qy        533 GGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGT 577

Db        144 TTCTGTAGTTGCCGCTGTTGATATTGGCGGTGATTGCGCTTTTGT 100


RESULT 7
BW314712/c
LOCUS       BW314712                617 bp    mRNA    linear   EST 11-NOV-2002
DEFINITION  BW314712 Nori Satoh unpublished cDNA library, heart Ciona
            intestinalis cDNA clone ciht039h07 5', mRNA sequence.
ACCESSION   BW314712
VERSION     BW314712.1  GI:24895396
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 617)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .617
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="ciht039h07"
                     /tissue_type="heart"
                     /clone_lib="Nori Satoh unpublished cDNA library, heart"
ORIGIN

  Query Match             4.0%;  Score 45.8;  DB 13;  Length 617;
  Best Local Similarity   43.2%;  Pred. No. 7.3;
  Matches  212;  Conservative    0;  Mismatches  279;  Indels    0;  Gaps    0;

Qy         87 GTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTC 146

Db        602 GTTGCTGTTTCTGTGTTCGGTGTATTNTGTGTTGTTGTTGTNGTAGTTGCTGCTGCT 543

Qy        147 GGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACG 206

Db        542 GCTGTTGTTGTTGCTGTAGTTGGTGGTGATGTGTTTTGTGTTGTTCTTGTATTAGGCGTT 483

Qy        207 GTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTG 266

Db        482 GTTGTTGATGTATTTCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGT 423

Qy        267 GCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCG 326

Db        422 GCTGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCT 363

Qy        327 GGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGT 386

Db        362 GTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTCCCTGTTGGT 303

Qy        387 CCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGAC 446

Db        302 GCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGTTGATGATGCTGTTGTTGTT 243

Qy        447 GGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGG 506

Db        242 GGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGCTGTTGTTGGCGCTGCT 183

Qy        507 CCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGAT 566
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Db        182 GTTGTTGTTGTTGATGTTGTTGGTGCTTCTGTAGTTGCCGCTGTTGATATTGGCGGTGAT 123

Qy        567 GTCGTTCGAGT 577
Db        122 TGCGCTTTTGT 112
```

RESULT 8
CA128348
LOCUS CA128348 1039 bp mRNA linear EST 24-SEP-2003
DEFINITION SCJLLR2006A05.g LR2 Saccharum officinarum cDNA clone SCJLLR2006A05 5', mRNA sequence.
ACCESSION CA128348
VERSION CA128348.1 GI:35009126
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE 1 (bases 1 to 1039)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 006 row: A column: 05
Seq primer: T7 Promoter Primer.
FEATURES Location/Qualifiers
source 1. .1039
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCJLLR2006A05"
/lab_host="DH10B"
/clone_lib="LR2"
/note="Organ: Leaf roll from field grown adult plants (small insert library); Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [Leaf roll from field grown adult plants (small insert library)]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
ORIGIN

Query Match 3.8%; Score 43.6; DB 13; Length 1039;
Best Local Similarity 45.6%; Pred. No. 30;
Matches 154; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

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Qy        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
Db        303 TCGGTGGAGACGTACAAGATCTACATCTTCAAGGTGCTGAAGCAGGTGCACCCGGACATC 362

Qy        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546
Db        363 TGCATCTCGTCCAAGGCCATGTCCATCATGAACTTCTTCATCAACGACATCTTCCATAAG 422

Qy        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
Db        423 CTGGCGGCGGAGGCGGCCAAACTGGCGCGCTACAACAAGAAGCCCACCATCACGTGCCGC 482

Qy        607 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 666
Db        483 GAGATCCAGACTTTCGTCCGCCTCGTCCTCCCCGGCGAGCTCGCCAAGCACGCCTTCTTC 542

Qy        667 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 726
Db        543 GAGGTGCACCAAGGCCGTTACCAAGTTCACCAGCTCCTATGCGAGCGATGGGACCTGCCT 602

Qy        727 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGT 764
Db        603 TAGTTTCGTTCATGAAGTACTAGTGTGTTGTCGTGTGT 640
```

RESULT 9
AI869699/c
LOCUS AI869699 486 bp mRNA linear EST 07-MAR-2000
DEFINITION wm02f07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2433253 3' similar to gb:J05016 PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AI869699
VERSION AI869699.1 GI:5543667
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 486)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 751 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 282.
FEATURES Location/Qualifiers
source 1. .486
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2433253"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Brn25"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATAGGTTTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN

Query Match 3.8%; Score 43.2; DB 9; Length 486;
Best Local Similarity 54.4%; Pred. No. 26;
Matches 87; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

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Qy        914 AGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGA 973
```

```
Db        430 ACAGAGATCTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGA 371

Qy        974 CGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTC 1033

Db        370 CCAAGGAAGAGCTTTGAAGGCCTGAGGTCTGCGAAAGGTGGGAGGAGGCAGACGCCCTGC 311

Qy       1034 GTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1073

Db        310 GTGGCCCATGGTCGGGGCGTCCACGCCGAGGCCGGCAACA 271


RESULT 10
BW265514/c
LOCUS       BW265514                658 bp    mRNA    linear   EST 09-NOV-2002
DEFINITION  BW265514 Nori Satoh unpublished cDNA library, gastrula and neurula
            Ciona intestinalis cDNA clone cign040o10 5', mRNA sequence.
ACCESSION   BW265514
VERSION     BW265514.1  GI:24845432
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 658)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .658
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cign040o10"
                     /tissue_type="whole body"
                     /dev_stage="gastrula and neurula"
                     /clone_lib="Nori Satoh unpublished cDNA library, gastrula
                     and neurula"
ORIGIN

  Query Match             3.8%;  Score 43.2;  DB 13;  Length 658;
  Best Local Similarity   44.1%;  Pred. No. 30;
  Matches  180;  Conservative    0;  Mismatches  228;  Indels    0;  Gaps    0;

Qy        165 GTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCT 224

Db        566 GTTGTTGTTGTTGTAGTTGCTGCTGCTGCTGTTGTTGTTGCTGTAGTTGGTGGTGATGTG 507

Qy        225 CCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGAC 284

Db        506 TTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATTTCGTGTTGTTGCT 447

Qy        285 CGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCT 344

Db        446 GTTGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTT 387

Qy        345 CTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGG 404

Db        386 CCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTT 327

Qy        405 TAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGAT 464

Db        326 GGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGCTGTTGTTGTT 267

Qy        465 AGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTG 524

Db        266 GGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGTTGTTGTTGTTGTTGTT 207

Qy        525 GTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTT 572

Db        206 GGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGT 159


RESULT 11
BW259047/c
LOCUS       BW259047                663 bp    mRNA    linear   EST 09-NOV-2002
DEFINITION  BW259047 Nori Satoh unpublished cDNA library, gastrula and neurula
            Ciona intestinalis cDNA clone cign001j16 5', mRNA sequence.
ACCESSION   BW259047
VERSION     BW259047.1  GI:24838965
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 663)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .663
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cign001j16"
                     /tissue_type="whole body"
                     /dev_stage="gastrula and neurula"
                     /clone_lib="Nori Satoh unpublished cDNA library, gastrula
                     and neurula"
ORIGIN

  Query Match             3.8%;  Score 43.2;  DB 13;  Length 663;
  Best Local Similarity   44.1%;  Pred. No. 31;
  Matches  180;  Conservative    0;  Mismatches  228;  Indels    0;  Gaps    0;

Qy        165 GTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCT 224

Db        566 GTTGTTGTTGTTGTAGTTGCTGCTGCTGCTGTTGTTGTTGCTGTAGTTGGTGGTGATGTG 507

Qy        225 CCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGAC 284

Db        506 TTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATTTCGTGTTGTTGCT 447

Qy        285 CGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCT 344

Db        446 GTTGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTT 387

Qy        345 CTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGG 404

Db        386 CCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTT 327

Qy        405 TAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGAT 464

Db        326 GGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGCTGTTGTTGTT 267

Qy        465 AGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTG 524

Db        266 GGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGTTGTTGTTGTTGTTGTT 207

Qy        525 GTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTT 572

Db        206 GGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGT 159
```

```
RESULT 12
CNS006ON
LOCUS       CNS006ON                910 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR14J21 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL065629
VERSION     AL065629.1  GI:4944698
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 910)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .910
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR14J21"
                     /clone_lib="RPCI-98"
                     /note="end : T7"
ORIGIN

  Query Match             3.8%;  Score 43.2;  DB 29;  Length 910;
  Best Local Similarity   19.2%;  Pred. No. 35;
  Matches   81;  Conservative  159;  Mismatches  180;  Indels    2;  Gaps    1;

Qy        315 GAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG 374
              | ||: |  : ||| ||| :|||||  | | |:|: |  : ||    |:  :::: |
Db        468 GGGGKGGGGKGGGGGGGGGHGGGGGSGGGTDTKTWTGGKSTGGGGGGGSSGGSSSKGGGC 527

Qy        375 GGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCA 434
              |:  :  || |:     : ||| :::| :  :::::  :  : ::| : :   | |:
Db        528 GSGSYGGGGGGYGGTGSGSGGGGSSSSGCSSSSSSSSSSSSCGSSSBGCBSSCGCGSCSY 587

Qy        435 GTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTC 494
              : ::  :||:   | :: :   ::     | :::|:|| :: ::: :| : : : :|
Db        588 SSSSTGSTGSCGCGSSSSSSSSSSCSSTSTSSSSTSGCGYSSSGSBSSSCSSTBTSSSTT 647

Qy        495 GTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAG 554
              :|:  : :|:: ::|:|  ||: |:|::: ::|::: : :: ::  : : ::: ::: :
Db        648 BTBTKBTSTYSTSYTST--TTSTTSTBSBTSYGSBBKSTSSTSSSTSSSTSSSSSSTSS 705

Qy        555 GAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAA 614
                  : : :::::||:   |: : ::|  |:: ::   : :    : : :| : :
Db        706 CTSTKBYSTSTBSYSBTTBTBTTSTSTBBTTSTBYTBBTTBYTKSTTSMTSTYTTBBSTS 765

Qy        615 GAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGA 674
              : :|  : :::  |  :| :|  :  : :: : |:    |: ::::::  :|: :   : :
Db        766 KBSTBTSTBKSTGTKTBTSBTTSCTSSSSSBSTSYSYSTSCBSSBSBSSTSYSBCTSTST 825

Qy        675 CAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTG 734
              : : :::::    :   ::| ::|:||    :| |: :||:::: |  :  ||  || |
Db        826 STSSBBSSBSSSSSCGTSBTSSSTSTTSTCTSTTCKTSTGBSSYGTGTSTYTTBTTTATT 885

Qy        735 CT 736
              :|
Db        886 ST 887


RESULT 13
BF593096/c
LOCUS       BF593096                509 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  7o56e02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578187 3'
            similar to TR:Q29305 Q29305 DISULFIDE ISOMERASE-RELATED PROTEIN ;,
            mRNA sequence.
ACCESSION   BF593096
VERSION     BF593096.1  GI:11685420
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 509)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 405.
FEATURES             Location/Qualifiers
     source          1. .509
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3578187"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Kid11"
                     /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
                     prepared, and ss circles were made in vitro. Following HAP
                     purification, this DNA was used as tracer in a subtractive
                     hybridization reaction. The driver was PCR-amplified cDNAs
                     from a pool of 5,000 clones made from the same library
                     (cloneIDs 1322376-1323911, 1456007-1456775, and
                     1500552-1502855). Subtraction by Bento Soares and M.
                     Fatima Bonaldo.  "
ORIGIN

  Query Match             3.8%;  Score 42.8;  DB 10;  Length 509;
  Best Local Similarity   54.4%;  Pred. No. 33;
  Matches   86;  Conservative    0;  Mismatches   72;  Indels    0;  Gaps    0;

Qy        916 AGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACG 975
              |||   |||||||  |||      | |     || |  || | |   ||    |   |||||
Db        425 AGAAATCTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGACC 366

Qy        976 GTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGT 1035
              |||  |      |||| || ||  |||| |    | | ||   | |  | | ||| |||
Db        365 AAGGAAGAGCTTTGAAGGCCTGAGGTCTGCGGAAGGTGGGAGGAGGCAGACGCCCTGCGT 306

Qy       1036 AGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1073
```

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                  | |||  |||| ||| || ||| |||| | ||  | |
Db        305 GGCCCATGGTCGGGGCGTCCACACCGAGGCCGGCAACA 268


RESULT 14
CA686322/c
LOCUS       CA686322                552 bp    mRNA    linear   EST 25-NOV-2002
DEFINITION  wlm96.pk032.g24 wlm96 Triticum aestivum cDNA clone wlm96.pk032.g24
            5' end, mRNA sequence.
ACCESSION   CA686322
VERSION     CA686322.1  GI:25275677
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 552)
  AUTHORS   Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
            Miao,G., Caraher,N. and Hanafey,M.K.
  TITLE     DuPont Wheat cDNA Sequence
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Scott V. Tingey
            Crop Genetics
            E. I. DuPont de Nemours and Company
            1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
            Tel: 302-631-2602
            Fax: 302-631-2607
            Email: Scott.V.Tingey@USA.dupont.com
            Seq primer: M13.
FEATURES             Location/Qualifiers
     source          1. .552
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /cultivar="Stephens"
                     /db_xref="taxon:4565"
                     /clone="wlm96.pk032.g24"
                     /tissue_type="leaf"
                     /clone_lib="wlm96"
                     /note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
                     XhoI; Wheat (Triticum aestivum L.) seedlings 96 hr after
                     inoculation w/ E. graminis"
ORIGIN

  Query Match             3.8%;  Score 42.8;  DB 14;  Length 552;
  Best Local Similarity   48.0%;  Pred. No. 35;
  Matches  119;  Conservative    0;  Mismatches  129;  Indels    0;  Gaps    0;

Qy        402 GGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAA 461
              |||||| | | ||| |||         || ||||  || | || | |  ||||  ||| |
Db        347 GGGTAGAGGCGTACGCGATGACCGAGAGGCCCAGCGGGGCGGGCCTGTTCAGTGGCCGCA 288

Qy        462 GATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTT 521
              | |    || | || ||  ||| ||  | |     || | | |        || |    |
Db        287 GGTGCAGTTGGTGCAGGTGCAGCTGGCGCCGCACTTGCACTTGCCGTCGTTCTCCGCGGC 228

Qy        522 CTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCA 581
              ||  |||      | |    ||       |  |  ||  | |  |||| |||    || ||
Db        227 CTCCTGCACCTCGAAGTGNCTCTTNTCGGTGTCGACCATGACGATGCCGTAGCCGTCGCC 168

Qy        582 CCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGA 641
              | | ||| ||  |   ||| |  |   ||||  |     |  |||||    |  |   |
Db        167 CTTCTTCACGCACTGGGTCTTGTCGGCGCAGTCGCAGTTGCCGCACTTGTCAGCCATGGC 108

Qy        642 CGTGTTGG 649
              || ||||
Db        107 GGTCTTGG 100


RESULT 15
CA012935/c
LOCUS       CA012935                642 bp    mRNA    linear   EST 23-OCT-2002
DEFINITION  HT06O08r HT Hordeum vulgare subsp. vulgare cDNA clone HT06O08
            5-PRIME, mRNA sequence.
ACCESSION   CA012935
VERSION     CA012935.1  GI:24290279
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. vulgare
  ORGANISM  Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 642)
  AUTHORS   Zhang,H., Potokina,E., Michalek,W., Weschke,W., Stein,N. and
            Graner,A.
  TITLE     Barley ESTs from germinating seeds
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Stein Nils
            Molecular Markers Group, Department Genbank
            Institute of Plant Genetics and Crop Plant Research (IPK)
            Correnssstr. 3, 06466, Gatersleben, Germany
            Tel: 039482-5522
            Fax: 039482-5595
            Email: stein@ipk-gatersleben.de
            Insert Length: 642   Std Error: 0.00
            Plate: 6  row: O  column: 8
            Seq primer: M13rev.
FEATURES             Location/Qualifiers
     source          1. .642
                     /organism="Hordeum vulgare subsp. vulgare"
                     /mol_type="mRNA"
                     /cultivar="barke"
                     /sub_species="vulgare"
                     /db_xref="GABI:261458"
                     /db_xref="taxon:112509"
                     /clone="HT06O08"
                     /tissue_type="endosperm early"
                     /dev_stage="0-16 hours after imbibition"
                     /lab_host="XL10-Gold"
                     /clone_lib="HT"
                     /note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of
                     cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning
                     artefact caused by the kit, in most cases the EcoRI site
                     is NOT present, as well as the EcoRIadapter used for
                     cloning. To excise the insert, restriction sites upstream
                     EcoRI should be used (e.g. BamHI, SalI,PstI). NOTE: Also
                     due to the cloning system used Blue/white selection for
                     recombinats is not 100% reliable."
ORIGIN

  Query Match             3.8%;  Score 42.6;  DB 13;  Length 642;
  Best Local Similarity   44.3%;  Pred. No. 41;
  Matches  174;  Conservative    0;  Mismatches  219;  Indels    0;  Gaps    0;

Qy        273 CGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGG 332
              | | ||| ||| | ||    |  |  | ||| |   |   ||| |||| |  ||  |
Db        567 CTTCGTCTTGAGCCACGGCTCAATGGACTTGTACTGCTGGTAGAAGTTGGTGAGGTCGAC 508

Qy        333 TCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACAT 392
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Qy        393 GTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCA 452
              || ||    |         |  | || |    | ||   || ||||   |  | ||| ||
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              |   ||| ||||   || | | |   | | | |  |       ||  |
Db        387 GGACCCGCAGATGCCCTCCCGGCAAGACCGGCGGAACGCCAGCGTCGAGTCGTGCTCCGA 328

Qy        513 GTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTT 572
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Db        267 GGACTGCAGGAACGGCCGGCCATGCGCGTCCGGGTTCCACCGGTATATCTGGAACTCCTT 208

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Search completed: May 10, 2004, 06:19:29
Job time : 2231 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:37 ; Search time 3069 Seconds
(without alignments)
16029.437 Million cell updates/sec

Title: US-10-679-999-16
Perfect score: 1135
Sequence: 1 CATATGGACAAAACTCACAC.....TCCGGGTTGTTAATGGATCC 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 5401154

Minimum DB seq length: 0
Maximum DB seq length: 1135

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	1109.4	97.7	1135	6	BD056521	BD056521 OB fusion
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4	662.4	58.4	748	6	AX304259	AX304259 Sequence
5	662.4	58.4	757	6	AR437967	AR437967 Sequence
6	662.4	58.4	757	6	AX304247	AX304247 Sequence
7	662.4	58.4	763	6	AR437969	AR437969 Sequence
8	662.4	58.4	763	6	AX304251	AX304251 Sequence
9	662.4	58.4	794	6	AR437913	AR437913 Sequence
10	662.4	58.4	794	6	AX303197	AX303197 Sequence
11	662.4	58.4	812	6	AR437917	AR437917 Sequence
12	662.4	58.4	812	6	AX303207	AX303207 Sequence
13	662.4	58.4	859	6	AX327583	AX327583 Sequence
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17	660.8	58.2	773	6	AR437971	AR437971 Sequence
18	660.8	58.2	773	6	AX304255	AX304255 Sequence
19	658.4	58.0	684	6	BD262999	BD262999 Dimeric t
20	658.4	58.0	684	6	AR437912	AR437912 Sequence
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22	658.4	58.0	684	6	AX303193	AX303193 Sequence
23	658.4	58.0	684	6	AX318309	AX318309 Sequence
24	658.4	58.0	684	6	AX320751	AX320751 Sequence
25	658.4	58.0	684	6	AX327476	AX327476 Sequence
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39	657	57.9	762	6	AX556168	AX556168 Sequence
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ALIGNMENTS

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LOCUS BD056523 1135 bp DNA linear PAT 27-AUG-2002
DEFINITION OB fusion protein compositions and methods.
ACCESSION BD056523
VERSION BD056523.1 GI:22602129
KEYWORDS JP 2001512417-A/11.
SOURCE Aequorea victoria
ORGANISM Aequorea victoria
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
REFERENCE 1 (bases 1 to 1135)
AUTHORS Mann,M.B. and Hecht,R.I.
TITLE OB fusion protein compositions and methods
JOURNAL Patent: JP 2001512417-A 11 21-AUG-2001;

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            AMGEN. INC
COMMENT     PN   JP 2001512417-A/11
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
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FEATURES            Location/Qualifiers
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  Query Match            100.0%;  Score 1135;  DB 6;  Length 1135;
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RESULT 2
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LOCUS       BD056521                1135 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056521
VERSION     BD056521.1  GI:22602127
KEYWORDS    JP 2001512417-A/9.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1135)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 9 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/9
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
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            CC   Strandedness: Double;
            CC   Topology: Linear;
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            FH   Key             Location/Qualifiers.
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RESULT 3
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LOCUS       AR437973                748 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1067 from patent US 6660843.
ACCESSION   AR437973
VERSION     AR437973.1  GI:40203312
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 748)
  AUTHORS   Feige,U. and Liu,C.-F.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: US 6660843-A 1067 09-DEC-2003;
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match 58.4%; Score 662.4; DB 6; Length 748;
Best Local Similarity 97.7%; Pred. No. 4.9e-132;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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RESULT 4
AX304259

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LOCUS       AX304259               748 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 1067 from Patent WO0183525.
ACCESSION   AX304259
VERSION     AX304259.1  GI:17383760
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Feige,U., Liu,C.F., Cheetham,J.C., Boone,T.C. and Gudas,J.M.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: WO 0183525-A 1067 08-NOV-2001;
            Amgen Inc., (US)
FEATURES             Location/Qualifiers
     source          1. .748
                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"
                     /note="Fc-MMP INHIBITOR"
     CDS             4. .735
                     /note="unnamed protein product"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAD13122.1"
                     /db_xref="GI:17383761"
                     /db_xref="REMTREMBL:CAD13122"
                     /translation="MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                     VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
                     KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
                     EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
                     QKSLSLSPGKGGGGGCTTHWGFTLC"
ORIGIN

  Query Match           58.4%;  Score 662.4;  DB 6;  Length 748;
  Best Local Similarity  97.7%;  Pred. No. 4.9e-132;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
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Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
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Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
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Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 5
AR437967
LOCUS       AR437967               757 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1055 from patent US 6660843.
ACCESSION   AR437967
VERSION     AR437967.1  GI:40203306
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 757)
  AUTHORS   Feige,U. and Liu,C.-F.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: US 6660843-A 1055 09-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .757
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           58.4%;  Score 662.4;  DB 6;  Length 757;
  Best Local Similarity  97.7%;  Pred. No. 4.9e-132;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
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Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 6
AX304247
LOCUS       AX304247                757 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 1055 from Patent WO0183525.
ACCESSION   AX304247
VERSION     AX304247.1  GI:17383748
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Feige,U., Liu,C.F., Cheetham,J.C., Boone,T.C. and Gudas,J.M.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: WO 0183525-A 1055 08-NOV-2001;
            Amgen Inc., (US)
FEATURES             Location/Qualifiers
     source          1. .757
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                     /db_xref="taxon:32630"
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     CDS             4. .750
                     /note="unnamed protein product"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAD13116.1"
                     /db_xref="GI:17383749"
                     /db_xref="REMTREMBL:CAD13116"
                     /translation="MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                     VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
                     KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
                     EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
                     QKSLSLSPGKGGGGGDFLPHYKNTSLGHRP"
ORIGIN

  Query Match           58.4%;  Score 662.4;  DB 6;  Length 757;
  Best Local Similarity  97.7%;  Pred. No. 4.9e-132;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
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Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 7
AR437969
LOCUS       AR437969                763 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1059 from patent US 6660843.
ACCESSION   AR437969
VERSION     AR437969.1  GI:40203308
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 763)
  AUTHORS   Feige,U. and Liu,C.-F.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: US 6660843-A 1059 09-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .763
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           58.4%;  Score 662.4;  DB 6;  Length 763;
  Best Local Similarity  97.7%;  Pred. No. 4.9e-132;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
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Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
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Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

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Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

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Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688

Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 8
AX304251
LOCUS       AX304251                763 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 1059 from Patent WO0183525.
ACCESSION   AX304251
VERSION     AX304251.1  GI:17383752
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Feige,U., Liu,C.F., Cheetham,J.C., Boone,T.C. and Gudas,J.M.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: WO 0183525-A 1059 08-NOV-2001;
            Amgen Inc., (US)
FEATURES             Location/Qualifiers
     source          1. .763
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Fc-IL-1 ANTAGONIST"
     CDS             4. .750
                     /note="unnamed protein product"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAD13118.1"
                     /db_xref="GI:17383753"
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                     KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
                     EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
                     QKSLSLSPGKGGGGGFEWTPGYWQPYALPL"
ORIGIN

  Query Match           58.4%;  Score 662.4;  DB 6;  Length 763;
  Best Local Similarity   97.7%;  Pred. No. 4.9e-132;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60

Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

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Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

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Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300

Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

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Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

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Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

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Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688

Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 9
AR437913
LOCUS       AR437913                794 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 5 from patent US 6660843.
ACCESSION   AR437913
VERSION     AR437913.1  GI:40203252
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 794)
  AUTHORS   Feige,U. and Liu,C.-F.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: US 6660843-A 5 09-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .794
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           58.4%;  Score 662.4;  DB 6;  Length 794;
  Best Local Similarity   97.7%;  Pred. No. 4.9e-132;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60

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Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
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Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
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Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
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Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
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Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
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Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
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Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 10
AX303197
LOCUS       AX303197                794 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 5 from Patent WO0183525.
ACCESSION   AX303197
VERSION     AX303197.1  GI:17383677
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Feige,U., Liu,C.F., Cheetham,J.C., Boone,T.C. and Gudas,J.M.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: WO 0183525-A 5 08-NOV-2001;
            Amgen Inc., (US)
FEATURES             Location/Qualifiers
     source          1. .794
                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"
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     CDS             39. .782
                     /note="unnamed protein product"
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                     /protein_id="CAD13102.1"
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                     /translation="MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
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                     KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
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                     QKSLSLSPGKGGGGGIEGPTLRQWLAARA"
ORIGIN

  Query Match             58.4%;  Score 662.4;  DB 6;  Length 794;
  Best Local Similarity   97.7%;  Pred. No. 4.9e-132;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
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Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
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Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
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Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
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Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
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Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
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Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 11
AR437917
LOCUS       AR437917                812 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 15 from patent US 6660843.
ACCESSION   AR437917
VERSION     AR437917.1  GI:40203256
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 812)
  AUTHORS   Feige,U. and Liu,C.-F.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: US 6660843-A 15 09-DEC-2003;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             58.4%;  Score 662.4;  DB 6;  Length 812;
  Best Local Similarity   97.7%;  Pred. No. 4.9e-132;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
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Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
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Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
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Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
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Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
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Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
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Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 12
AX303207
LOCUS       AX303207                812 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 15 from Patent WO0183525.
ACCESSION   AX303207
VERSION     AX303207.1  GI:17383685
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Feige,U., Liu,C.F., Cheetham,J.C., Boone,T.C. and Gudas,J.M.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: WO 0183525-A 15 08-NOV-2001;
            Amgen Inc., (US)

FEATURES             Location/Qualifiers
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     CDS             39. .800
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                     /translation="MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                     VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
                     KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
                     EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
                     QKSLSLSPGKGGGGGGGTYSCHFGPLTWVCKPQGG"
ORIGIN

  Query Match             58.4%;  Score 662.4;  DB 6;  Length 812;
  Best Local Similarity   97.7%;  Pred. No. 4.9e-132;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
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Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
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Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
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Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
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Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
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Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
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Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
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RESULT 13
AX327583
LOCUS       AX327583                859 bp    DNA     linear   PAT 07-JAN-2002
DEFINITION  Sequence 108 from Patent WO0181377.
ACCESSION   AX327583
VERSION     AX327583.1  GI:18097963
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Feige,U., Kohno,T., Lacey,D.L. and Boone,T.C.
  TITLE     Integrin/adhesion antagonists
  JOURNAL   Patent: WO 0181377-A 108 01-NOV-2001;
            Amgen, Inc. (US)
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     CDS             4. .852
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ORIGIN

  Query Match           58.4%;  Score 662.4;  DB 6;  Length 859;
  Best Local Similarity   97.7%;  Pred. No. 4.8e-132;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
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Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
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Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
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Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
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Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
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Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 14
BD263009
LOCUS       BD263009                861 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and
            having thrombopoietic activity.
ACCESSION   BD263009
VERSION     BD263009.1  GI:33072777
KEYWORDS    JP 2002536960-A/11.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 861)
  AUTHORS   Liu,C.F., Feige,U. and Cheetham,J.
  TITLE     Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and
            having thrombopoietic activity
  JOURNAL   Patent: JP 2002536960-A 11 05-NOV-2002;
            AMGEN INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002536960-A/11
            PD   05-NOV-2002
            PF   22-OCT-1999 JP 2000578340
            PR   23-OCT-1998 US    60/105348
            PI   CHUAN FA LIU,ULRICH FEIGE,JANET CHEETHAM
            PC   C12N15/09,A61K38/00,A61P7/00,C07K14/52,C07K19/00,C12N1/15, PC
             C12N1/19,
            PC   C12N1/21,C12N5/10,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC
            Description of Artificial Sequence: oligonucleotide FH   Key
                 Location/Qualifiers
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            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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  Query Match           58.4%;  Score 662.4;  DB 6;  Length 861;
  Best Local Similarity   97.7%;  Pred. No. 4.8e-132;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
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Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

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Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
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Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
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Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
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Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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RESULT 15
AR437914
LOCUS       AR437914                 861 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 7 from patent US 6660843.
ACCESSION   AR437914
VERSION     AR437914.1  GI:40203253
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 861)
  AUTHORS   Feige,U. and Liu,C.-F.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: US 6660843-A 7 09-DEC-2003;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           58.4%;  Score 662.4;  DB 6;  Length 861;
  Best Local Similarity   97.7%;  Pred. No. 4.8e-132;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
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Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
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Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
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Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
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Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
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Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
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Search completed: May 10, 2004, 03:26:25
Job time : 3071 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:35 ; Search time 333.5 Seconds
(without alignments)
14457.886 Million cell updates/sec

Title: US-10-679-999-16
Perfect score: 1135
Sequence: 1 CATATGGACAAAACTCACAC.....TCCGGGTTGTTAATGGATCC 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 5802412

Minimum DB seq length: 0
Maximum DB seq length: 1135

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
2: geneseqn1990s:*
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8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1135	100.0	1135	2	AAV32903	Aav32903 Recombina
2	1109.4	97.7	1135	2	AAV32902	Aav32902 Recombina
3	1109.4	97.7	1135	2	AAV69686	Aav69686 Recombina
4	662.4	58.4	748	6	ABL35776	Abl35776 Fc-MMP in
5	662.4	58.4	757	3	AAA69501	Aaa69501 Fc-TNF-al
6	662.4	58.4	757	6	ABL35770	Abl35770 Fc-TNF-al
7	662.4	58.4	763	3	AAA69503	Aaa69503 Fc-IL-1 a
8	662.4	58.4	794	3	AAA69444	Aaa69444 Fc-TMP nu
9	662.4	58.4	794	6	ABL35761	Abl35761 Fc-TPO mi
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15	662.4	58.4	861	6	ABL35762	Abl35762 Fc-TMP-TM
16	660.8	58.2	748	3	AAA69507	Aaa69507 Fc-MMP in
17	660.8	58.2	763	6	ABL35772	Abl35772 Fc-interl
18	660.8	58.2	773	3	AAA69505	Aaa69505 Fc-VEGF a
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20	658.4	58.0	684	3	AAA29220	Aaa29220 Human IgG
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23	658.4	58.0	684	6	ABA03672	Aba03672 Human IgG
24	658.4	58.0	684	6	ABK24097	Abk24097 Human cDN
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26	658.4	58.0	684	6	ABL35760	Abl35760 Human imm
27	658.4	58.0	684	6	AAI67658	Aai67658 Human imm
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29	658.4	58.0	684	7	ABT33856	Abt33856 Human IgG
30	657.6	57.9	816	6	AAD23841	Aad23841 Fc-calcit
31	657.6	57.9	884	3	AAA69451	Aaa69451 Fc-EMP-EM
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33	657.2	57.9	1050	2	AAQ28684	Aaq28684 LFA-3-Ig
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35	657.2	57.9	1050	4	AAF28326	Aaf28326 Human LFA
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37	657.2	57.9	1050	6	ABK15720	Abk15720 cDNA enco
38	657	57.9	705	6	AAD30460	Aad30460 Human imm
39	657	57.9	711	2	AAX87655	Aax87655 DNA encod
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ALIGNMENTS

RESULT 1
AAV32903
ID AAV32903 standard; cDNA; 1135 BP.
XX
AC AAV32903;
XX
DT 18-NOV-1998 (first entry)
XX
DE Recombinant human MetFc-OB variant 3 cDNA.
XX
KW Recombinant human MetFc-OB variant 3 cDNA; chimeric; immunoglobulin;
KW high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
KW diabetes; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 4. .1128
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FT mat_peptide 7. .1125
FT /*tag= b
FT misc_feature 685. .1125
FT /*tag= c
FT /note= "Encodes for the OB part of the fusion protein"
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PN WO9828427-A1.
XX
PD 02-JUL-1998.
XX
PF 11-DEC-1997; 97WO-US023183.
XX
PR 20-DEC-1996; 96US-00770973.
XX
PA (AMGE-) AMGEN INC.
XX
PI Mann MB, Hecht RI;
XX
DR WPI; 1998-377658/32.
DR P-PSDB; AAW49076.
XX
PT New fusion proteins of OB and Fc - used for treating e.g. excess weight,
PT diabetes, arterial sclerosis, arterial plaque, high blood lipid level,
PT gall stones or stroke.
XX

PS Disclosure; Fig 6A-6C; 107pp; English.
XX
CC The present sequence represents a recombinant human MetFc-OB variant 3
CC cDNA which encodes a recombinant human Fc-OB fusion variant 3 protein
CC having the L16E, E99A, K101A and K103A substitutions when compared with
CC the template protein shown in AAW49075. The invention provides Fc-OB
CC fusion proteins whereby the Fc region of an immunoglobulin or its
CC analogue is linked, either directly or indirectly using a linker, to the
CC N-terminus of an OB protein or its analogue. The Fc-OB fusion proteins
CC are claimed to demonstrate increased stability and clearance rate and
CC decreased degradation as compared to OB protein or a fusion of Fc to the
CC C-terminus of the OB protein. These Fc-OB fusion proteins are also
CC claimed to be useful for treating excess weight in an individual or
CC animal or for treating co-morbidities associated with excess fat such as
CC diabetes, high blood lipid level, arterial sclerosis and stroke
XX
SQ Sequence 1135 BP; 270 A; 365 C; 283 G; 217 T; 0 U; 0 Other;

Query Match 100.0%; Score 1135; DB 2; Length 1135;
Best Local Similarity 100.0%; Pred. No. 2.4e-253;
Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
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Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Db        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900

Qy        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960
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Qy        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020
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Db       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080

Qy       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
```

RESULT 2
AAV32902
ID AAV32902 standard; cDNA; 1135 BP.
XX
AC AAV32902;
XX
DT 18-NOV-1998 (first entry)
XX
DE Recombinant human MetFc-OB variant 2 cDNA.
XX
KW Recombinant human MetFc-OB variant 2 cDNA; chimeric; immunoglobulin;
KW high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
KW diabetes; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	CDS	4. .1128
FT		/*tag= a
FT		/product= "Recombinant human Fc-OB variant 2"
FT	mat_peptide	7. .1125
FT		/*tag= b
FT	misc_feature	685. .1125
FT		/*tag= c
FT		/note= "Encodes for the OB part of the fusion protein"

XX
PN WO9828427-A1.
XX
PD 02-JUL-1998.
XX
PF 11-DEC-1997; 97WO-US023183.
XX
PR 20-DEC-1996; 96US-00770973.
XX
PA (AMGE-) AMGEN INC.
XX
PI Mann MB, Hecht RI;
XX
DR WPI; 1998-377658/32.
DR P-PSDB; AAW49075.
XX
PT New fusion proteins of OB and Fc - used for treating e.g. excess weight,
PT diabetes, arterial sclerosis, arterial plaque, high blood lipid level,
PT gall stones or stroke.
XX
PS Disclosure; Fig 5A-5C; 107pp; English.

```
XX
CC   The present sequence represents a recombinant human MetFc-OB variant 2
CC   cDNA which encodes a recombinant human Fc-OB fusion variant 2 protein
CC   having a 5 residue deletion of residues 2-6 of the wild-type Fc-OB
CC   protein sequence shown in AAW49073. The invention provides Fc-OB fusion
CC   proteins whereby the Fc region of an immunoglobulin or its analogue is
CC   linked, either directly or indirectly using a linker, to the N-terminus
CC   of an OB protein or its analogue. The Fc-OB fusion proteins are claimed
CC   to demonstrate increased stability and clearance rate and decreased
CC   degradation as compared to OB protein or a fusion of Fc to the C-terminus
CC   of the OB protein. These Fc-OB fusion proteins are also claimed to be
CC   useful for treating excess weight in an individual or animal or for
CC   treating co-morbidities associated with excess fat such as diabetes, high
CC   blood lipid level, arterial sclerosis and stroke
XX
SQ   Sequence 1135 BP; 271 A; 361 C; 283 G; 220 T; 0 U; 0 Other;

  Query Match             97.7%;  Score 1109.4;  DB 2;  Length 1135;
  Best Local Similarity   98.6%;  Pred. No. 2.1e-247;
  Matches 1119;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || ||||||||||||||    || ||||| .
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720

Qy        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780

Qy        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840

Qy        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900

Qy        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960

Qy        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020

Qy       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080

Qy       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135


RESULT 3
AAV69686
ID   AAV69686 standard; DNA; 1135 BP.
XX
AC   AAV69686;
XX
DT   05-FEB-1999  (first entry)
XX
DE   Recombinant human metFc-OB protein variant encoding DNA.
XX
KW   Recombinant; metFc-OB protein; Fc region; immunoglobulin; Ig; OB;
KW   obesity; human; adiposity; blood lipid; diabetes type II; insulin;
KW   hypoglycaemic; antihypertensive; diuretic; appetite suppressant;
KW   suspension; variant; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             4. .1128
FT                   /*tag=  a
FT                   /product= "metFc-OB protein variant"
XX
PN   WO9846257-A1.
XX
PD   22-OCT-1998.
XX
PF   16-APR-1998;   98WO-US007828.
XX
PR   17-APR-1997;   97US-00843971.
PR   14-APR-1998;   98US-00059467.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Brems DN,  French DL,  Speed MA;
XX
DR   WPI; 1998-594525/50.
DR   P-PSDB; AAW83963.
XX
PT   Concentrated suspension of fusion of obesity protein with Fc
PT   immunoglobulin fragment - stable at physiological pH, used for e.g.
PT   reduction of weight and blood lipid levels, and for treatment of type II
PT   diabetes.
XX
PS   Disclosure; Fig 6A-C; 47pp; English.
XX
CC   This DNA encodes a recombinant metFc-OB protein variant which consists of
CC   an Fc region of human immunoglobulin (Ig) fused to a human OB (obesity)
CC   protein. The invention provides a human OB protein suspension that
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CC   contains at least 0.5 mg/ml of the human OB protein derivatised by
CC   attachment of the Fc region of an Ig to the N-terminus of OB, and has a
CC   pH 6-8. The suspensions are used to reduce weight, adiposity and blood
CC   lipid levels, to treat or prevent diabetes type II, and to increase lean
CC   mass and insulin sensitivity. They may be used in conjunction with
CC   insulin, hypoglycaemics, antihypertensives, diuretics, appetite
CC   suppressants etc. These suspensions are stable and active at
CC   physiological pH and are ready-for-use formulations that do not require
CC   freezing or freeze drying. As they are very concentrated, only small
CC   volumes are required and they provide a sustained-release effect, with
CC   increased potency and reduced frequency of injection
XX
SQ   Sequence 1135 BP; 271 A; 361 C; 283 G; 220 T; 0 U; 0 Other;

  Query Match             97.7%;  Score 1109.4;  DB 2;  Length 1135;
  Best Local Similarity   98.6%;  Pred. No. 2.1e-247;
  Matches 1119;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              ||||||||||||||||||||||| ||||| || ||||||||||||||    || |||||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720

Qy        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780

Qy        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840

Qy        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900

Qy        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960

Qy        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020

Qy       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080

Qy       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135


RESULT 4
ABL35776
ID   ABL35776 standard; DNA; 748 BP.
XX
AC   ABL35776;
XX
DT   05-APR-2002  (first entry)
XX
DE   Fc-MMP inhibitor fusion amino acid SEQ ID NO:1068.
XX
KW   Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW   erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW   TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW   TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW   MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW   cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW   antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW   neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW   cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW   sleep disorder; neurological degenerative disease; anaemia;
KW   thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW   Fanconi's syndrome; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200183525-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US014310.
XX
PR   03-MAY-2000; 2000US-00563286.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Féige U,  Liu C,  Cheetham JC,  Boone TC,  Gudas JM;
XX
DR   WPI; 2002-130313/17.
DR   P-PSDB; ABB73426.
XX
PT   Novel vehicle-peptide molecule or its multimers useful for treating
PT   inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT   diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS   Example 7; Fig 25A-B; 176pp; English.
XX
CC   The present invention describes a vehicle-peptide molecule (I) or its
CC   multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC   cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC   antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
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CC   neuroprotective activities. (I) can be used as a therapeutic or
CC   prophylactic agent as well as for screening purposes. (I) is useful for
CC   diagnosing diseases characterised by dysfunction of their associated
CC   protein of interest, for identifying normal or abnormal proteins of
CC   interest, as a part of diagnostic kit to detect the presence of their
CC   proteins of interest in a biological sample. Additionally, (I) is useful
CC   for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC   rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC   infertility, and neurological degenerative diseases. (I), comprising EPO-
CC   mimetic compounds are useful for treating disorders characterised by low
CC   red blood cell levels such as anaemia. The TPO-mimetic comprising
CC   compounds are useful for treating conditions that involve an existing
CC   megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC   deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC   tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC   and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC   represent amino acid and nucleic acid sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 748 BP; 180 A; 240 C; 201 G; 127 T; 0 U; 0 Other;

  Query Match             58.4%;  Score 662.4;  DB 6;  Length 748;
  Best Local Similarity   97.7%;  Pred. No. 7.9e-144;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              ||||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

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RESULT 5
AAA69501
ID   AAA69501 standard; DNA; 757 BP.
XX
AC   AAA69501;
XX
DT   31-OCT-2000  (first entry)
XX
DE   Fc-TNF-alpha inhibitor fusion nucleotide sequence SEQ ID NO:1055.
XX
KW   Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW   autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW   immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW   inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW   cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW   vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW   thrombosis; pharmaceutical; ds.
XX
OS   Synthetic.
XX
PN   WO200024782-A2.
XX
PD   04-MAY-2000.
XX
PF   25-OCT-1999;   99WO-US025044.
XX
PR   23-OCT-1998;   98US-0105371P.
PR   22-OCT-1999;   99US-00428082.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C,  Cheetham J,  Boone TC;
XX
DR   WPI; 2000-350702/30.
DR   P-PSDB; AAB17951.
XX
PT   Novel composition of matter comprising an Fc domain and pharmacologically
PT   active peptides, useful for treating cancer and autoimmune diseases.
XX
PS   Example 4; Page 566-568; 608pp; English.
XX
CC   The present invention describes composition of matter (I) comprising an
CC   Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC   (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC   independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC   (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC   P3, and P4 = are each independently sequences of pharmacologically active
CC   peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC   c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC   of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC   thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC   cells from the present invention can be used for producing pharmaceutical
CC   compositions. The compositions are useful for treating cancer, asthma,
CC   thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC   a Fab domain) can provide a longer half-life or incorporate functions
CC   such as Fc receptor binding, protein A binding, complement fixation, and
CC   possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC   AAB18003 represent nucleotide and amino acid sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 757 BP; 185 A; 244 C; 200 G; 128 T; 0 U; 0 Other;

  Query Match             58.4%;  Score 662.4;  DB 3;  Length 757;
  Best Local Similarity   97.7%;  Pred. No. 7.9e-144;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              ||||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
Qy       121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
Db       121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
Qy       181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
Db       181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
Qy       241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
Db       241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
Qy       301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
Db       301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
Qy       361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
Db       361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
Qy       421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
Db       421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
Qy       481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
Db       481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
Qy       541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
Db       541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
Qy       601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
Db       601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
Qy       661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
Db       661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

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RESULT 6
ABL35770
ID   ABL35770 standard; DNA; 757 BP.
XX
AC   ABL35770;
XX
DT   05-APR-2002  (first entry)
XX
DE   Fc-TNF-alpha inhibitor fusion amino acid SEQ ID NO:1056.
XX
KW   Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW   erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW   TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW   TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW   MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW   cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW   antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW   neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW   cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW   sleep disorder; neurological degenerative disease; anaemia;
KW   thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW   Fanconi's syndrome; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200183525-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US014310.
XX
PR   03-MAY-2000; 2000US-00563286.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C,  Cheetham JC,  Boone TC,  Gudas JM;
XX
DR   WPI; 2002-130313/17.
DR   P-PSDB; ABB73420.
XX
PT   Novel vehicle-peptide molecule or its multimers useful for treating
PT   inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT   diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS   Example 4; Fig 19A-B; 176pp; English.
XX
CC   The present invention describes a vehicle-peptide molecule (I) or its
CC   multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC   cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC   antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC   neuroprotective activities. (I) can be used as a therapeutic or
CC   prophylactic agent as well as for screening purposes. (I) is useful for
CC   diagnosing diseases characterised by dysfunction of their associated
CC   protein of interest, for identifying normal or abnormal proteins of
CC   interest, as a part of diagnostic kit to detect the presence of their
CC   proteins of interest in a biological sample. Additionally, (I) is useful
CC   for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC   rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC   infertility, and neurological degenerative diseases. (I), comprising EPO-
CC   mimetic compounds are useful for treating disorders characterised by low
CC   red blood cell levels such as anaemia. The TPO-mimetic comprising
CC   compounds are useful for treating conditions that involve an existing
CC   megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC   deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC   tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC   and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC   represent amino acid and nucleic acid sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 757 BP; 185 A; 244 C; 200 G; 128 T; 0 U; 0 Other;

  Query Match            58.4%;  Score 662.4;  DB 6;  Length 757;
  Best Local Similarity  97.7%;  Pred. No. 7.9e-144;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
Db         1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60
Qy        61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
Db        61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
Qy       121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
Db       121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
Qy       181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
Db       181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
Qy       241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
Db       241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
Qy       301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
Db       301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
Qy       361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
Db       361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

RESULT 7
AAA69503
ID AAA69503 standard; DNA; 763 BP.
XX
AC AAA69503;
XX
DT 31-OCT-2000 (first entry)
XX
DE Fc-IL-1 antagonist fusion nucleotide sequence SEQ ID NO:1059.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical; ds.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
DR P-PSDB; AAB17953.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Example 5; Page 572-573; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 763 BP; 182 A; 243 C; 208 G; 130 T; 0 U; 0 Other;

```
  Query Match             58.4%;  Score 662.4;  DB 3;  Length 763;
  Best Local Similarity   97.7%;  Pred. No. 7.9e-144;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || ||||||||||||||||    || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||  |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

RESULT 8
AAA69444
ID AAA69444 standard; DNA; 794 BP.
XX
AC AAA69444;
XX
DT 31-OCT-2000 (first entry)
XX
DE Fc-TMP nucleotide sequence SEQ ID NO:5.

```
XX
KW   Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW   autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW   immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW   inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW   cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW   vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW   thrombosis; pharmaceutical; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200024782-A2.
XX
PD   04-MAY-2000.
XX
PF   25-OCT-1999;   99WO-US025044.
XX
PR   23-OCT-1998;   98US-0105371P.
PR   22-OCT-1999;   99US-00428082.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C,  Cheetham J,  Boone TC;
XX
DR   WPI; 2000-350702/30.
DR   P-PSDB; AAB16958.
XX
PT   Novel composition of matter comprising an Fc domain and pharmacologically
PT   active peptides, useful for treating cancer and autoimmune diseases.
XX
PS   Example 2; Page 178-179; 608pp; English.
XX
CC   The present invention describes composition of matter (I) comprising an
CC   Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC   (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC   independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC   (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC   P3, and P4 = are each independently sequences of pharmacologically active
CC   peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC   c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC   of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC   thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC   cells from the present invention can be used for producing pharmaceutical
CC   compositions. The compositions are useful for treating cancer, asthma,
CC   thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC   a Fab domain) can provide a longer half-life or incorporate functions
CC   such as Fc receptor binding, protein A binding, complement fixation, and
CC   possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC   AAB18003 represent nucleotide and amino acid sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 794 BP; 195 A; 242 C; 213 G; 144 T; 0 U; 0 Other;

  Query Match             58.4%;  Score 662.4;  DB 3;  Length 794;
  Best Local Similarity   97.7%;  Pred. No. 8e-144;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 9
ABL35761
ID   ABL35761 standard; DNA; 794 BP.
XX
AC   ABL35761;
XX
DT   05-APR-2002  (first entry)
XX
DE   Fc-TPO mimetic peptide (Fc-TMP) nucleic acid SEQ ID NO:5.
XX
KW   Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW   erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW   TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW   TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW   MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW   cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW   antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW   neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW   cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW   sleep disorder; neurological degenerative disease; anaemia;
KW   thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW   Fanconi's syndrome; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200183525-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US014310.
XX
PR   03-MAY-2000; 2000US-00563286.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C,  Cheetham JC,  Boone TC,  Gudas JM;
XX
DR   WPI; 2002-130313/17.
```

DR P-PSDB; ABB73411.
XX
PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS Example 2; Fig 7; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 794 BP; 195 A; 242 C; 213 G; 144 T; 0 U; 0 Other;

Query Match 58.4%; Score 662.4; DB 6; Length 794;
Best Local Similarity 97.7%; Pred. No. 8e-144;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
```

RESULT 10
AAA69448
ID AAA69448 standard; DNA; 812 BP.
XX
AC AAA69448;
XX
DT 31-OCT-2000 (first entry)
XX
DE Fc-EMP nucleotide sequence SEQ ID NO:15.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
DR P-PSDB; AAB16964.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Example 3; Page 190-191; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention

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XX
SQ   Sequence 812 BP; 198 A; 246 C; 218 G; 150 T; 0 U; 0 Other;

  Query Match            58.4%;  Score 662.4;  DB 3;  Length 812;
  Best Local Similarity  97.7%;  Pred. No. 8.1e-144;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 11
ABL35765
ID   ABL35765 standard; DNA; 812 BP.
XX
AC   ABL35765;
XX
DT   05-APR-2002  (first entry)
XX
DE   Fc-EPO mimetic peptide (Fc-EMP) nucleic acid SEQ ID NO:15.
XX
KW   Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW   erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW   TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW   TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW   MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW   cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW   antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW   neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW   cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW   sleep disorder; neurological degenerative disease; anaemia;
KW   thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW   Fanconi's syndrome; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200183525-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US014310.
XX
PR   03-MAY-2000; 2000US-00563286.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C,  Cheetham JC,  Boone TC,  Gudas JM;
XX
DR   WPI; 2002-130313/17.
DR   P-PSDB; ABB73415.
XX
PT   Novel vehicle-peptide molecule or its multimers useful for treating
PT   inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT   diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS   Example 3; Fig 13; 176pp; English.
XX
CC   The present invention describes a vehicle-peptide molecule (I) or its
CC   multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC   cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC   antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC   neuroprotective activities. (I) can be used as a therapeutic or
CC   prophylactic agent as well as for screening purposes. (I) is useful for
CC   diagnosing diseases characterised by dysfunction of their associated
CC   protein of interest, for identifying normal or abnormal proteins of
CC   interest, as a part of diagnostic kit to detect the presence of their
CC   proteins of interest in a biological sample. Additionally, (I) is useful
CC   for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC   rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC   infertility, and neurological degenerative diseases. (I), comprising EPO-
CC   mimetic compounds are useful for treating disorders characterised by low
CC   red blood cell levels such as anaemia. The TPO-mimetic comprising
CC   compounds are useful for treating conditions that involve an existing
CC   megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC   deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC   tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC   and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC   represent amino acid and nucleic acid sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 812 BP; 198 A; 246 C; 218 G; 150 T; 0 U; 0 Other;

  Query Match            58.4%;  Score 662.4;  DB 6;  Length 812;
  Best Local Similarity  97.7%;  Pred. No. 8.1e-144;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
```

```
RESULT 12
ABK24109
ID   ABK24109 standard; DNA; 859 BP.
XX
AC   ABK24109;
XX
DT   29-AUG-2003  (revised)
DT   09-APR-2002  (first entry)
XX
DE   DNA encoding Echistatin/IgG Fc fusion protein.
XX
KW   IgG Fc; ds; anticoagulant; thrombolytic; cytostatic; antiinflammatory;
KW   immunosuppressive; osteopathic; antagonist; laminin; saw-scaled viper;
KW   echistatin; integrin; selectin; vinculin; platelet aggregation;
KW   angiogenesis; tumour; inflammation; autoimmune disease;
KW   rheumatoid arthritis; osteoporosis.
XX
OS   Echis carinatus.
OS   Homo sapiens.
OS   Chimeric.
XX
PN   WO200181377-A2.
XX
PD   01-NOV-2001.
XX
PF   23-APR-2001; 2001WO-US013069.
XX
PR   21-APR-2000; 2000US-0198919P.
PR   03-MAY-2000; 2000US-0201394P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Kohno T,  Lacey DL,  Boone TC;
XX
DR   WPI; 2002-062025/08.
DR   P-PSDB; AAU81169.
XX
PT   Composition comprising integrin or adhesion antagonistic peptide and
PT   vehicle, useful for treating or preventing platelet aggregation, has a
PT   longer half-life than free peptide.
XX
PS   Example 1; Page 45-46; 68pp; English.
XX
CC   The invention relates to a composition comprising an integrin/adhesion
CC   antagonistic peptide (I) and a vehicle e.g. IgG Fc. The peptides are
CC   based on laminin or saw-scaled viper echistatin and target integrin,
CC   selectin or vinculin.Also included are compounds of formula (Ia) and
CC   their multimers (X^1)_a-F^1-(X^2)_b where; F^1 = Fc domain; X^1 and X^2 =
CC   -(L^1)_c-P^1, (L^1)_c-P^1-(L^2)_d-P^2, (L^1)_c-P^1-(L^2)_d-P^2-(L^3)_e-
CC   P^3 or (L^1)_c-P^1-(L^2)_d-P^2-(L^3)_e-P^3-(L^4)_f-P^4; P^1-P^4 = same or
CC   different (I); L^1-L^4 = same or different linkers; a-f = 0 or 1,
CC   provided at least one of a and b = 1, a nucleic acid that encodes (Ia),
CC   an expression vector containing the nucleic acid, host cells containing
CC   the vector, producing a pharmaceutically active compound (B) by
CC   covalently linking at least one Fc domain to at least one amino acid
CC   sequence of a selected randomized (I) and any of six laminin-related
CC   peptides (Ib). The compositions are used prophylactically and
CC   therapeutically in the same way as (I), e.g. to inhibit platelet
CC   aggregation or angiogenesis (tumours), or to treat inflammation and
CC   autoimmune diseases (e.g. rheumatoid arthritis) and many different forms
CC   of osteoporosis, also for diagnosis. Attaching the vehicle (especially Fc
CC   domain) to (I) increases the half-life (free (I) are normally degraded
CC   very quickly in vivo). The present sequence encodes all or part of an
CC   antagonist peptide-IgG Fc fusion compound of the invention. (Updated on
CC   29-AUG-2003 to standardise OS field)
XX
SQ   Sequence 859 BP; 220 A; 258 C; 232 G; 149 T; 0 U; 0 Other;
```

Query Match 58.4%; Score 662.4; DB 6; Length 859;
Best Local Similarity 97.7%; Pred. No. 8.2e-144;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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```
Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              ||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

RESULT 13
AAA29229
ID AAA29229 standard; DNA; 861 BP.
XX
AC AAA29229;
XX
DT 04-SEP-2000 (first entry)
XX
DE Human IgG1 Fc TMP fusion coding sequence.
XX
KW Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet;
KW megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV;
KW anti-anaemic; dermatological; immunosuppressive; anti-inflammatory; ds.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   39. .848
FT   /*tag= a
XX
PN WO200024770-A2.
XX
PD 04-MAY-2000.
XX
PF 22-OCT-1999; 99WO-US024834.
XX
PR 23-OCT-1998; 98US-0105348P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Liu C, Feige U, Cheetham J;
XX
DR WPI; 2000-365108/31.
DR P-PSDB; AAY96531.
XX
PT Thrombopoietic peptides which activate mpl receptors and increase the
PT production of platelets or platelet precursors, useful for treatment of
PT diseases which involve thombocytopenia.
XX
PS Example 2A; Page 49-50; 91pp; English.
XX
CC A compound which binds to an mpl receptor comprising a thrombopoietin
CC mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is
CC new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to
CC 14 residues in length comprising X_2-X_1_0, X_2-X_1_1, X_2-X_1_2, X_2-
CC X_1_3, X_2-X_1_4, X_1-X_1_0, X_1-X_1_1, X_1-X_1_2, X_1-X_1_3, and X_1-
CC X_1_4. X_1 = I, A, V, L, S or R; X_2 = E, D, K or V; X_3 = G or A; X_4 =
CC P; X_5 = T or S; X_6 = L, I, V, A or F; X_7 = R or K; X_8 = Q, N, or E;
CC X_9 = W, Y or F; X_1_0 = L, I, V, A, F, M, or K; X_1_1 = A, I, V, L, F,
CC S, T, K, H, or E; X_1_2 = A, I, V, L, F, G, S, or Q; X_1_3 = R, K, T, V,
CC N, Q or G; X_1_4 = A, I, V, L, F, T, R, E, or G; L_1 = linker comprising
CC 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and activate
CC the c-Mpl receptor which mediates the activity of endogenous
CC thrombopoietin. The TMPs are useful for increasing the production of
CC platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which
CC is useful for treatment of diseases which involve thombocytopenia, e.g.
CC aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency
CC virus associated ITP, and systemic lupus erythematosus
XX
SQ Sequence 861 BP; 206 A; 259 C; 241 G; 155 T; 0 U; 0 Other;

  Query Match   58.4%; Score 662.4; DB 3; Length 861;
  Best Local Similarity 97.7%; Pred. No. 8.2e-144;

  Matches 672; Conservative   0; Mismatches   16; Indels   0; Gaps   0;

```
Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              ||||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
```

RESULT 14
AAA69445
ID AAA69445 standard; DNA; 861 BP.
XX
AC AAA69445;
XX
DT 31-OCT-2000 (first entry)
XX
DE Fc-TMP-TMP nucleotide sequence SEQ ID NO:7.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200024782-A2.

XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
DR P-PSDB; AAB16959.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Example 2; Page 180-182; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 861 BP; 206 A; 259 C; 241 G; 155 T; 0 U; 0 Other;

Query Match 58.4%; Score 662.4; DB 3; Length 861;
Best Local Similarity 97.7%; Pred. No. 8.2e-144;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || |||||||||||||||    || || |||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
```

RESULT 15
ABL35762
ID ABL35762 standard; DNA; 861 BP.
XX
AC ABL35762;
XX
DT 05-APR-2002 (first entry)
XX
DE Fc-TMP-TMP nucleic acid SEQ ID NO:7.
XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome; gene; dg.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200183525-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014310.
XX
PR 03-MAY-2000; 2000US-00563286.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX
DR WPI; 2002-130313/17.
DR P-PSDB; ABB73412.
XX
PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS Example 2; Fig 8; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or

CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 861 BP; 206 A; 259 C; 241 G; 155 T; 0 U; 0 Other;

Query Match 58.4%; Score 662.4; DB 6; Length 861;
Best Local Similarity 97.7%; Pred. No. 8.2e-144;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy    1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
          ||||||||||||||||||||||| ||||| || ||||||||||||||||   || || |||
Db   36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy   61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy  121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy  181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy  241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db  276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy  301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
          |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy  361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy  421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy  481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy  541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy  601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy  661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
          ||||||||||||||||||||||||||||
Db  696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
```

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Job time : 336.5 secs

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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:36 ; Search time 59.25 Seconds
(without alignments)
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Title: US-10-679-999-16
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1245136

Minimum DB seq length: 0
Maximum DB seq length: 1135

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	662.4	58.4	748	4	US-09-428-082B-1067	Sequence 1067, Ap
2	662.4	58.4	757	4	US-09-428-082B-1055	Sequence 1055, Ap
3	662.4	58.4	763	4	US-09-428-082B-1059	Sequence 1059, Ap
4	662.4	58.4	794	4	US-09-428-082B-5	Sequence 5, Appli
5	662.4	58.4	812	4	US-09-428-082B-15	Sequence 15, Appl
6	662.4	58.4	861	4	US-09-428-082B-7	Sequence 7, Appli
7	660.8	58.2	773	4	US-09-428-082B-1063	Sequence 1063, Ap
8	658.4	58.0	684	4	US-09-428-082B-1	Sequence 1, Appli
9	658.4	58.0	684	4	US-09-847-249A-1	Sequence 1, Appli
10	657.6	57.9	885	4	US-09-428-082B-21	Sequence 21, Appl
11	657.2	57.9	1050	1	US-07-940-861-42	Sequence 42, Appl
12	657.2	57.9	1050	1	US-08-459-512-42	Sequence 42, Appl
13	657.2	57.9	1050	2	US-08-459-657-42	Sequence 42, Appl
14	657.2	57.9	1050	2	US-08-460-132-42	Sequence 42, Appl
15	657.2	57.9	1050	3	US-08-466-465-7	Sequence 7, Appli
16	657.2	57.9	1050	5	PCT-US92-02050-42	Sequence 42, Appl
17	657	57.9	705	4	US-09-023-655-1223	Sequence 1223, Ap
18	657	57.9	1019	3	US-09-178-869-1	Sequence 1, Appli
19	657	57.9	1019	4	US-09-761-413-1	Sequence 1, Appli
20	657	57.9	1080	4	US-09-180-100-14	Sequence 14, Appl
21	656.8	57.9	757	4	US-09-428-082B-1061	Sequence 1061, Ap
22	656.8	57.9	761	4	US-09-428-082B-1057	Sequence 1057, Ap
23	656.8	57.9	763	4	US-09-428-082B-1069	Sequence 1069, Ap
24	656.8	57.9	789	4	US-09-428-082B-11	Sequence 11, Appl
25	656.8	57.9	807	4	US-09-428-082B-17	Sequence 17, Appl
26	656.8	57.9	855	4	US-09-428-082B-9	Sequence 9, Appli
27	656.8	57.9	881	4	US-09-428-082B-19	Sequence 19, Appl
28	655.8	57.8	706	4	US-09-122-144-1	Sequence 1, Appli
29	655.4	57.7	693	1	US-08-322-805-3	Sequence 3, Appli
30	655.4	57.7	693	2	US-08-429-499-3	Sequence 3, Appli
31	655.4	57.7	693	3	US-09-152-733-3	Sequence 3, Appli
32	655.4	57.7	699	2	US-08-595-043A-49	Sequence 49, Appl
33	654.6	57.7	773	4	US-09-428-082B-1065	Sequence 1065, Ap
34	653.8	57.6	1135	1	US-08-236-311-8	Sequence 8, Appli
35	653.8	57.6	1135	3	US-08-457-918-8	Sequence 8, Appli
36	652.4	57.5	768	2	US-08-284-391B-32	Sequence 32, Appl
37	652.4	57.5	768	3	US-09-218-950-32	Sequence 32, Appl
38	652.2	57.5	699	4	US-09-522-217-33	Sequence 33, Appl
39	652.2	57.5	699	4	US-09-404-641-45	Sequence 45, Appl
40	652.2	57.5	699	4	US-09-923-246-33	Sequence 33, Appl
41	652.2	57.5	699	4	US-10-295-723-33	Sequence 33, Appl
42	652.2	57.5	733	4	US-09-227-357-1	Sequence 1, Appli
43	652.2	57.5	733	4	US-09-527-236A-27	Sequence 27, Appl
44	652.2	57.5	733	4	US-09-280-839-4	Sequence 4, Appli
45	652.2	57.5	733	4	US-09-411-977-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-428-082B-1067
; Sequence 1067, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1067
; LENGTH: 748
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc MMP INHIBITOR
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(732)
; OTHER INFORMATION:
US-09-428-082B-1067

Query Match 58.4%; Score 662.4; DB 4; Length 748;
Best Local Similarity 97.7%; Pred. No. 8.5e-161;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
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Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

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Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
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Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
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Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
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Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
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Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
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Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
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Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

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Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
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Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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RESULT 4
US-09-428-082B-5
; Sequence 5, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 794
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc-TMP
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(779)
; OTHER INFORMATION:
US-09-428-082B-5

Query Match 58.4%; Score 662.4; DB 4; Length 794;
Best Local Similarity 97.7%; Pred. No. 8.7e-161;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
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Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
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Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
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RESULT 5
US-09-428-082B-15
; Sequence 15, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371

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;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 812
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc-EMP
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (39)..(797)
;   OTHER INFORMATION:
US-09-428-082B-15

  Query Match             58.4%;  Score 662.4;  DB 4;  Length 812;
  Best Local Similarity   97.7%;  Pred. No. 8.7e-161;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

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Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
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Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
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Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
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Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 6
US-09-428-082B-7
; Sequence 7, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/09/428,082B
;  CURRENT FILING DATE:  1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 861
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc-TMP-TMP
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (39)..(842)
;   OTHER INFORMATION:
US-09-428-082B-7

  Query Match             58.4%;  Score 662.4;  DB 4;  Length 861;
  Best Local Similarity   97.7%;  Pred. No. 8.9e-161;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

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Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
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Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
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Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
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Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
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Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        421 AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG 480

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Db        481 GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC 540

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Db        661 AGCCTCTCCCTGTCTCCGGGTAAA 684


RESULT 9
US-09-847-249A-1
; Sequence 1, Application US/09847249A
; Patent No. 6677136
; GENERAL INFORMATION:
;  APPLICANT: MARSHALL, WILLIAM S.
;  APPLICANT:  STARK, KEVIN LEE
;  TITLE OF INVENTION: GLUCAGON ANTAGONIST
;  FILE REFERENCE: A-693
;  CURRENT APPLICATION NUMBER: US/09/847,249A
;  CURRENT FILING DATE:  2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,436
;  PRIOR FILING DATE: 2000-05-03
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 684
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(684)
;   OTHER INFORMATION:
US-09-847-249A-1

  Query Match             58.0%;  Score 658.4;  DB 4;  Length 684;
  Best Local Similarity   97.7%;  Pred. No. 8.8e-160;
  Matches  668;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          4 ATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCA 63
              |||||||||||||||||||| ||||| || ||||||||||||||    || || ||||||
Db          1 ATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCA 60

Qy         64 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 120

Qy        124 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG 180

Qy        184 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG 240

Qy        244 TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTAC 303
              |||||||||||||||||||||||||||||||||||||||||||||||||| | |||||||
Db        241 TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC 300

Qy        304 GCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC 363
                  ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC 360

Qy        364 AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC 420

Qy        424 AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG 480

Qy        484 GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC 540

Qy        544 TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG 600

Qy        604 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG 660

Qy        664 AGCCTCTCCCTGTCTCCGGGTAAA 687
              ||||||||||||||||||||||||
Db        661 AGCCTCTCCCTGTCTCCGGGTAAA 684


RESULT 10
US-09-428-082B-21
; Sequence 21, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/09/428,082B
;  CURRENT FILING DATE:  1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
;   LENGTH: 885
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc-EMP-EMP
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (39)..(869)
;   OTHER INFORMATION:
US-09-428-082B-21

  Query Match             57.9%;  Score 657.6;  DB 4;  Length 885;
  Best Local Similarity   97.2%;  Pred. No. 1.5e-159;
  Matches  669;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||| ||||| |||||||| || ||||||   || || |||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275
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Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCTCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              ||||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
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RESULT 11
US-07-940-861-42
; Sequence 42, Application US/07940861
; Patent No. 5547853
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: WALLNER, Barbara P.
; APPLICANT: MILLER, Glenn T.
; APPLICANT: ROSA, Margaret D.
; TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
; TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 875 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022-6250
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/940,861
; FILING DATE: 21-OCT-1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02050
; FILING DATE: 12-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/667,971
; FILING DATE: 12-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,967
; FILING DATE: 07-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY, James F., Jr.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B151CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)715-0600
; TELEFAX: (212)715-0673
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1050 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1041
US-07-940-861-42

Query Match 57.9%; Score 657.2; DB 1; Length 1050;
Best Local Similarity 97.4%; Pred. No. 2.1e-159;
Matches 668; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Qy          2 ATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGT 61
              || | |||||||||||||||||||||||||||||||| || ||||||   || ||  ||||
Db        356 ATGTCGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGT 415

Qy         62 CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGG 475

Qy        122 TCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACG 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 TCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACG 535

Qy        182 TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCA 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCA 595

Qy        242 CGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTT 301
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||| | | |
Db        596 CGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGT 655

Qy        302 ACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG 361
              ||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 ACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG 715

Qy        362 CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGA 421
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Db        716 CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGA 775

Qy        422 CCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCG 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 CCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCG 835

Qy        482 TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGG 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        836 TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGG 895

Qy        542 ACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGC 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 ACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGC 955

Qy        602 AGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGA 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 AGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGA 1015

Qy        662 AGAGCCTCTCCCTGTCTCCGGGTAAA 687
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Db       1016 AGAGCCTCTCCCTGTCTCCGGGTAAA 1041
```

RESULT 12

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US-08-459-512-42
; Sequence 42, Application US/08459512
; Patent No. 5728677
;  GENERAL INFORMATION:
;    APPLICANT:  BIOGEN, INC.
;    APPLICANT:  WALLNER, Barbara P.
;    APPLICANT:  MILLER, Glenn T.
;    APPLICANT:  ROSA, Margaret D.
;    TITLE OF INVENTION:  CD2-BINDING DOMAIN OF LYMPHOCYTE
;    TITLE OF INVENTION:  FUNCTION ASSOCIATED ANTIGEN 3
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Neave
;      STREET:  875 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10022-6250
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/459,512
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/02050
;      FILING DATE:  12-MAR-1992
;      APPLICATION NUMBER:  US 07/667,971
;      FILING DATE:  12-MAR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/770,967
;      FILING DATE:  07-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HALEY, James F., Jr.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  B151CIP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)715-0600
;      TELEFAX:  (212)715-0673
;      TELEX:  14-8367
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1050 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1041
US-08-459-512-42

  Query Match             57.9%;  Score 657.2;  DB 1;  Length 1050;
  Best Local Similarity   97.4%;  Pred. No. 2.1e-159;
  Matches  668;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          2 ATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGT 61
              || | ||||||||||||||||||||||||||| || ||||||   || || ||||
Db        356 ATGTCGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGT 415

Qy         62 CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGG 475

Qy        122 TCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACG 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 TCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACG 535

Qy        182 TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCA 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCA 595

Qy        242 CGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTT 301
              ||||||| |||||||||||||||||||||||||||||||||||||||||| | | |
Db        596 CGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGT 655

Qy        302 ACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG 361
              ||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 ACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG 715

Qy        362 CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGA 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGA 775

Qy        422 CCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCG 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 CCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCG 835

Qy        482 TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGG 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        836 TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGG 895

Qy        542 ACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGC 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 ACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGC 955

Qy        602 AGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGA 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 AGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGA 1015

Qy        662 AGAGCCTCTCCCTGTCTCCGGGTAAA 687
              |||||||||||||||||||||||||
Db       1016 AGAGCCTCTCCCTGTCTCCGGGTAAA 1041


RESULT 13
US-08-459-657-42
; Sequence 42, Application US/08459657
; Patent No. 5914111
;  GENERAL INFORMATION:
;    APPLICANT:  BIOGEN, INC.
;    APPLICANT:  WALLNER, Barbara P.
;    APPLICANT:  MILLER, Glenn T.
;    APPLICANT:  ROSA, Margaret D.
;    TITLE OF INVENTION:  CD2-BINDING DOMAIN OF LYMPHOCYTE
;    TITLE OF INVENTION:  FUNCTION ASSOCIATED ANTIGEN 3
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Neave
;      STREET:  875 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10022-6250
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/459,657
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/02050
;      FILING DATE:  12-MAR-1992
;      APPLICATION NUMBER:  US 07/667,971
;      FILING DATE:  12-MAR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/770,967
;      FILING DATE:  07-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
```

```
;       NAME:  HALEY, James F., Jr.
;       REGISTRATION NUMBER:  27,794
;       REFERENCE/DOCKET NUMBER:  B151CIP2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212)715-0600
;       TELEFAX:  (212)715-0673
;       TELEX:  14-8367
;   INFORMATION FOR SEQ ID NO:  42:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1050 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..1041
US-08-459-657-42

  Query Match             57.9%;  Score 657.2;  DB 2;  Length 1050;
  Best Local Similarity   97.4%;  Pred. No. 2.1e-159;
  Matches  668;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          2 ATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGT 61
              || | |||||||||||||||||||||||||||||| || ||||||   || || ||||
Db        356 ATGTCGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGT 415

Qy         62 CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGG 475

Qy        122 TCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACG 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 TCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACG 535

Qy        182 TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCA 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCA 595

Qy        242 CGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTT 301
              ||||||| ||||||||||||||||||||||||||||||||||||||||||| |   |
Db        596 CGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGT 655

Qy        302 ACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG 361
              ||    |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 ACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG 715

Qy        362 CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGA 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        422 CCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCG 481
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Db        776 CCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCG 835

Qy        482 TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGG 541
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Db        836 TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGG 895

Qy        542 ACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGC 601
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Qy        602 AGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGA 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        662 AGAGCCTCTCCCTGTCTCCGGGTAAA 687
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Db       1016 AGAGCCTCTCCCTGTCTCCGGGTAAA 1041
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RESULT 14
US-08-460-132-42
; Sequence 42, Application US/08460132
; Patent No. 5928643
;  GENERAL INFORMATION:
;    APPLICANT:  BIOGEN, INC.
;    APPLICANT:  WALLNER, Barbara P.
;    APPLICANT:  MILLER, Glenn T.
;    APPLICANT:  ROSA, Margaret D.
;    TITLE OF INVENTION:  CD2-BINDING DOMAIN OF LYMPHOCYTE
;    TITLE OF INVENTION:  FUNCTION ASSOCIATED ANTIGEN 3
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Neave
;      STREET:  875 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10022-6250
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,132
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/940,861
;      FILING DATE:  21-OCT-1992
;      APPLICATION NUMBER:  PCT/US92/02050
;      FILING DATE:  12-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/667,971
;      FILING DATE:  12-MAR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/770,967
;      FILING DATE:  07-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HALEY, James F., Jr.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  B151CIP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)715-0600
;      TELEFAX:  (212)715-0673
;      TELEX:  14-8367
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1050 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1041
US-08-460-132-42

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  Best Local Similarity   97.4%;  Pred. No. 2.1e-159;
  Matches  668;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

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Db        356 ATGTCGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGT 415

Qy         62 CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGG 121
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Qy        122 TCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACG 181
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Qy        182 TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCA 241
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Db        596 CGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGT 655

Qy        302 ACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAG 361
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Qy        362 CCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGA 421
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Qy        422 CCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCG 481
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Db        776 CCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCG 835

Qy        482 TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGG 541
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Db        836 TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGG 895

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Qy        602 AGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGA 661
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RESULT 15
US-08-466-465-7
; Sequence 7, Application US/08466465
; Patent No. 6162432
;  GENERAL INFORMATION:
;    APPLICANT:  Wallner, Barbara P.
;    APPLICANT:  Cooper, Kevin D.
;    TITLE OF INVENTION:  Method of Prophylaxis or Treatment of Antigen
;    TITLE OF INVENTION:  Presenting Cell Driven Skin Conditions Using
;    TITLE OF INVENTION:  Inhibitors of the CD2/LFA-3 Interaction
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/466,465
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/08755
;      FILING DATE:  06-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/862,022
;      FILING DATE:  12-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/770,969
;      FILING DATE:  07-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Myers, Louis (PLM)
;      REGISTRATION NUMBER:  35,965
;      REFERENCE/DOCKET NUMBER:  BGP-111CP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-5941
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1050 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1041
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;      NAME/KEY:  sig-peptide
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;      LOCATION:  85..1041
;      OTHER INFORMATION:  /note= "LFA3TIP"
;    FEATURE:
;      NAME/KEY:  misc-feature
;      LOCATION:  360..361
;      OTHER INFORMATION:  /note= "LFA-3/IgG fusion point"
US-08-466-465-7

  Query Match             57.9%;  Score 657.2;  DB 3;  Length 1050;
  Best Local Similarity   97.4%;  Pred. No. 2.1e-159;
  Matches  668;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          2 ATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGT 61
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Qy         62 CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGG 121
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Qy        182 TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCA 241
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Db        836 TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGG 895

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Qy        662 AGAGCCTCTCCCTGTCTCCGGGTAAA 687
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Db       1016 AGAGCCTCTCCCTGTCTCCGGGTAAA 1041
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Job time : 61.25 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2004, 16:13:07 ; Search time 473.75 Seconds
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Title: US-10-679-999-16
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Sequence: 1 CATATGGACAAAACTCACAC.....TCCGGGTTGTTAATGGATCC 1135

Scoring table: IDENTITY_NUC
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Searched: 2941586 seqs, 2264995651 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1109.4	97.7	1135	13	US-10-679-999-13	Sequence 13, Appl
3	662.4	58.4	748	12	US-10-645-761-1067	Sequence 1067, Ap
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6	662.4	58.4	748	13	US-10-651-723-1067	Sequence 1067, Ap
7	662.4	58.4	748	17	US-10-666-696-1067	Sequence 1067, Ap
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27	662.4	58.4	812	17	US-10-666-696-15	Sequence 15, Appl
28	662.4	58.4	837	15	US-10-269-806-151	Sequence 151, App
29	662.4	58.4	859	9	US-09-840-277-108	Sequence 108, App
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33	662.4	58.4	861	13	US-10-651-723-7	Sequence 7, Appli
34	662.4	58.4	861	17	US-10-666-696-7	Sequence 7, Appli
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38	660.8	58.2	773	13	US-10-651-723-1063	Sequence 1063, Ap
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45	658.4	58.0	684	12	US-10-645-761-1	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
US-10-679-999-16
; Sequence 16, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 16:
;        SEQUENCE CHARACTERISTICS:
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;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;          MOLECULE TYPE: cDNA
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;             NAME/KEY:  misc_feature
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Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720

Qy        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780

Qy        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840

Qy        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900

Qy        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960

Qy        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020

Qy       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080

Qy       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
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Db       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135


RESULT 2
US-10-679-999-13
; Sequence 13, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1135 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION:  4
;             OTHER INFORMATION:  /note= "Met = ATG"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-679-999-13

  Query Match             97.7%;  Score 1109.4;  DB 13;  Length 1135;
  Best Local Similarity   98.6%;  Pred. No. 1.4e-305;
  Matches 1119;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;
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Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || ||||||||||||||    || |||||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
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Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720

Qy        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780

Qy        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840

Qy        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900

Qy        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960

Qy        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020

Qy       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080

Qy       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
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RESULT 3
US-10-645-761-1067
; Sequence 1067, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1067
; LENGTH: 748
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc MMP INHIBITOR
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(732)
; OTHER INFORMATION:
US-10-645-761-1067

Query Match 58.4%; Score 662.4; DB 12; Length 748;
Best Local Similarity 97.7%; Pred. No. 2.4e-178;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
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Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

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Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 4
US-10-609-217-1067
; Sequence 1067, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/609,217
;  CURRENT FILING DATE:  2003-06-27
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1067
;   LENGTH: 748
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc MMP INHIBITOR
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(732)
;   OTHER INFORMATION:
US-10-609-217-1067

  Query Match             58.4%;  Score 662.4;  DB 13;  Length 748;
  Best Local Similarity   97.7%;  Pred. No. 2.4e-178;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
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Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
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Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
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Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
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Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
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Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 5
US-10-632-388-1067
; Sequence 1067, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/632,388
;  CURRENT FILING DATE:  2003-07-31
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1067
;   LENGTH: 748
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc MMP INHIBITOR
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(732)
;   OTHER INFORMATION:
US-10-632-388-1067

  Query Match             58.4%;  Score 662.4;  DB 13;  Length 748;
  Best Local Similarity   97.7%;  Pred. No. 2.4e-178;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
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Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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RESULT 6
US-10-651-723-1067
; Sequence 1067, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1067
; LENGTH: 748
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc MMP INHIBITOR
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(732)
; OTHER INFORMATION:
US-10-651-723-1067

Query Match 58.4%; Score 662.4; DB 13; Length 748;
Best Local Similarity 97.7%; Pred. No. 2.4e-178;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              ||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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RESULT 7
US-10-666-696-1067
; Sequence 1067, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1067
; LENGTH: 748
; TYPE: DNA

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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc-MMP INHIBITOR
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(732)
;   OTHER INFORMATION:
US-10-666-696-1067

  Query Match             58.4%;  Score 662.4;  DB 17;  Length 748;
  Best Local Similarity   97.7%;  Pred. No. 2.4e-178;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              ||||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
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Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 8
US-10-645-761-1055
; Sequence 1055, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/645,761
;  CURRENT FILING DATE:  2003-08-18
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1055
;   LENGTH: 757
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: FC-TNF-ALPA INHIBITORS
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(747)
;   OTHER INFORMATION:
US-10-645-761-1055

  Query Match             58.4%;  Score 662.4;  DB 12;  Length 757;
  Best Local Similarity   97.7%;  Pred. No. 2.5e-178;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              ||||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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RESULT 9
US-10-609-217-1055
; Sequence 1055, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/609,217
;  CURRENT FILING DATE:  2003-06-27
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1055
;   LENGTH: 757
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: FC-TNF-ALPA INHIBITORS
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(747)
;   OTHER INFORMATION:
US-10-609-217-1055

  Query Match             58.4%;  Score 662.4;  DB 13;  Length 757;
  Best Local Similarity   97.7%;  Pred. No. 2.5e-178;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 10
US-10-632-388-1055
; Sequence 1055, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/632,388
;  CURRENT FILING DATE:  2003-07-31
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1055
;   LENGTH: 757
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: FC-TNF-ALPA INHIBITORS
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(747)
;   OTHER INFORMATION:
US-10-632-388-1055

  Query Match             58.4%;  Score 662.4;  DB 13;  Length 757;
  Best Local Similarity   97.7%;  Pred. No. 2.5e-178;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
```

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Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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RESULT 11
US-10-651-723-1055
; Sequence 1055, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1055
; LENGTH: 757
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-TNF-ALPA INHIBITORS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(747)
; OTHER INFORMATION:
US-10-651-723-1055

Query Match 58.4%; Score 662.4; DB 13; Length 757;
Best Local Similarity 97.7%; Pred. No. 2.5e-178;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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RESULT 12
US-10-666-696-1055
; Sequence 1055, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1055
; LENGTH: 757
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc-TNF-ALPHA INHIBITORS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(747)
; OTHER INFORMATION:
US-10-666-696-1055

Query Match 58.4%; Score 662.4; DB 17; Length 757;
Best Local Similarity 97.7%; Pred. No. 2.5e-178;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
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Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 13
US-10-645-761-1059
; Sequence 1059, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/645,761
;  CURRENT FILING DATE:  2003-08-18
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1059
;   LENGTH: 763
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: FC-IL-1 ANTAGONIST
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(747)
;   OTHER INFORMATION:
US-10-645-761-1059

  Query Match             58.4%;  Score 662.4;  DB 12;  Length 763;
  Best Local Similarity   97.7%;  Pred. No. 2.5e-178;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 14
US-10-609-217-1059
; Sequence 1059, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/609,217
;  CURRENT FILING DATE:  2003-06-27
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
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;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1059
;    LENGTH: 763
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: FC-IL-1 ANTAGONIST
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (4)..(747)
;    OTHER INFORMATION:
US-10-609-217-1059

  Query Match             58.4%;  Score 662.4;  DB 13;  Length 763;
  Best Local Similarity   97.7%;  Pred. No. 2.5e-178;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              ||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 15
US-10-632-388-1059
; Sequence 1059, Application US/10632388
; Publication No. US20040053845A1
```

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; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/632,388
;  CURRENT FILING DATE:  2003-07-31
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1059
;    LENGTH: 763
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: FC-IL-1 ANTAGONIST
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (4)..(747)
;    OTHER INFORMATION:
US-10-632-388-1059

  Query Match             58.4%;  Score 662.4;  DB 13;  Length 763;
  Best Local Similarity   97.7%;  Pred. No. 2.5e-178;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
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Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
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Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
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Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
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Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
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Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
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Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
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Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
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Search completed: May 11, 2004, 09:06:44
Job time : 475.75 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 18:55:54 ; Search time 2223.5 Seconds
(without alignments)
15243.344 Million cell updates/sec

Title: US-10-679-999-16
Perfect score: 1135
Sequence: 1 CATATGGACAAAACTCACAC.....TCCGGGTTGTTAATGGATCC 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 54259654

Minimum DB seq length: 0
Maximum DB seq length: 1135

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
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19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	657	57.9	871	12	BG753979	BG753979 602709506
2	657	57.9	983	13	BQ708975	BQ708975 AGENCOURT
3	656.2	57.8	843	12	BM007897	BM007897 603617582
4	656	57.8	941	13	BQ712021	BQ712021 AGENCOURT
5	655.4	57.7	925	13	BQ709152	BQ709152 AGENCOURT
6	654.6	57.7	973	13	BQ706204	BQ706204 AGENCOURT
7	654.4	57.7	858	13	BX346946	BX346946 BX346946
8	653.8	57.6	919	13	BQ709339	BQ709339 AGENCOURT
9	653.2	57.6	897	13	BQ709144	BQ709144 AGENCOURT
10	652.2	57.5	947	13	BQ709771	BQ709771 AGENCOURT
11	652	57.4	881	13	BQ711291	BQ711291 AGENCOURT
c 12	650	57.3	1013	13	BX360518	BX360518 BX360518
13	649.6	57.2	757	12	BG674795	BG674795 602620925
14	649.6	57.2	914	13	BQ712363	BQ712363 AGENCOURT
15	647.8	57.1	856	13	BQ709859	BQ709859 AGENCOURT
16	645	56.8	892	12	BG397723	BG397723 602438784
17	645	56.8	897	12	BM008412	BM008412 603617406
18	645	56.8	902	13	BU146962	BU146962 AGENCOURT
c 19	644.2	56.8	1015	13	BX367600	BX367600 BX367600
c 20	643	56.7	860	13	BX437583	BX437583 BX437583
c 21	642.6	56.6	954	12	BG746184	BG746184 602723696
c 22	642.6	56.6	985	13	BX457369	BX457369 BX457369
c 23	642.6	56.6	1034	13	BX337959	BX337959 BX337959
24	642.4	56.6	873	13	BQ708562	BQ708562 AGENCOURT
c 25	642.2	56.6	951	12	BG746233	BG746233 602723760
26	641.2	56.5	940	13	BQ705928	BQ705928 AGENCOURT
c 27	640.6	56.4	898	13	BX415442	BX415442 BX415442
28	639.6	56.4	958	13	BQ706140	BQ706140 AGENCOURT
29	639.6	56.4	961	13	BQ710233	BQ710233 AGENCOURT
c 30	639	56.3	885	13	BX437308	BX437308 BX437308
31	638	56.2	941	13	BQ711680	BQ711680 AGENCOURT
c 32	637.6	56.2	879	13	BX336029	BX336029 BX336029
33	636.2	56.1	926	12	BG755166	BG755166 602711488
34	635.6	56.0	857	13	BX429638	BX429638 BX429638
35	635	55.9	1014	12	BM914505	BM914505 AGENCOURT
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c 37	632.6	55.7	1009	13	BX456658	BX456658 BX456658
38	632	55.7	965	12	BG754808	BG754808 602714385
c 39	630.8	55.6	883	13	BX454398	BX454398 BX454398
40	630.8	55.6	925	13	BQ709853	BQ709853 AGENCOURT
c 41	630.6	55.6	1063	13	BX358861	BX358861 BX358861
c 42	629.6	55.5	877	13	BX324928	BX324928 BX324928
c 43	629.6	55.5	921	13	BX359858	BX359858 BX359858
c 44	629.4	55.5	980	13	BX325701	BX325701 BX325701
c 45	628	55.3	890	13	BX366845	BX366845 BX366845

ALIGNMENTS

RESULT 1
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LOCUS BG753979 871 bp mRNA linear EST 15-MAY-2001
DEFINITION 602709506F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4846201 5', mRNA sequence.
ACCESSION BG753979
VERSION BG753979.1 GI:14064632
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 871)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1686 row: k column: 02
High quality sequence stop: 848.

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FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4846201"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             57.9%;  Score 657;  DB 12;  Length 871;
  Best Local Similarity   97.8%;  Pred. No. 2.8e-127;
  Matches  666;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
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Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
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Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
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Db        157 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 216

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
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Db        217 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 276

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
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Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
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Db        337 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 396

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
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Db        397 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 456

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
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Db        457 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 516

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
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Db        517 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 576

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
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Db        577 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 636

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
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Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
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RESULT 2
BQ708975
LOCUS       BQ708975                983 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8353514 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279683
            5', mRNA sequence.
ACCESSION   BQ708975
VERSION     BQ708975.1  GI:21847874
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 983)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2469  row: k  column: 12
            High quality sequence stop: 604.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6279683"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             57.9%;  Score 657;  DB 13;  Length 983;
  Best Local Similarity   97.8%;  Pred. No. 3e-127;
  Matches  666;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
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Db         24 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 83

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
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Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 203

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 263

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
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Db        264 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 323

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
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Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
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Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
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Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
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RESULT 3
BM007897

LOCUS	BM007897 843 bp mRNA linear EST 30-OCT-2001
DEFINITION	603617582F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450469 5', mRNA sequence.
ACCESSION	BM007897
VERSION	BM007897.1 GI:16522238
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 843)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Mark Watson cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM1939 row: d column: 22 High quality sequence stop: 833.

FEATURES	Location/Qualifiers
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ORIGIN

Query Match 57.8%; Score 656.2; DB 12; Length 843;
Best Local Similarity 97.4%; Pred. No. 4.1e-127;
Matches 667; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
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Db        108 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 167

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
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Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
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Db        228 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 287

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 347

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
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Db        348 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 407

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 467

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 527

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        528 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 587

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        588 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 647

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
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Db        648 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 707

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        708 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCATTACACGCAGAAGAGC 767

Qy        667 CTCTCCCTGTCTCCGGGTAAAGTAC 691
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Db        768 CTCTCCCTGTCTCCGGGTAAATGAC 792
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RESULT 4
BQ712021

LOCUS	BQ712021 941 bp mRNA linear EST 16-JUL-2002
DEFINITION	AGENCOURT_8418162 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281403 5', mRNA sequence.
ACCESSION	BQ712021
VERSION	BQ712021.1 GI:21850920
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 941)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Mark Watson cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2474 row: c column: 04
High quality sequence stop: 638.

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FEATURES             Location/Qualifiers
     source          1. .941
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6281403"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN
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Query Match 57.8%; Score 656; DB 13; Length 941;
Best Local Similarity 97.7%; Pred. No. 4.7e-127;
Matches 665; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
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Db         50 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 109

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 169

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 229

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 289

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        290 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 349

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 409

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
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Db        410 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 469

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        470 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 529

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
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Db        530 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 589

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
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Db        590 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 649

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        650 AACGTCTTCTCATGCTCCGTGATGCATGANGCTCTGCACAACCACTACACGCAGAAGAGC 709

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
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Db        710 CTCTCCCTGTCTCCGGGTAAA 730
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RESULT 5
BQ709152
LOCUS       BQ709152                925 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8485151 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301245
            5', mRNA sequence.
ACCESSION   BQ709152
VERSION     BQ709152.1  GI:21848051
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 925)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2516  row: m  column: 22
            High quality sequence stop: 739.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6301245"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN
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Query Match 57.7%; Score 655.4; DB 13; Length 925;
Best Local Similarity 97.7%; Pred. No. 6.3e-127;
Matches 665; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db         48 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 107

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        108 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 167

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 227

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 287

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        288 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 347

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        348 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 407

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 467

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
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Db        468 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 527

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        528 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 587

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        588 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 647

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        648 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 707

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
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Db        708 CTCTCCCTGTCTCCGGGTAAA 728
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RESULT 6
BQ706204
LOCUS       BQ706204                973 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8352308 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277592
            5', mRNA sequence.
ACCESSION   BQ706204
VERSION     BQ706204.1  GI:21845103
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 973)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2464  row: d  column: 09
            High quality sequence stop: 640.
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                     /clone="IMAGE:6277592"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN
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  Query Match             57.7%;  Score 654.6;  DB 13;  Length 973;
  Best Local Similarity   94.4%;  Pred. No. 9.4e-127;
  Matches  678;  Conservative    0;  Mismatches   40;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
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Db        108 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 167

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 227

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 287

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 347

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        348 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 407

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 467

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 527

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        528 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 587

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        588 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 647

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        648 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGNG 707

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
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Db        708 AACGTCTTCTCATGCTCCGTGATGCATGAAGCTCTGCACAACCACTACACGCAGAAGAGC 767

Qy        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAAACCT 724
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Db        768 CTCTCCCTGTCTCCGGGTAAATGAGTGCGACGGGCGGGAAAGCCCCCCTCCCCAGGCT 825
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RESULT 7
BX346946
LOCUS       BX346946                858 bp    mRNA    linear   EST 05-MAY-2003
DEFINITION  BX346946 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI039YP09 5-PRIME, mRNA sequence.
ACCESSION   BX346946
VERSION     BX346946.1  GI:30377150
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 858)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
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          Invitrogen. This sequence belongs to sequence cluster 7198.r For
          more information about this cluster, see
          http://www.genoscope.cns.fr/
          cgi-bin/cluster.cgi?seq=CS0AT021ZE05_T01957_1&cluster=7198.r.
          Contact : Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
          Faraday Avenue Genoscope sequence ID : CS0AT021ZE05_T01957_1.
FEATURES             Location/Qualifiers
     source          1. .858
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI039YP09"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             57.7%;  Score 654.4;  DB 13;  Length 858;
  Best Local Similarity   97.5%;  Pred. No. 9.9e-127;
  Matches  664;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db         65 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 124

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 184

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
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Db        185 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 244

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
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Db        245 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 304

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        305 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 364

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 424

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
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Db        425 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 484

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 544

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 604

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 664

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        665 AACGTCTTCTCATGCTNCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 724

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
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Db        725 CTCTCCCTGTCTTCGGGTAAA 745
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RESULT 8
BQ709339
LOCUS       BQ709339                919 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_7976429 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214450
            5', mRNA sequence.
ACCESSION   BQ709339
VERSION     BQ709339.1  GI:21848238
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 919)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2381  row: m  column: 11
            High quality sequence stop: 576.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6214450"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             57.6%;  Score 653.8;  DB 13;  Length 919;
  Best Local Similarity   97.5%;  Pred. No. 1.4e-126;
  Matches  664;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db         57 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 116

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 176

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        177 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 236

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 296

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        297 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 356

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 416
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Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 476

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 536

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 596

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        597 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAAGTGGCAGCAGGGG 656

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        657 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 716

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
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Db        717 CTCTCCCTGTCTCCGGGTAAA 737
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RESULT 9
BQ709144
LOCUS BQ709144 897 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8474994 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301566 5', mRNA sequence.
ACCESSION BQ709144
VERSION BQ709144.1 GI:21848043
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 897)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2517 row: k column: 07
High quality sequence stop: 628.
FEATURES Location/Qualifiers
source 1. .897
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6301566"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
ORIGIN

Query Match 57.6%; Score 653.2; DB 13; Length 897;
Best Local Similarity 97.4%; Pred. No. 1.8e-126;
Matches 664; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db         50 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 109

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 169

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 229

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 289

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        290 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 349

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 409

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 469

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        470 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 529

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        530 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 589

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        590 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 649

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        650 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 709

Qy        667 CTCTCCCTGTCTCCGGGTAAAG 688
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Db        710 CTCTCCCTGTCTCCGGTAAATG 731
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RESULT 10
BQ709771
LOCUS BQ709771 947 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8353965 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278583 5', mRNA sequence.
ACCESSION BQ709771
VERSION BQ709771.1 GI:21848670
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 947)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

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           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM2466  row: m  column: 16
           High quality sequence start: 3
           High quality sequence stop: 675.
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                     /clone="IMAGE:6278583"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             57.5%;  Score 652.2;  DB 13;  Length 947;
  Best Local Similarity   97.4%;  Pred. No. 3e-126;
  Matches  663;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||||| || ||||||    || || |||||||||
Db        197 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 256

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 316

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 376

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 436

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||||||  |   |||
Db        437 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 496

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 556

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 616

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 676

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 736

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        737 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 796

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        797 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACCACCACTACACGCAGAAGAGC 856

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
              |||||||||||  ||||||||
Db        857 CTCTCCCTGTCCTCGGGTAAA 877


RESULT 11
BQ711291
LOCUS       BQ711291                881 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8347186 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279096
            5', mRNA sequence.
ACCESSION   BQ711291
VERSION     BQ711291.1  GI:21850190
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 881)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2468  row: c  column: 01
            High quality sequence stop: 721.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6279096"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             57.4%;  Score 652;  DB 13;  Length 881;
  Best Local Similarity   97.8%;  Pred. No. 3.2e-126;
  Matches  661;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||||| || ||||||    || || |||||||||
Db        137 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 196

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 256

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 316

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 376

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||||||  |   |||
Db        377 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 436
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Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 496

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 556

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 616

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 676

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 736

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        737 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 796

Qy        667 CTCTCCCTGTCTCCGG 682
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Db        797 CTCTCCCTGTCTCCGG 812
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RESULT 12
BX360518/c
LOCUS BX360518 1013 bp mRNA linear EST 05-MAY-2003
DEFINITION BX360518 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI071YG21 3-PRIME, mRNA sequence.
ACCESSION BX360518
VERSION BX360518.1 GI:30372442
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1013)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7198.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI071AD11NP1&cluster=7198.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI071AD11NP1.
FEATURES Location/Qualifiers
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match 57.3%; Score 650; DB 13; Length 1013;
Best Local Similarity 96.5%; Pred. No. 8.8e-126;

Matches 657; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

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Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
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Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
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Db        648 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 589

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
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Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
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Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
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Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
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Db        108 CTCTCCCYBTCTCCGGGTAAA 88
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RESULT 13
BG674795
LOCUS BG674795 757 bp mRNA linear EST 01-MAY-2001
DEFINITION 602620925F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4746150 5', mRNA sequence.
ACCESSION BG674795
VERSION BG674795.1 GI:13906191
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 757)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.

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           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM10594  row: b  column: 07
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                     Average insert size 1.5kb.  Library constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match           57.2%;  Score 649.6;  DB 12;  Length 757;
  Best Local Similarity   97.1%;  Pred. No. 9.6e-126;
  Matches  661;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
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Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
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Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
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Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
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Db        217 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 276

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
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Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
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RESULT 14
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BQ712363
LOCUS       BQ712363                 914 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8475100 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301405
            5', mRNA sequence.
ACCESSION   BQ712363
VERSION     BQ712363.1  GI:21851262
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 914)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2517  row: d  column: 14
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                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match           57.2%;  Score 649.6;  DB 13;  Length 914;
  Best Local Similarity   97.1%;  Pred. No. 1e-125;
  Matches  661;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
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Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
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Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
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RESULT 15
BQ709859
LOCUS       BQ709859                 856 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8349888 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6280560
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ACCESSION   BQ709859
VERSION     BQ709859.1  GI:21848758
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 856)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
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                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match            57.1%;  Score 647.8;  DB 13;  Length 856;
  Best Local Similarity  96.8%;  Pred. No. 2.4e-125;
  Matches  661;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

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Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
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Search completed: May 10, 2004, 06:19:31
Job time : 2226 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:37 ; Search time 3069 Seconds
(without alignments)
16029.437 Million cell updates/sec

Title: US-10-679-999-17
Perfect score: 1135
Sequence: 1 GTATACCTGTTTTGAGTGTG.....AGGCCCAACAATTACCTAGG 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 5401154

Minimum DB seq length: 0
Maximum DB seq length: 1135

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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1: gb_ba:*
2: gb_htg:*
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35: em_htg_rod:*
36: em_htg_mam:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1135	100.0	1135	6	BD056524	BD056524 OB fusion
	2	1109.4	97.7	1135	6	BD056522	BD056522 OB fusion
	3	662.4	58.4	861	6	BD263010	BD263010 Dimeric t
	4	658.4	58.0	684	6	BD263000	BD263000 Dimeric t
	5	440.8	38.8	454	6	BD004077	BD004077 Methods o
	6	440.8	38.8	454	6	BD056516	BD056516 OB fusion
	7	378.4	33.3	491	6	BD004075	BD004075 Methods o
	8	378.4	33.3	491	6	BD056514	BD056514 OB fusion
	9	49.2	4.3	908	8	AB029092	AB029092 Cucumis s
	10	49.2	4.3	1110	8	AB029147	AB029147 Cucumis s
	11	43	3.8	468	6	I27620	I27620 Sequence 12
	12	43	3.8	746	6	A51599	A51599 Sequence 9
c	13	39	3.4	688	6	A86256	A86256 Sequence 91
c	14	39	3.4	688	6	AR155749	AR155749 Sequence
c	15	39	3.4	688	6	E66274	E66274 Genome DNA
c	16	38.8	3.4	1057	6	E02180	E02180 DNA sequenc
c	17	38.8	3.4	1057	6	E02181	E02181 DNA sequenc
c	18	38.6	3.4	462	10	AY300753	AY300753 Mesocrice
c	19	38.6	3.4	564	10	AY300754	AY300754 Mesocrice
c	20	38.4	3.4	533	6	AR365256	AR365256 Sequence
	21	37	3.3	900	4	AF510666	AF510666 Equus cab
c	22	36.8	3.2	675	1	USO539323	AJ539323 Unculture
c	23	36.6	3.2	1018	8	AF479764	AF479764 Triticum
c	24	36.4	3.2	744	6	BD180141	BD180141 Highly th
c	25	36	3.2	675	1	USO538112	AJ538112 Unculture
c	26	36	3.2	1065	1	AY392156	AY392156 Streptomy
c	27	35.8	3.2	453	1	AY123833	AY123833 Nitrososp
	28	35.8	3.2	558	6	AX090818	AX090818 Sequence
	29	35.8	3.2	558	6	AX092882	AX092882 Sequence
c	30	35.8	3.2	954	10	RNSHUNA3	U26358 Rattus norv
	31	35.6	3.1	789	6	AX756672	AX756672 Sequence
	32	35.6	3.1	810	6	AX575331	AX575331 Sequence
	33	35.6	3.1	813	6	AX467493	AX467493 Sequence
	34	35.6	3.1	813	6	AX575327	AX575327 Sequence
	35	35.6	3.1	815	6	AX527763	AX527763 Sequence
	36	35.6	3.1	815	6	AX527765	AX527765 Sequence
	37	35.6	3.1	882	6	BD105732	BD105732 A method
	38	35.6	3.1	882	6	BD105740	BD105740 Immunoglo
	39	35.2	3.1	495	1	UBA317920	AJ317920 unculture
	40	35.2	3.1	726	6	AX473062	AX473062 Sequence
c	41	35.2	3.1	792	4	OAR507201	AJ507201 Ovis arie
c	42	35.2	3.1	829	3	SMU63575	U63575 Stylonychia
c	43	35.2	3.1	1005	6	AX653238	AX653238 Sequence
	44	35	3.1	531	1	AY080950	AY080950 Unculture
	45	35	3.1	531	1	AY080958	AY080958 Unculture

ALIGNMENTS

RESULT 1
BD056524
LOCUS BD056524 1135 bp DNA linear PAT 27-AUG-2002
DEFINITION OB fusion protein compositions and methods.
ACCESSION BD056524
VERSION BD056524.1 GI:22602130
KEYWORDS JP 2001512417-A/12.
SOURCE Aequorea victoria
ORGANISM Aequorea victoria
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
REFERENCE 1 (bases 1 to 1135)
AUTHORS Mann,M.B. and Hecht,R.I.
TITLE OB fusion protein compositions and methods
JOURNAL Patent: JP 2001512417-A 12 21-AUG-2001;

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            AMGEN INC
COMMENT     PN   JP 2001512417-A/12
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .1135
                        /organism="Aequorea victoria"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:6100"
ORIGIN

  Query Match             100.0%;  Score 1135;  DB 6;  Length 1135;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-266;
  Matches 1135;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATACCTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGC 60
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Db          1 GTATACCTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGC 60

Qy         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120

Qy        121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180

Qy        181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240

Qy        241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGA 300

Qy        301 ATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360
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Db        301 ATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360

Qy        361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420
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Db        361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420

Qy        421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480
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Db        421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480

Qy        481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540
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Db        481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540

Qy        541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600
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Db        541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600

Qy        601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660
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Qy        661 TTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTT 720
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Db        721 TGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCG 780

Qy        781 AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC 840
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Db        781 AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC 840

Qy        841 AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA 900
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Db        841 AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA 900

Qy        901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT 960
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Db        901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT 960

Qy        961 AAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCG 1020
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Db        961 AAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCG 1020

Qy       1021 CCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCA 1080
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Db       1021 CCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCA 1080

Qy       1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
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Db       1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135


RESULT 2
BD056522
LOCUS       BD056522                1135 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056522
VERSION     BD056522.1  GI:22602128
KEYWORDS    JP 2001512417-A/10.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1135)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 10 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/10
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .1135
                        /organism="Aequorea victoria"
                        /mol_type="genomic DNA"
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ORIGIN

  Query Match             97.7%;  Score 1109.4;  DB 6;  Length 1135;
  Best Local Similarity   98.6%;  Pred. No. 3.2e-260;
  Matches 1119;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

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Db          1 GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGA 60

Qy         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120
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Qy        121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180
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Db        121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180

Qy        181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240

Qy        241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGA 300
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Db        241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC 300

Qy        301 ATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360

Qy        361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420
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Qy        421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480
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Db        421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480

Qy        481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540
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Qy        541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600
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Db        541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600

Qy        601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660
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Qy        721 TGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCG 780
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Db        721 TGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCG 780

Qy        781 AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC 840
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Db        781 AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC 840

Qy        841 AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA 900
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Qy        901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT 960
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Db        901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT 960

Qy        961 AAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCG 1020
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Db        961 AAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCG 1020

Qy       1021 CCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCA 1080
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Qy       1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
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Db       1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
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RESULT 3
BD263010
LOCUS BD263010 861 bp DNA linear PAT 17-JUL-2003
DEFINITION Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and having thrombopoietic activity.
ACCESSION BD263010
VERSION BD263010.1 GI:33072778
KEYWORDS JP 2002536960-A/12.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 861)
AUTHORS Liu,C.F., Feige,U. and Cheetham,J.
TITLE Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and having thrombopoietic activity
JOURNAL Patent: JP 2002536960-A 12 05-NOV-2002;
AMGEN INC
COMMENT OS Artificial Sequence
PN JP 2002536960-A/12
PD 05-NOV-2002
PF 22-OCT-1999 JP 2000578340
PR 23-OCT-1998 US 60/105348
PI CHUAN FA LIU,ULRICH FEIGE,JANET CHEETHAM
PC C12N15/09,A61K38/00,A61P7/00,C07K14/52,C07K19/00,C12N1/15, PC C12N1/19,
PC C12N1/21,C12N5/10,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC
Description of Artificial Sequence: oligonucleotide FH Key Location/Qualifiers
FT source 1. .861
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .861
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 58.4%; Score 662.4; DB 6; Length 861;
Best Local Similarity 97.7%; Pred. No. 5.2e-151;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy          1 GTATACCTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGC 60
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Db         36 GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC 95

Qy         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120
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Qy        121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 215

Qy        181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240
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Db        216 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 275

Qy        241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGA 300
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Db        276 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC 335

Qy        301 ATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360
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Qy        361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420
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Qy        421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480
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Db        516 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 575
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Qy        541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600
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Db        576 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 635

Qy        601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660
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Db        636 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 695

Qy        661 TTCTCGGAGAGGGACAGAGGCCCATTTC 688
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Db        696 TTCTCGGAGAGGGACAGAGGCCCATTTC 723


RESULT 4
BD263000
LOCUS       BD263000                684 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Dimeric thrombopoietin peptide mimetics binding to MPl receptor and
            having thrombopoietic activity.
ACCESSION   BD263000
VERSION     BD263000.1  GI:33072768
KEYWORDS    JP 2002536960-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 684)
  AUTHORS   Liu,C.F., Feige,U. and Cheetham,J.
  TITLE     Dimeric thrombopoietin peptide mimetics binding to MPl receptor and
            having thrombopoietic activity
  JOURNAL   Patent: JP 2002536960-A 2 05-NOV-2002;
            AMGEN INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002536960-A/2
            PD   05-NOV-2002
            PF   22-OCT-1999 JP 2000578340
            PR   23-OCT-1998 US    60/105348
            PI   CHUAN FA LIU,ULRICH FEIGE,JANET CHEETHAM
            PC   C12N15/09,A61K38/00,A61P7/00,C07K14/52,C07K19/00,C12N1/15, PC
             C12N1/19,
            PC   C12N1/21,C12N5/10,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC
            Description of Artificial Sequence: oligonucleotide FH   Key
                 Location/Qualifiers
            FT   source          1. .684
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .684
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match           58.0%;  Score 658.4;  DB 6;  Length 684;
  Best Local Similarity  97.7%;  Pred. No. 5e-150;
  Matches  668;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          4 TACCTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGT 63
              |||||||||||||||||| ||||| || ||||||||||||||   || || ||||||
Db          1 TACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGT 60

Qy         64 CAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG 120

Qy        124 TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC 180

Qy        184 CTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGC 240

Qy        244 ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATG 303
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        241 ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATG 300

Qy        304 CGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGG 363
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGG 360

Qy        364 TTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGG 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGG 420

Qy        424 TTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC 480

Qy        484 CTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTG 540

Qy        544 AGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC 600

Qy        604 CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTC 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTC 660

Qy        664 TCGGAGAGGGACAGAGGCCCATTT 687
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Db        661 TCGGAGAGGGACAGAGGCCCATTT 684


RESULT 5
BD004077
LOCUS       BD004077                454 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Methods of increasing sensitivity of an individual to OB protein by
             up-regulating OB protein receptor.
ACCESSION   BD004077
VERSION     BD004077.1  GI:18632038
KEYWORDS    JP 2001501177-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 454)
  AUTHORS   Pelleymounter,M.A.
  TITLE     Methods of increasing sensitivity of an individual to OB protein by
            up-regulating OB protein receptor
  JOURNAL   Patent: JP 2001501177-A 4 30-JAN-2001;
            AMGEN INC
COMMENT     OS   Unidentified
            PN   JP 2001501177-A/4
            PD   30-JAN-2001
            PF   26-AUG-1997 JP 1998511882
            PR   30-AUG-1996 US    08/705981
            PI   MARY ANN PELLEYMOUNTER
            PC   A61K38/00,A61K31/425,A61P1/16,A61P3/04,A61P3/06,A61P3/10, PC
            A61P9/10,
            PC   A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .454
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match           38.8%;  Score 440.8;  DB 6;  Length 454;
  Best Local Similarity  98.5%;  Pred. No. 7.3e-97;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
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Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
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Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
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Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454
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RESULT 6
BD056516

LOCUS	BD056516 454 bp DNA linear PAT 27-AUG-2002
DEFINITION	OB fusion protein compositions and methods.
ACCESSION	BD056516
VERSION	BD056516.1 GI:22602122
KEYWORDS	JP 2001512417-A/4.
SOURCE	Aequorea victoria
ORGANISM	Aequorea victoria
	Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae; Aequoreidae; Aequorea.
REFERENCE	1 (bases 1 to 454)
AUTHORS	Mann,M.B. and Hecht,R.I.
TITLE	OB fusion protein compositions and methods
JOURNAL	Patent: JP 2001512417-A 4 21-AUG-2001; AMGEN INC
COMMENT	PN JP 2001512417-A/4 PD 21-AUG-2001 PF 11-DEC-1997 JP 1998528896 PR 20-DEC-1996 US 08/770973 PI MICHAEL BENJAMIN MANN,RANDY IRA HECHT PC C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC A61P43/00, PC C12N15/09,C12N15/00,A61K37/02 CC Strandedness: Double; CC Topology: Linear; FH Key Location/Qualifiers.
FEATURES	Location/Qualifiers
source	1. .454 /organism="Aequorea victoria" /mol_type="genomic DNA" /db_xref="taxon:6100"

ORIGIN

Query Match 38.8%; Score 440.8; DB 6; Length 454;
Best Local Similarity 98.5%; Pred. No. 7.3e-97;
Matches 445; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
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Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
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Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
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Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454
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RESULT 7
BD004075

LOCUS	BD004075 491 bp DNA linear PAT 31-JAN-2002
DEFINITION	Methods of increasing sensitivity of an individual to OB protein by up-regulating OB protein receptor.
ACCESSION	BD004075
VERSION	BD004075.1 GI:18632036
KEYWORDS	JP 2001501177-A/2.
SOURCE	unidentified
ORGANISM	unidentified unclassified.
REFERENCE	1 (bases 1 to 491)
AUTHORS	Pelleymounter,M.A.
TITLE	Methods of increasing sensitivity of an individual to OB protein by up-regulating OB protein receptor
JOURNAL	Patent: JP 2001501177-A 2 30-JAN-2001; AMGEN INC
COMMENT	OS Unidentified PN JP 2001501177-A/2 PD 30-JAN-2001 PF 26-AUG-1997 JP 1998511882 PR 30-AUG-1996 US 08/705981 PI MARY ANN PELLEYMOUNTER PC A61K38/00,A61K31/425,A61P1/16,A61P3/04,A61P3/06,A61P3/10, PC A61P9/10, PC A61K37/02 CC Strandedness: Single; CC Topology: Linear; FH Key Location/Qualifiers FT source 1. .491 FT /organism='Unidentified'.
FEATURES	Location/Qualifiers
source	1. .491 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"

ORIGIN

Query Match 33.3%; Score 378.4; DB 6; Length 491;
Best Local Similarity 89.8%; Pred. No. 1.3e-81;
Matches 406; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
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Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
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Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              |||||||||||||||||||||||||||| | ||||||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              |||||||||||||| | |||||||||| |||||||||  ||||||  | ||||||  |||||||
Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
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Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
                | | |||||||||| |||  | ||| || |||| ||||||||||||||||||   ||
Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
              |||||||||||||||||||||||||||||||||||||||||||||||||||||  |||  |||
Db        400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
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Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491


RESULT 8
BD056514
LOCUS       BD056514                491 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056514
VERSION     BD056514.1  GI:22602120
KEYWORDS    JP 2001512417-A/2.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 491)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 2 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/2
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .491
                        /organism="Aequorea victoria"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:6100"
ORIGIN

  Query Match           33.3%;  Score 378.4;  DB 6;  Length 491;
  Best Local Similarity  89.8%;  Pred. No. 1.3e-81;
  Matches  406;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||    | ||||||||  |||||  || ||
Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              |||||||||||||||||||||||||||| | ||||||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              |||||||||||||| | |||||||||| |||||||||  ||||||  | ||||||  |||||||
Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
              |||||||||||||||||||||||||| ||||||||||||||||||||  ||||||
Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
                | | |||||||||| |||  | ||| || |||| ||||||||||||||||||   ||
Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
              |||||||||||||||||||||||||||||||||||||||||||||||||||||  |||  |||
Db        400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
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Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491


RESULT 9
AB029092
LOCUS       AB029092                908 bp    mRNA    linear   PLN 15-APR-2003
DEFINITION  Cucumis sativus mRNA for arabinogalactan protein, complete cds.
ACCESSION   AB029092
VERSION     AB029092.2  GI:29893813
KEYWORDS    .
SOURCE      Cucumis sativus (cucumber)
  ORGANISM  Cucumis sativus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
REFERENCE   1
  AUTHORS   Park,M.H., Suzuki,Y., Chono,M., Knox,J.P. and Yamaguchi,I.
  TITLE     CsAGP1, a Gibberellin-Responsive Gene from Cucumber Hypocotyls,
            Encodes a Classical Arabinogalactan Protein and Is Involved in Stem
            Elongation
  JOURNAL   Plant Physiol. 131 (3), 1450-1459 (2003)
  MEDLINE   22531811
   PUBMED   12644694
REFERENCE   2  (bases 1 to 908)
  AUTHORS   Chono,M., Suzuki,Y. and Yamaguchi,I.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-JUN-1999) Makiko Chono, University of Tokyo, Applied
            Biological Chemistry; Yayoi 1-1-1, Bunkyo-ku, Tokyo 113-8657, Japan
            (E-mail:mchono@pgr1.ch.a.u-tokyo.ac.jp, Tel:+81-3-5841-5160,
            Fax:+81-3-5841-8025)
COMMENT     On Apr 16, 2003 this sequence version replaced gi:5443647.
FEATURES             Location/Qualifiers
     source          1. .908
                     /organism="Cucumis sativus"
                     /mol_type="mRNA"
                     /db_xref="taxon:3659"
                     /clone="203-1/5"
                     /note="obtained by differential display analysis"
     CDS             21. .752
                     /codon_start=1
                     /product="arabinogalactan protein"
                     /protein_id="BAC75541.1"
                     /db_xref="GI:29893814"
                     /translation="MGRQSVIALVLICAVVAGVGGQSPAAAPTTTPAATPPVAATYPP
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VASPPVEVPAPAPSKKKSKKHRAPAPSPALLGPPAPPSEAPAGSEEGPAPSPSLEDKS
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ORIGIN

Query Match 4.3%; Score 49.2; DB 8; Length 908;
Best Local Similarity 45.7%; Pred. No. 0.36;
Matches 171; Conservative 0; Mismatches 203; Indels 0; Gaps 0;

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Qy      118 CTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACC 177
Db      283 CACCAGCCAGCACTCCTCCGACTGCTTCCGTTCCTGCCAGCTCTCCTCCGGCTGCTTCCG 342

Qy      178 ATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTG 237
Db      343 TTCCACCTAGCTCTCCACCAGCTGCTACCGTTCCGGCTAGCTCTCCGCCTGTTCCAGTTC 402

Qy      238 TCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTT 297
Db      403 CGGTTAGTTCTCCACCAGTTTCAGTACCGGTGAGCTCTCCTCCAGTACCAACTCCAACGG 462

Qy      298 CGAATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGG 357
Db      463 AATCTCCTCCCGCTCCCGAAAGTTCTCCTCCTGCCCCAGTCGCGTCGCCTCCTGTTGAGG 522

Qy      358 TTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTC 417
Db      523 TTCCTGCCCCGGCACCTAGCAAGAAGAAGTCAAAGAAGCACAGAGCACCAGCTCCTTCTC 582

Qy      418 GACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAG 477
Db      583 CAGCGTTGCTTGGTCCACCTGCGCCTCCTTCTGAAGCTCCTGCAGGAAGCGAGGAAGGTC 642

Qy      478 CGGCACCTCACCCT 491
Db      643 CTGCGCCCAGCCCT 656
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RESULT 10
AB029147
LOCUS AB029147 1110 bp mRNA linear PLN 23-JUN-1999
DEFINITION Cucumis sativus mRNA expressed in cucumber hypocotyls, complete cds.
ACCESSION AB029147
VERSION AB029147.1 GI:5139694
KEYWORDS .
SOURCE Cucumis sativus (cucumber)
ORGANISM Cucumis sativus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
REFERENCE 1 (bases 1 to 1110)
AUTHORS Chono,M., Suzuki,Y. and Yamaguchi,I.
TITLE Molecular cloning of genes expressed in cucumber hypocotyls
JOURNAL Published Only in DataBase (1999)
REFERENCE 2 (bases 1 to 1110)
AUTHORS Chono,M., Suzuki,Y. and Yamaguchi,I.
TITLE Direct Submission
JOURNAL Submitted (18-JUN-1999) Makiko Chono, University of Tokyo, Applied Biological Chemistry; Yayoi 1-1-1, Bunkyo-ku, Tokyo 113-8657, Japan (E-mail:mchono@pgr1.ch.a.u-tokyo.ac.jp, Tel:+81-3-5841-5160, Fax:+81-3-5841-8025)
FEATURES Location/Qualifiers
source 1. .1110
/organism="Cucumis sativus"
/mol_type="mRNA"
/db_xref="taxon:3659"
CDS 21. .752
/note="expressed in cucumber hypocotyls"
/codon_start=1
/protein_id="BAA81686.1"
/db_xref="GI:5139695"
/translation="MGRQSVIALVLICAVVAGVGGQSPAAAPTTTPAATPPVAATYPP PAASPVSTPTNPSPAAAPQKPATPAPVSTPPASAPPAVAPVASPPASTPPTASVPASS

PPAASVPPSSPPAATVPASSPPVPVPVSSPPVSVPVSSPPVPTPTESPPAPESSPPAP
VASPPVEVPAPAPSKKKSKKHRAPAPSPALLGPPAPPSEAPAGSEEGPAPSPSLEDKS
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ORIGIN

Query Match 4.3%; Score 49.2; DB 8; Length 1110;
Best Local Similarity 45.7%; Pred. No. 0.36;
Matches 171; Conservative 0; Mismatches 203; Indels 0; Gaps 0;

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Qy      118 CTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACC 177
Db      283 CACCAGCCAGCACTCCTCCGACTGCTTCCGTTCCTGCCAGCTCTCCTCCGGCTGCTTCCG 342

Qy      178 ATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTG 237
Db      343 TTCCACCTAGCTCTCCACCAGCTGCTACCGTTCCGGCTAGCTCTCCGCCTGTTCCAGTTC 402

Qy      238 TCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTT 297
Db      403 CGGTTAGTTCTCCACCAGTTTCAGTACCGGTGAGCTCTCCTCCAGTACCAACTCCAACGG 462

Qy      298 CGAATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGG 357
Db      463 AATCTCCTCCCGCTCCCGAAAGTTCTCCTCCTGCCCCAGTCGCGTCGCCTCCTGTTGAGG 522

Qy      358 TTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTC 417
Db      523 TTCCTGCCCCGGCACCTAGCAAGAAGAAGTCAAAGAAGCACAGAGCACCAGCTCCTTCTC 582

Qy      418 GACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAG 477
Db      583 CAGCGTTGCTTGGTCCACCTGCGCCTCCTTCTGAAGCTCCTGCAGGAAGCGAGGAAGGTC 642

Qy      478 CGGCACCTCACCCT 491
Db      643 CTGCGCCCAGCCCT 656
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RESULT 11
I27620
LOCUS I27620 468 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 12 from patent US 5565335.
ACCESSION I27620
VERSION I27620.1 GI:1818396
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 468)
AUTHORS Capon,D.J. and Gregory,T.J.
TITLE Adhesion variants
JOURNAL Patent: US 5565335-A 12 15-OCT-1996;
FEATURES Location/Qualifiers
source 1. .468
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 3.8%; Score 43; DB 6; Length 468;
Best Local Similarity 49.5%; Pred. No. 12;
Matches 143; Conservative 0; Mismatches 140; Indels 6; Gaps 1;

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Qy      379 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 438
Db      127 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 186

Qy      439 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 492
Db      187 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 246

Qy      493 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 552
Db      247 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 306
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Qy        553 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 612
              ||| |  ||||  |||||  || ||  ||  |||       |   || |    || |||
Db        307 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 366

Qy        613 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 661
              | | | |||   || |  ||| |||  |||  |  | |  |||  |||
Db        367 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 415


RESULT 12
A51599
LOCUS       A51599                   746 bp    DNA     linear   PAT 10-MAR-1997
DEFINITION  Sequence 9 from Patent WO9616990.
ACCESSION   A51599
VERSION     A51599.1  GI:2304408
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 746)
  AUTHORS   Ellis,J.H. and Lewis,A.P.
  TITLE     HUMANIZED ANTIBODIES TO CD38
  JOURNAL   Patent: WO 9616990-A 9 06-JUN-1996;
            WELLCOME FOUND (GB)
COMMENT     Other publication AU 3933695 960619.
FEATURES             Location/Qualifiers
     source          1. .746
                     /organism="unidentified"
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Qy        379 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 438
              | ||||   || | || | | || |||||    ||  || |||             | |
Db        429 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 488

Qy        439 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 492
              |    |||||| | ||   |||||||||||| ||   |   ||  ||||      |||
Db        489 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 548

Qy        493 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 552
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Db        549 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 608

Qy        553 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 612
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Db        609 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 668

Qy        613 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 661
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Db        669 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 717


RESULT 13
A86256/c
LOCUS       A86256                   688 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 915 from Patent EP0866129.
ACCESSION   A86256
VERSION     A86256.1  GI:6734855
KEYWORDS    .
SOURCE      Eremothecium gossypii (Ashbya gossypii)
  ORGANISM  Eremothecium gossypii
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Eremothecium.
REFERENCE   1  (bases 1 to 688)
  AUTHORS   Mohr,C. and Knechtle,P.
  TITLE     Genomic DNA sequences of Ashbya gossypii and uses thereof
  JOURNAL   Patent: EP 0866129-A 915 23-SEP-1998;
            CIBA GEIGY AG (CH)
FEATURES             Location/Qualifiers
     source          1. .688
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                     /mol_type="unassigned DNA"
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ORIGIN

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  Matches  132;  Conservative    0;  Mismatches  155;  Indels    0;  Gaps    0;

Qy         78 GGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCA 137
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Db        526 GTGGTTGCTGTGATTGTGGTTTCAATTGTGGTTGTGGTTGGTGTTGTGTCTGCTGCTGTG 467

Qy        138 CCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCA 197
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Db        466 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCGTCTGCTGCTGCGTCT 407

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Db        406 GCTGCTGCGGTTGTGGTTGTTGCGCCTGCGCCTGCGCCAGTTGTGGCTGATGAGGCTGTA 347

Qy        258 GCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGTACGCGCCAGAG 317
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Db        346 AACCAAGCTGTTGTTGTTGTTGTAGTTGCGGTTGAGGTTGGGGCTGCTGCTGCTGTTGTG 287

Qy        318 GTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGT 364
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Db        286 GTTGTTGTGGTTGTTGTGTTTGTTGCTGTGGTTGTGGTGGTGGTGGT 240


RESULT 14
AR155749/c
LOCUS       AR155749                 688 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 915 from patent US 6239264.
ACCESSION   AR155749
VERSION     AR155749.1  GI:15123802
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 688)
  AUTHORS   Philippsen,P., Pohlmann,R., Steiner-Lange,S., Mohr,C., Wendland,J.,
            Knechtle,P. and Rebischung,C.
  TITLE     Genomic DNA sequences of ashbya gossypii and uses thereof
  JOURNAL   Patent: US 6239264-A 915 29-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .688
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ORIGIN

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  Matches  132;  Conservative    0;  Mismatches  155;  Indels    0;  Gaps    0;

Qy         78 GGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCA 137
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Qy        138 CCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCA 197
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Qy        198 CGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTC 257
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Qy        258 GCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGTACGCGCCAGAG 317
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Db        346 AACCAAGCTGTTGTTGTTGTTGTAGTTGCGGTTGAGGTTGGGGCTGCTGCTGCTGTTGTG 287
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Qy        318 GTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGT 364
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Db        286 GTTGTTGTGGTTGTTGTGTTTGTTGCTGTGGTTGTGGTGGTGGTGGT 240


RESULT 15
E66274/c
LOCUS       E66274                   688 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Genome DNA sequence of Ashbya gossypii and use thereof.
ACCESSION   E66274
VERSION     E66274.1  GI:13020615
KEYWORDS    JP 1999225770-A/914.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 688)
  AUTHORS   Peter,P., Reiner,P., Sabine,S., Christine,M., Juergen,W.,
            Phillip,K. and Corinne,R.
  TITLE     Genome DNA sequence of Ashbya gossypii and use thereof
  JOURNAL   Patent: JP 1999225770-A 914 24-AUG-1999;
            NOVARTIS AG
COMMENT     OS   PAG1570RP
            PN   JP 1999225770-A/914
            PD   24-AUG-1999
            PF   05-JAN-1998 JP 1998076818
            PR   31-DEC-1996 CH        16/97
            PI   PETER PHILLIPSEN,REINER POHLMANN,SABINE STEINER,CHRISTINE
            MORE, PI   JUERGEN WENDLAND,PHILLIP KUNEHHITORU,CORINNE REBISHUN PC
              C12N15/09,C12N1/15,C12Q1/18,C12Q1/68//(C12N15/09,C12R1:645), PC
            (C12N15/09,C12R1:865),(C12N1/15,C12R1:645),C12N15/00, PC
            (C12N15/00,C12R1:645),
            PC   (C12N15/00,C12R1:865)
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
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            FT                   /organism='PAG1570RP'.
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                     /db_xref="taxon:32644"
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  Matches  132;  Conservative    0;  Mismatches  155;  Indels    0;  Gaps    0;

Qy         78 GGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCA 137
              | | ||   ||   |||||    | | | ||   |||    |   ||||  ||  |
Db        526 GTGGTTGCTGTGATTGTGGTTTCAATTGTGGTTGTGGTTGGTGTTGTGTCTGCTGCTGTG 467

Qy        138 CCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCA 197
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Qy        198 CGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTC 257
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Db        406 GCTGCTGCGGTTGTGGTTGTTGCGCCTGCGCCTGCGCCAGTTGTGGCTGATGAGGCTGTA 347

Qy        258 GCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGTACGCGCCAGAG 317
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Db        346 AACCAAGCTGTTGTTGTTGTTGTAGTTGCGGTTGAGGTTGGGGCTGCTGCTGCTGTTGTG 287

Qy        318 GTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGT 364
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Db        286 GTTGTTGTGGTTGTTGTGTTTGTTGCTGTGGTTGTGGTGGTGGTGGT 240


Search completed: May 10, 2004, 03:26:27
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:35 ; Search time 333.5 Seconds
(without alignments)
14457.886 Million cell updates/sec

Title: US-10-679-999-17
Perfect score: 1135
Sequence: 1 GTATACCTGTTTTGAGTGTG.....AGGCCCAACAATTACCTAGG 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 5802412

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	53.6	4.7	138	7	AAL51057	Aal51057 Cyclic si
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c	4	38.4	3.4	543	2	AAQ23092	Aaq23092 Antigen t
c	5	37.6	3.3	717	7	ADA07157	Ada07157 Ptilosarc
	6	35.8	3.2	558	4	AAF61431	Aaf61431 Synthetic
	7	35.8	3.2	558	4	AAF61428	Aaf61428 Synthetic
c	8	35.6	3.1	486	4	AAF75507	Aaf75507 Polygluta
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	10	35.6	3.1	810	6	ABZ22164	Abz22164 Human elo
	11	35.6	3.1	813	6	AAD42270	Aad42270 Human ELG
	12	35.6	3.1	813	6	ABZ22162	Abz22162 Human elo
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	16	35.4	3.1	926	6	ABZ11846	Abz11846 Human pol
	17	35.4	3.1	1014	4	ABL15657	Abl15657 Drosophil
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	20	34.4	3.0	249	3	AAA34062	Aaa34062 Human ade
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	24	34.2	3.0	780	7	ACA37806	Aca37806 Prokaryot
c	25	34.2	3.0	1098	7	ADA70957	Ada70957 Rice gene
c	26	34	3.0	693	4	AAF87193	Aaf87193 Human ion
	27	33.8	3.0	541	9	ADE07341	Ade07341 Novel cod
c	28	33.6	3.0	486	8	ACH44360	Ach44360 Human foe
c	29	33.6	3.0	578	4	AAI60937	Aai60937 Human pol
c	30	33.4	2.9	795	2	AAV55830	Aav55830 FLGA inse
c	31	33.4	2.9	799	2	AAV55831	Aav55831 Nucleotid
	32	33.2	2.9	1023	4	AAS54245	Aas54245 Pseudomon
c	33	33.2	2.9	1090	3	AAF15027	Aaf15027 Trichoder
c	34	33	2.9	422	3	AAC79295	Aac79295 Human lun
c	35	33	2.9	422	4	AAD23371	Aad23371 Human lun
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c	37	33	2.9	422	9	ADE87899	Ade87899 Human lun
	38	33	2.9	513	6	ABK70225	Abk70225 Human lun
c	39	33	2.9	714	4	ABL07831	Abl07831 Drosophil
c	40	32.8	2.9	480	7	ACA42677	Aca42677 Prokaryot
c	41	32.8	2.9	575	8	ACH42111	Ach42111 Human foe
	42	32.8	2.9	825	7	ABZ66726	Abz66726 Orthosomy
c	43	32.8	2.9	978	4	ABL29343	Abl29343 Drosophil
c	44	32.8	2.9	1100	4	AAK51553	Aak51553 Human pol
c	45	32.8	2.9	1125	3	AAA57483	Aaa57483 cDNA enco

ALIGNMENTS

RESULT 1
AAL51057
ID AAL51057 standard; DNA; 138 BP.
XX
AC AAL51057;
XX
DT 20-FEB-2003 (first entry)
XX
DE Cyclic single-strand anti-tumour antibody-related coding sequence #6.
XX
KW Cyclic single-strand anti-tumour antibody; anti-tumour Fab; ds;
KW anti-human Cd3 Fab; anti-human CD28 Fab; immunotherapy; tumour;
KW ovarian cancer.
XX
OS Unidentified.
XX
PN WO200283738-A1.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-CN000252.
XX
PR 11-APR-2001; 2001CN-00110554.
XX
PA (GENE-) INST GENETICS CAS.
PA (BEIJ-) BEIJING ABT GENETIC ENG TECHNOLOGY CO LT.
XX
PI Huang H, Cheng J, Wang X, Song L, Zhang Z, Lin Q, Gu Y;
XX
DR WPI; 2003-075525/07.
DR P-PSDB; AAO16031.
XX
PT Cyclic single-strand tri-specific antibody made from antitumor Fab,
PT single-strand antibody and modified anti-human CD3 or CD28 Fab,
PT applicable in early-stage diagnosis, and prevention or treatment of
PT tumors e.g. ovarian cancer.
XX
PS Disclosure; Fig 4A; 49pp; Chinese.
XX
CC The invention comprises a cyclic single-strand anti-tumour antibody, the
CC antibody of the invention is obtained by combining anti-tumour Fab and
CC modified anti-human Cd3 or CD28 Fab. The antibody is useful in the
CC immunotherapy of tumours - particularly ovarian cancer, including the
CC sensitive early-stage diagnosis and post-operative eradication of
CC disease. The present DNA sequence encodes a peptide which was used in the
CC invention

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XX
SQ   Sequence 138 BP; 35 A; 37 C; 39 G; 27 T; 0 U; 0 Other;

  Query Match             4.7%;  Score 53.6;  DB 7;  Length 138;
  Best Local Similarity   93.3%;  Pred. No. 4.7e-05;
  Matches   56;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        235 TTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCG 294
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Db         61 TTGTCGTGCATGGCCCAACATTCGCAGGAGTGGCATGACGTGGTCCTGACCGACTTACCG 120


RESULT 2
AAT20112
ID   AAT20112 standard; cDNA to mRNA; 268 BP.
XX
AC   AAT20112;
XX
DT   29-JUL-1996  (first entry)
XX
DE   Human gene signature HUMGS01256.
XX
KW   Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW   human; cloning; mapping; non-biased library; diagnosis; detection;
KW   cell typing; abnormal cell function; ss.
XX
OS   Homo sapiens.
XX
PN   WO9514772-A1.
XX
PD   01-JUN-1995.
XX
PF   11-NOV-1994;   94WO-JP001916.
XX
PR   12-NOV-1993;   93JP-00355504.
XX
PA   (MATS/) MATSUBARA K.
PA   (OKUB/) OKUBO K.
XX
PI   Matsubara K,  Okubo K;
XX
DR   WPI; 1995-206931/27.
XX
PT   Single-stranded DNA for identifying gene signatures - isolated from 3'-
PT   directed human cDNA library that reflects relative abundance of corresp.
PT   mRNA in specific human tissues.
XX
PS   Claim 1; Page 563; 2245pp; Japanese.
XX
CC   A single-stranded DNA (or its complementary strand or the corresp. double
CC   -stranded DNA) which comprises one of the 7837 "GS" sequences given in
CC   AAT19001-T26837 and which is able to hybridise to part of human genomic
CC   DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were
CC   obtained from 3'-directed cDNA libraries prepared from various human
CC   tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using
CC   poly(T) as the sole primer. Since the 3'- untranslated sequence is unique
CC   to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise
CC   with specific mRNAs. Each library is constructed so as to reflect
CC   accurately the relative abundance of different mRNAs in the particular
CC   tissue from which it was derived. The appearance frequency of a given GS
CC   in a cDNA library can be determined (esp. using primers and probes
CC   derived from the GS sequences) as a means of diagnosing abnormal cell
CC   function or for recognising different cell types
XX
SQ   Sequence 268 BP; 68 A; 54 C; 70 G; 62 T; 0 U; 14 Other;

  Query Match             3.6%;  Score 40.6;  DB 2;  Length 268;
  Best Local Similarity   53.9%;  Pred. No. 0.31;
  Matches   82;  Conservative    0;  Mismatches   70;  Indels    0;  Gaps    0;

Qy        922 CTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGAC 981
              |||||||  |||     | |    || |  || | |   ||    |   |||||   |||
Db          4 CTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGACCAAGGAA 63

Qy        982 GGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCA 1041
              |     ||||  ||  ||  ||||  |    | |  ||   | |  | |  |||  |||  | |||
Db         64 GAGCTTTGAAGGCCTGAGGTCTGCGNAAGGTGGGAGGAGGCAGACGCCCTGCGTGGCCCA 123

Qy       1042 ATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1073
                |||| |||  ||  ||  ||||  |  ||   | |
Db        124 TGGTCGGGGCGTCCACGCCGAGGCCGGCAACA 155


RESULT 3
AAQ03405/c
ID   AAQ03405 standard; DNA; 1057 BP.
XX
AC   AAQ03405;
XX
DT   25-MAR-2003  (revised)
DT   10-MAR-2003  (revised)
DT   19-AUG-1990  (first entry)
XX
DE   Streptomyces gene encoding prepro xylanase.
XX
KW   Secretory expression vector; actinomycetes; Streptomyces; xylanase gene;
KW   endo-1,4-beta-D-xylanase; EC-3.2.1.8; endo-1,3-beta-D-xylanase;
KW   EC-3.2.1.32.
XX
OS   Streptomyces sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             416. .475
FT                   /*tag=  a
XX
PN   JP02002377-A.
XX
PD   08-JAN-1990.
XX
PF   08-JUN-1988;   88JP-00140990.
XX
PR   08-JUN-1988;   88JP-00140990.
XX
PA   (BANY ) BANYU PHARM CO LTD.
XX
DR   WPI; 1990-053427/08.
DR   P-PSDB; AAR03202.
XX
PT   DNA fragment for manifestation secretory vector for actinomycetes - using
PT   Streptomyces spp. as host.
XX
PS   Page 876; Fig 3; 17pp; Japanese.
XX
CC   Streptomyces or E. coli transformed with a secretory expression vector
CC   contg. the sequence efficiently secrete the protein into the culture
CC   medium. This sequence is identical to that of patent JO 2002-379-A.
CC   (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003
CC   to correct PR field.)
XX
SQ   Sequence 1057 BP; 186 A; 390 C; 336 G; 145 T; 0 U; 0 Other;

  Query Match             3.4%;  Score 38.8;  DB 2;  Length 1057;
  Best Local Similarity   44.5%;  Pred. No. 1.8;
  Matches  154;  Conservative    0;  Mismatches  192;  Indels    0;  Gaps    0;

Qy        255 GTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGTACGCGCCA 314
              | ||  | |  ||   | | ||    ||  |  |  | |||      || | |||   |
Db        784 GGCGTTGTACCGGGTCGTCTTGTAGATGTCGTAGGTGCCGCCGTCGCTGTGGACGGTGCC 725

Qy        315 GAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG 374
              |||  |  | || |||  |||  |  || |   | || || | |  ||   |     |
Db        724 CCGGTACTCGCCGGTGGGCCGGTAGCTGCCCCAGTTGTCGACGATGTAGTACTCGACGAG 665

Qy        375 GGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCA 434
              |   | |  |||||   || |      |     | |  | | |||| ||||      |
Db        664 CGGGTTGGAGGTCCAGCCGTAGAGGCAGCCGTAGCCGTTGCCCGACGGGTTGAACCAGCC 605
```

```
Qy        435 GTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTC 494
              |  | || |||||| || |   |||  | | |    ||  | || |  |   |   |  |
Db        604 GGTGTACCGGACGGTCCGGCGCCCGCCGTTGGCCCAGCCCTTGCCGGCCACGAAGTTGCC 545

Qy        495 GTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAG 554
              |      |||  ||  || ||  | |   |         | || | ||  |  |
Db        544 GCAGTTGGTCCACCGGGTGCTGTAGCTGCCGCCGCCGTTGAGCGTCATGGAGACGGACCC 485

Qy        555 GAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600
              |  |  |  | |   |  ||||| | || ||   |||| | | |||
Db        484 GCCGCCGTCGGTCCAGAACGAGTAGTACATGCCGTCGTACCCGGTC 439
```

RESULT 4
AAQ23092/c
ID AAQ23092 standard; DNA; 543 BP.
XX
AC AAQ23092;
XX
DT 25-MAR-2003 (revised)
DT 17-AUG-1992 (first entry)
XX
DE Antigen tc-7a gene.
XX
KW Oocysts; MAb 12-07; sporozoite; ss.
XX
OS Eimeria tenella.
XX
PN WO9204460-A.
XX
PD 19-MAR-1992.
XX
PF 05-SEP-1991; 91WO-US006430.
XX
PR 12-SEP-1990; 90US-00581693.
XX
PA (GEMX) GENEX CORP.
XX
PI Jacobson JW, Strausberg RL, Wilson SD, Pope SH, Strausberg SL;
PI Ruff MD, Augustine PC, Danforth HD;
XX
DR WPI; 1992-114365/14.
DR P-PSDB; AAR22392.
XX
PT Vaccine against avian coccidiosis - comprising recombinant eimeria
PT antigen ac-18 or ac-6b gene, or microorganisms expressing them.
XX
PS Claim 5; Page 39 + Fig 5; 56pp; English.
XX
CC To identify antigens of E. tenella, expression libraries were prepd. in
CC lambda vector, lambda gt11, using cDNA prepd. from polyA mRNA isolated
CC from E. tenella oocysts. The cDNA expression library was screened with
CC monoclonal antibody (MAb) 12-07 which was raised against the sporozoite
CC stage of E. tenella. The library to be screened was plated on a host that
CC allows lysis and plaque formation. During induction of the antigens
CC encoded by the phage, the plaques were identified by screening the
CC filters with Mab 12-07. The cDNA inserts from the MAb 12-07 positive
CC phage were cloned into bacteriophage M13 and subjected to sequence
CC analysis. Following sequence analysis, E. tenella antigen tc-7a was
CC identified. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 543 BP; 229 A; 135 C; 161 G; 18 T; 0 U; 0 Other;

Query Match 3.4%; Score 38.4; DB 2; Length 543;
Best Local Similarity 46.9%; Pred. No. 1.8;
Matches 120; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

```
Qy         89 TCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGG 148
              |||    ||  |||  |  |     |  || | |     ||  || |  |||   | |
Db        450 TCCCCCAGGCTTACCTGCTGCTGATGCTGCTGCTGCTCTTGCTGCAGCTGCTGTTGTTGC 391

Qy        149 TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT 208
              |||| ||  ||  |||  | |  | ||| |||| || ||||   | | |
Db        390 TGCTGTTGCTGCTTGTGTTTTCGCTTTCTCTGCTTCTGCTGCTGCTCCTGCTGCTCCTTC 331

Qy        209 TCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGC 268
              | | |   ||  || |   |  ||| |  | ||  | || |  || |  || ||
Db        330 GGTTTCTGTTCGTGCTTCCGCTGCCTTTGCTGCTCCTGCTGCTCCTGCTGCGGCTGTCGC 271

Qy        269 AGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGTACGCGCCAGAGGTTGTTTCGGG 328
              | |  |||| |||    |  | | ||| |  |||   ||  |||  | || | | |
Db        270 TGCAGCTGGTGCTGCTGCAGCTCCTGTTGCTGCTGCTGCTGCTGCAGCTGGTGCTGCTGC 211

Qy        329 AGGGTCGGGGGTAGCT 344
              ||     |  | ||||
Db        210 AGCTGGTGCTGCAGCT 195
```

RESULT 5
ADA07157/c
ID ADA07157 standard; DNA; 717 BP.
XX
AC ADA07157;
XX
DT 06-NOV-2003 (first entry)
XX
DE Ptilosarcus gurneyi GFP codon optimised nucleotide sequence.
XX
KW fusion nucleic acid; Renilla; Ptilosarcus; green fluorescent protein;
KW GFP; retroviral vector; internal ribosome entry site element;
KW IRES element; type 2A sequence; protease recognition site;
KW antiinflammatory; cytostatic; immunomodulator; antibacterial; virucide;
KW protozoacide; gene therapy; immunological disease; inflammatory disease;
KW infectious disease; cancer; drug resistance; toxicity; gene; ds.
XX
OS Synthetic.
OS Ptilosarcus gurneyi.
XX
PN WO200290535-A1.
XX
PD 14-NOV-2002.
XX
PF 09-MAY-2002; 2002WO-US014766.
XX
PR 10-MAY-2001; 2001US-0290287P.
PR 24-APR-2002; 2002US-00133973.
XX
PA (RIGE-) RIGEL PHARM INC.
XX
PI Anderson D;
XX
DR WPI; 2003-103518/09.
XX
PT New fusion nucleic acid, useful as reporter for intracellular assays or
PT in drug resistance or toxicity studies, comprises a gene of interest and
PT a gene encoding codon optimized Renilla muelleri or Ptilosarcus green
PT fluorescent protein.
XX
PS Example 1; Fig 3; 130pp; English.
XX
CC The present invention describes a fusion nucleic acid (I) comprising a
CC gene of interest, and a gene encoding codon optimised Renilla muelleri or
CC Ptilosarcus green fluorescent proteins (GFP). Also described: (1) a
CC retroviral or nucleic acid vector comprising the fusion nucleic acid
CC having a promoter and a Renilla or Ptilosarcus GFP gene, and optionally,
CC a separation site, and a gene of interest; (2) a library of fusion
CC nucleic acids comprising the fusion nucleic acid described above; (3) a
CC library of cells comprising the library of fusion nucleic acids in (2);
CC (4) a cell comprising the above fusion nucleic acid; and (5) screening
CC for bioactive agents, comprising combining a candidate bioactive agent
CC and a cell comprising the fusion nucleic acid, and screening the cells
CC for an altered phenotype. Preferably the GFP is codon optimised for
CC expression in human cells. Preferably the nucleic acid vector comprises a
CC separation site comprising an internal ribosome entry site (IRES)
CC element, a type 2A sequence, or a protease recognition site. (I) has

CC antiinflammatory, cytostatic, immunomodulator, antibacterial, virucide
CC and protozoacide activities, and can be used in gene therapy. The fusion
CC nucleic acids are useful as reporters for intracellular assays, for
CC screening libraries of cells using Renilla or Ptilosarcus GFPs, in
CC immunological, inflammatory, infectious disease, or cancer applications,
CC in drug resistance or toxicity studies, or in identifying candidate
CC agents that alter phenotypes of cells. The vectors are used to express
CC the proteins and the nucleic acids in e.g. plants, insects or cells. The
CC present sequence represents a GFP nucleotide sequence which is given in
CC the exemplification of the present invention.
XX
SQ Sequence 717 BP; 158 A; 229 C; 220 G; 110 T; 0 U; 0 Other;

Query Match 3.3%; Score 37.6; DB 7; Length 717;
Best Local Similarity 52.6%; Pred. No. 3.3;
Matches 82; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 467 GGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGT 526
Db 649 GCTCCACGAAGCTGCCCTCCTCCACGTAGGTCTTCTCCAGGCGGTGGTGGATGAAGTGGT 590

Qy 527 GCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGT 586
Db 589 ACTCGGGGAACTCCTTCACGCCGCCCTTGCTGCGGTAGAAGGTCTTCATGTGGCAGCTGT 530

Qy 587 TCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGA 622
Db 529 AGTAGTTGCCGCTCTCCAGCTTGTACACCAGGTCCA 494

RESULT 6
AAF61431
ID AAF61431 standard; DNA; 558 BP.
XX
AC AAF61431;
XX
DT 08-JUN-2001 (first entry)
XX
DE Synthetic MspA coding region SEQ ID 4.
XX
KW MspA; Gram positive bacterium; channel forming protein; porin;
KW nanostructure; automation; ds.
XX
OS Synthetic.
XX
PN DE19943520-A1.
XX
PD 01-MAR-2001.
XX
PF 11-SEP-1999; 99DE-01043520.
XX
PR 31-AUG-1999; 99DE-01041416.
XX
PA (NIED/) NIEDERWEIS M.
PA (BOSS/) BOSSMANN S.
XX
PI Niederweis M, Bossmann S;
XX
DR WPI; 2001-266957/28.
DR P-PSDB; AAB70808.
XX
PT Production of bacterial channel-forming proteins, useful for making
PT nanostructures comprises heterologous expression or by extraction from
PT mycobacteria.
XX
PS Disclosure; Page 11; 18pp; German.
XX
CC This invention describes a novel method for the production of a channel-
CC forming protein (I), present in Gram-positive bacteria which comprises
CC heterologous expression and purification from mycobacteria. The invention
CC describes (1) (I) produced this way; and (2) a gene encoding (I),
CC particularly a porin (Ia), from Gram-positive bacteria. (I) are used to
CC prepare nanostructures useful in testing and detection. (I) can be
CC isolated simply and quickly, with better yield than in known processes,
CC and the method is suitable for automation (of chromatographic
CC purification). Expression of (I) in Escherichia coli provides a 10-20
CC fold increase in yield, relative to recovery of native protein, and
CC extraction with surfactants is very selective, reducing contamination by
CC other proteins and eliminating the need for organic solvents. (I) can be
CC dissolved in organic solvents, precipitated with acetone and heated for
CC 10 min in 3% sodium dodecylsulfate solution, all without denaturation.
CC This sequence encodes a synthetic MspA protein which is used to
CC illustrate the method of the invention
XX
SQ Sequence 558 BP; 92 A; 166 C; 156 G; 144 T; 0 U; 0 Other;

Query Match 3.2%; Score 35.8; DB 4; Length 558;
Best Local Similarity 51.6%; Pred. No. 9.8;
Matches 82; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

Qy 392 TGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACC 451
Db 351 TGCTGATCTGGGCAACGGTCCGGGTATCCAGGAAGTTGCTACCTTCTCTGTAGACGTCTC 410

Qy 452 AGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCT 511
Db 411 TGGTGCTGAAGGTGGTGTTGCTGTTTCTAACGCTCACGGCACCGTTACCGGTGCGGCTGG 470

Qy 512 TGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGC 550
Db 471 CGGTGTTCTGCTGCGTCCGTTCGCTCGTCTGATCGCTTC 509

RESULT 7
AAF61428
ID AAF61428 standard; DNA; 558 BP.
XX
AC AAF61428;
XX
DT 08-JUN-2001 (first entry)
XX
DE Synthetic MspA DNA coding region SEQ ID 4.
XX
KW Nanostructure; channel-forming protein; Gram-positive bacterium;
KW miniaturized material; miniaturized machine; sensor; nanowire; MspA;
KW molecular sieve; ds.
XX
OS Synthetic.
XX
PN DE19941448-A1.
XX
PD 01-MAR-2001.
XX
PF 31-AUG-1999; 99DE-01041448.
XX
PR 31-AUG-1999; 99DE-01041448.
XX
PA (BOSS/) BOSSMANN S.
PA (NIED/) NIEDERWEIS M.
XX
PI Bossmann S, Niederweis M;
XX
DR WPI; 2001-283025/30.
DR P-PSDB; AAB70806.
XX
PT Producing regular nanostructures, useful e.g. as miniature wires or
PT catalysts for sensors, by depositing bacterial channel-forming protein on
PT substrate.
XX
PS Disclosure; Page 14; 24pp; German.
XX
CC This invention describes a novel method for the production of regular
CC nanostructures (A) which comprises preparing a channel-forming protein
CC (I) from a Gram-positive bacterium and applying it to a substrate. The
CC invention also describes (1) (A) produced this way; and (2) use of (I)
CC for preparation of nanoparticles and (A) on substrates. (A) are useful

```
CC   e.g. in production of miniaturized materials and machines, e.g.
CC   electronic or physical devices such as sensors and nanowires, also as
CC   'cages' and host compounds for catalysts and molecular sieves. (I) have
CC   excellent chemical and thermal stability, e.g. they can be dissolved in
CC   organic solvent, precipitated with acetone and boiled in detergent
CC   solutions without denaturation. They can be modified, by mutation, at
CC   selected positions to alter local chemical or physical properties, e.g.
CC   to improve self-assembly or association with other materials; are easily
CC   penetrated by light (so photochemical reactions can be performed inside
CC   the proteins), and can self assemble on electrodes to allow performance
CC   of electrochemical reactions, e.g. deposition of metals. Production of
CC   (I) by heterologous expression is very efficient (10-20 fold greater
CC   yield than recovery of native protein) and allows automated purification
CC   by chromatography. Extraction of (I) using detergents is very selective,
CC   eliminating need for organic solvents and reducing contamination by other
CC   proteins. This sequence encodes a synthetic MspA channel forming protein
CC   which is used to illustrate the method of the invention
XX
SQ   Sequence 558 BP; 92 A; 166 C; 156 G; 144 T; 0 U; 0 Other;

  Query Match             3.2%;  Score 35.8;  DB 4;  Length 558;
  Best Local Similarity   51.6%;  Pred. No. 9.8;
  Matches   82;  Conservative    0;  Mismatches   77;  Indels    0;  Gaps    0;

Qy        392 TGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACC 451
              ||  |  | |||  | || ||   |   | ||   ||| | |  ||    | ||||   |
Db        351 TGCTGATCTGGGCAACGGTCCGGGTATCCAGGAAGTTGCTACCTTCTCTGTAGACGTCTC 410

Qy        452 AGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCT 511
              | | | |||| | | || |||||  |      |||||     ||||||| ||  | ||
Db        411 TGGTGCTGAAGGTGGTGTTGCTGTTTCTAACGCTCACGGCACCGTTACCGGTGCGGCTGG 470

Qy        512 TGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGC 550
              | || | | |||   | |   || || |     ||| |
Db        471 CGGTGTTCTGCTGCGTCCGTTCGCTCGTCTGATCGCTTC 509


RESULT 8
AAF75507/c
ID   AAF75507 standard; DNA; 486 BP.
XX
AC   AAF75507;
XX
DT   09-MAY-2001  (first entry)
XX
DE   Polyglutamine tract coding sequence #2.
XX
KW   Animal model; polyglutamine tract; neurodegenerative disorder; HDJ1;
KW   heat shock protein 40; tetratricopeptide repeat protein 2; TPR2; stroke;
KW   myeloid leukaemia factor 1; MLF; human; fruit fly; Alzheimer's disease;
KW   Parkinson's disease; CJD; BSE; Huntington's disease; head trauma; cancer;
KW   ds.
XX
OS   Drosophila sp.
XX
PN   WO200112238-A1.
XX
PD   22-FEB-2001.
XX
PF   14-AUG-2000; 2000WO-US022496.
XX
PR   12-AUG-1999;   99US-0148933P.
PR   12-AUG-1999;   99US-0148934P.
PR   18-JAN-2000; 2000US-0177047P.
PR   19-MAY-2000; 2000US-0205720P.
XX
PA   (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
PI   Benzer S,  Kazemi-Esfarjani P;
XX
DR   WPI; 2001-147537/15.
XX
PT   Identifying genes or other compounds that modulate polyglutamine
PT   toxicity, useful for treating Alzheimer's disease, Parkinson's disease
PT   and Creutzfeldt-Jakob disease.
XX
PS   Disclosure; Fig 1A; 275pp; English.
XX
CC   The present invention describes a method of screening for genes which
CC   modulate polyglutamine toxicity using animal models with polyglutamine
CC   sequences that cause toxicity in the animal. The model is preferably
CC   Drosophila, and toxic polyglutamine sequences include the human and
CC   Drosophila heat shock protein 40/HDJ1, tetratricopeptide repeat protein 2
CC   (TPR2) and myeloid leukaemia factor 1 (MLF) genes. The model is useful
CC   for identifying treatments for neurodegenerative and proliferative
CC   disorders, including Alzheimer's disease, Parkinson's disease,
CC   Creutzfeldt-Jacob's disease (CJD), bovine spongiform encephalopathy
CC   (BSE), Huntington's disease, Machado-Joseph disease, spinocerebellar
CC   ataxias, dentatorubropallidoluysian atrophy, Kennedy's disease, stroke,
CC   head trauma and cancer
XX
SQ   Sequence 486 BP; 193 A; 164 C; 108 G; 21 T; 0 U; 0 Other;

  Query Match             3.1%;  Score 35.6;  DB 4;  Length 486;
  Best Local Similarity   44.2%;  Pred. No. 11;
  Matches  146;  Conservative    0;  Mismatches  184;  Indels    0;  Gaps    0;

Qy         82 TTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTG 141
              ||   | | |||| |  |      |  |   | |   || | ||    ||  |  |   ||
Db        375 TTGCTGCTGCTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTG 316

Qy        142 CACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTA 201
              |  | | |||| |||   | | | |  ||||    |||  |||| |   || |   |
Db        315 CTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGCTGCTGCTG 256

Qy        202 TTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAG 261
              || | ||| |  ||       | ||  |  |||||  ||   ||    |   || || |
Db        255 TTGCTGTTGTTGTTGCTGTTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTGCTG 196

Qy        262 GAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGTACGCGCCAGAGGTTG 321
              |  |  |    || | |||       | | | |     ||     ||  | |  ||||
Db        195 CTGCTGTTGCTGTTGCTGCTGCTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTG 136

Qy        322 TTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTT 381
              | | |  |  | |  | |||  | | || |  | | | |||  |   |  |  ||
Db        135 CTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTG 76

Qy        382 GGTGTCCACATGTGGGACGGGGGTAGGGCC 411
                | |   || |||   |  |  |||||
Db         75 TTGCTGCTGCTGGGGGGGTTGACGGTGGGCC 46


RESULT 9
AAD56497
ID   AAD56497 standard; DNA; 789 BP.
XX
AC   AAD56497;
XX
DT   27-AUG-2003  (first entry)
XX
DE   Human VLCFABE MOOSE00004 DNA from ctg13284.
XX
KW   Human; very long chain fatty acid biosynthesis enzyme; VLFA; VLCFABE;
KW   non-insulin dependent diabetes mellitus; NIDDM; adrenoleukodystrophy;
KW   ALD; autosomal dominant macular dystrophy; adMD; Alzheimer's disease;
KW   coronary heart disease; stroke; myocardial infarction; gene therapy;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .789
FT                   /*tag=  a
FT                   /product= "Human VLCFABE protein"
FT                   /note= "No start and stop codon"
FT                   /partial
```

XX
PN WO2003040392-A2.
XX
PD 15-MAY-2003.
XX
PF 04-NOV-2002; 2002WO-IB004610.
XX
PR 06-NOV-2001; 2001US-0332864P.
XX
PA (DECO-) DECODE GENETICS EHF.
XX
PI Betts M, Sigurdsson GT;
XX
DR WPI; 2003-430674/40.
DR P-PSDB; AAE37330.
XX
PT New isolated nucleic acid molecule comprising a very long chain fatty
PT acid biosynthesis enzyme nucleic acid, useful for treating a disease
PT associated with the biosynthesis enzyme nucleic acid.
XX
PS Claim 1; Page 86; 90pp; English.
XX
CC The invention relates to very long chain fatty acid (VLFA) biosynthesis
CC enzymes (VLCFABE) and polynucleotides encoding such proteins. Sequences
CC of the invention are useful for treating VLCFABE diseases such as non-
CC insulin dependent diabetes mellitus (NIDDM), adrenoleukodystrophy (ALD),
CC autosomal dominant macular dystrophy (adMD), Alzheimer's disease and
CC coronary heart diseases such as stroke and myocardial infarction. They
CC are also used in gene therapy. The present sequence is human VLCFABE DNA
XX
SQ Sequence 789 BP; 204 A; 215 C; 172 G; 198 T; 0 U; 0 Other;

Query Match 3.1%; Score 35.6; DB 7; Length 789;
Best Local Similarity 48.1%; Pred. No. 13;
Matches 101; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

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Qy          60 CAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACT 119
               ||   | || | |   |  ||     |||||  |       | |||   | |     |   |
Db         438 CAAGAACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCAT 497

Qy         120 CCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCAT 179
               |  ||  ||  || ||   ||| |  | |       ||   | ||      | | || ||||
Db         498 CATGTACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCAT 557

Qy         180 GCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTC 239
               || | |  |   ||| ||  | || | | | | | | || ||| || ||  ||| |  |
Db         558 GCTCATCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCAC 617

Qy         240 GTGCATGGCACACCAGTCGCAGGAGTGGCA 269
               || |||       |||   ||||  || ||
Db         618 GTACATCTGGAGGCAGGATCAGGGATGCCA 647
```

RESULT 10
ABZ22164
ID ABZ22164 standard; cDNA; 810 BP.
XX
AC ABZ22164;
XX
DT 12-MAR-2003 (first entry)
XX
DE Human elongase HSELO1-like protein encoding cDNA SEQ ID NO:5.
XX
KW Human; elongase; elongase HSELO1-like protein; enzyme; cytostatic;
KW antidiabetic; antiasthmatic; anti-HIV; antiparkinsonian; nootropic;
KW neuroprotective; tranquilliser; antimigraine; analgesic; neuroleptic;
KW cerebroprotective; gene therapy; cancer; diabetes; CNS disorder; asthma;
KW metabolic disease; central nervous system disorder; COPD; dementia;
KW Parkinson's disease; multiple sclerosis; stroke; Alzheimer's disease;
KW Huntington's disease; Creutzfeldt-Jakob disease; HIV; schizophrenia;
KW psychosis; attention deficit disorder; headache pain; migraine; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .810
FT /*tag= a
FT /partial
FT /product= "elongase HSELO1-like protein"
FT /note= "no stop codon given"
XX
PN WO200262974-A2.
XX
PD 15-AUG-2002.
XX
PF 07-FEB-2002; 2002WO-EP001262.
XX
PR 08-FEB-2001; 2001US-0267135P.
XX
PA (FARB) BAYER AG.
XX
PI Zhu Z;
XX
DR WPI; 2002-636596/68.
DR P-PSDB; ABP56418.
XX
PT New isolated human elongase HSELO1-like polynucleotide and encoded
PT peptide, useful for treating, preventing and ameliorating diseases such
PT as COPD, cancer, metabolic disease, diabetes, CNS disorders, or asthma.
XX
PS Claim 1; Fig 5; 128pp; English.
XX
CC The present sequence encodes a human elongase HSELO1-like protein (I).
CC (I) has cytostatic, antidiabetic, antiasthmatic, anti-HIV, nootropic,
CC antiparkinsonian, neuroprotective, tranquilliser, antimigraine,
CC analgesic, neuroleptic and cerebroprotective activities, and can be used
CC in gene therapy. (I) can be used in the treatment of a disease, such as
CC cancer, diabetes, central nervous system (CNS) disorder, asthma,
CC metabolic disease or COPD. The human elongase HSELO1-like protein is
CC useful in preventing, treating or ameliorating the diseases cited above,
CC including Parkinson's disease, dementia, multiple sclerosis, stroke, HIV,
CC Alzheimer's disease, Huntington's disease, Creutzfeldt-Jakob disease,
CC schizophrenia, psychosis, attention deficit disorders, pain associated
CC with CNS disorders, with cancer, or headache pain, e.g. migraine. It can
CC also be useful in identifying test compounds that may act as activators
CC or inhibitors at the enzyme's active site, or in raising specific
CC antibodies that can block and effectively reduce its activity
XX
SQ Sequence 810 BP; 195 A; 231 C; 181 G; 203 T; 0 U; 0 Other;

Query Match 3.1%; Score 35.6; DB 6; Length 810;
Best Local Similarity 48.1%; Pred. No. 13;
Matches 101; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

```
Qy          60 CAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACT 119
               ||   | || | |   |  ||     |||||  |       | |||   | |     |   |
Db         480 CAAGAACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCAT 539

Qy         120 CCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCAT 179
               |  ||  ||  || ||   ||| |  | |       ||   | ||      | | || ||||
Db         540 CATGTACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCAT 599

Qy         180 GCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTC 239
               || | |  |   ||| ||  | || | | | | | | || ||| || ||  ||| |  |
Db         600 GCTCATCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCAC 659

Qy         240 GTGCATGGCACACCAGTCGCAGGAGTGGCA 269
               || |||       |||   ||||  || ||
Db         660 GTACATCTGGAGGCAGGATCAGGGATGCCA 689
```

RESULT 11
AAD42270
ID AAD42270 standard; DNA; 813 BP.
XX
AC AAD42270;

```
XX
DT   04-NOV-2002  (first entry)
XX
DE   Human ELG6 gene.
XX
KW   Human; elongase; therapy; enzyme; polyunsaturated fatty acid; sinusitis;
KW   PUFA disorder; cardiovascular disorder; articular cartilage degradation;
KW   peripheral vascular disease; atherosclerosis; coronary artery disease;
KW   inflammatory disorder; pancreatitis; asthma; gastrointestinal disorder;
KW   osteoarthritis; rheumatoid arthritis; congenital liver disease; cancer;
KW   acne; Sjogren's syndrome; body weight disorder; cerebrovascular disease;
KW   acute respiratory distress syndrome; hypercholesterolaemia; alcoholism;
KW   postviral fatigue; psychiatric disorder; pre-menstrual syndrome; eczema;
KW   Alzheimer's syndrome; hypertriglyceridaemia; cystic fibrosis; anorexia;
KW   autoimmune disorder; obesity; cachexia; viral disease; endometriosis;
KW   dyslipidaemia; atopic disorder; diabetes; ELG6; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .813
FT                   /*tag=  a
FT                   /product= "ELG6 protein"
XX
PN   WO200244320-A2.
XX
PD   06-JUN-2002.
XX
PF   29-NOV-2001; 2001WO-CA001705.
XX
PR   29-NOV-2000; 2000US-0253728P.
XX
PA   (XENO-) XENON GENETICS INC.
XX
PI   Winther MD,  Knickle LC,  Haardt M,  De Antueno RJ,  Jenkins DK;
PI   Nwaka SO,  Allen SJ,  Ponton A,  Goldberg YP;
XX
DR   WPI; 2002-547693/58.
DR   P-PSDB; AAE24550.
XX
PT   Novel elongase polypeptide, genes and their control regions useful in
PT   determining compositions for treating polyunsaturated fatty acid disorder
PT   e.g. cardiovascular, inflammation, gastrointestinal disorders and cancer.
XX
PS   Claim 1; Page 160; 173pp; English.
XX
CC   The invention relates to novel elongase polypeptides, genes and their
CC   control regions. Sequences of the invention are used in the diagnosis and
CC   treatment of polyunsaturated fatty acid (PUFA) disorders such as
CC   cardiovascular disorders (e.g. atherosclerosis, coronary artery disease),
CC   inflammatory disorders (e.g. sinusitis, pancreatitis, asthma,
CC   osteoarthritis, rheumatoid arthritis, acne), Sjogren's syndrome, body
CC   weight disorders (e.g. obesity, cachexia and anorexia), viral diseases
CC   and postviral fatigue, gastrointestinal disorders, eczema, psychiatric
CC   disorders, cancer, congenital liver disease, alcoholism, Alzheimer's
CC   syndrome, cystic fibrosis, endometriosis, pre-menstrual syndrome,
CC   hypercholesterolaemia, hypertriglyceridaemia, dyslipidaemia, peripheral
CC   vascular disease, cerebrovascular disease, autoimmune disorders, acute
CC   respiratory distress syndrome, atopic disorders, articular cartilage
CC   degradation, diabetes and diabetic complication. The present sequence is
CC   human elongase gene (ELG6)
XX
SQ   Sequence 813 BP; 196 A; 231 C; 182 G; 204 T; 0 U; 0 Other;

  Query Match             3.1%;  Score 35.6;  DB 6;  Length 813;
  Best Local Similarity   48.1%;  Pred. No. 13;
  Matches  101;  Conservative    0;  Mismatches  109;  Indels    0;  Gaps    0;

Qy         60 CAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACT 119
              ||   | || | |   |  ||     |||||  |       | |||   | |      |   |
Db        480 CAAGAACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCAT 539

Qy        120 CCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCAT 179
              |  ||  ||  || ||   ||| |  | |       ||   | ||     | | || ||||
Db        540 CATGTACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCAT 599

Qy        180 GCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTC 239
              || | |   ||| ||  | || | | | | | | || ||| || ||  |||  |  |
Db        600 GCTCATCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCAC 659

Qy        240 GTGCATGGCACACCAGTCGCAGGAGTGGCA 269
              || |||       |||   ||||  || ||
Db        660 GTACATCTGGAGGCAGGATCAGGGATGCCA 689


RESULT 12
ABZ22162
ID   ABZ22162 standard; cDNA; 813 BP.
XX
AC   ABZ22162;
XX
DT   12-MAR-2003  (first entry)
XX
DE   Human elongase HSELO1-like protein encoding cDNA SEQ ID NO:1.
XX
KW   Human; elongase; elongase HSELO1-like protein; enzyme; cytostatic;
KW   antidiabetic; antiasthmatic; anti-HIV; antiparkinsonian; nootropic;
KW   neuroprotective; tranquilliser; antimigraine; analgesic; neuroleptic;
KW   cerebroprotective; gene therapy; cancer; diabetes; CNS disorder; asthma;
KW   metabolic disease; central nervous system disorder; COPD; dementia;
KW   Parkinson's disease; multiple sclerosis; stroke; Alzheimer's disease;
KW   Huntington's disease; Creutzfeldt-Jakob disease; HIV; schizophrenia;
KW   psychosis; attention deficit disorder; headache pain; migraine; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .813
FT                   /*tag=  a
FT                   /product= "elongase HSELO1-like protein"
XX
PN   WO200262974-A2.
XX
PD   15-AUG-2002.
XX
PF   07-FEB-2002; 2002WO-EP001262.
XX
PR   08-FEB-2001; 2001US-0267135P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Zhu Z;
XX
DR   WPI; 2002-636596/68.
DR   P-PSDB; ABP56418.
XX
PT   New isolated human elongase HSELO1-like polynucleotide and encoded
PT   peptide, useful for treating, preventing and ameliorating diseases such
PT   as COPD, cancer, metabolic disease, diabetes, CNS disorders, or asthma.
XX
PS   Claim 1; Fig 1; 128pp; English.
XX
CC   The present sequence encodes a human elongase HSELO1-like protein (I).
CC   (I) has cytostatic, antidiabetic, antiasthmatic, anti-HIV, nootropic,
CC   antiparkinsonian, neuroprotective, tranquilliser, antimigraine,
CC   analgesic, neuroleptic and cerebroprotective activities, and can be used
CC   in gene therapy. (I) can be used in the treatment of a disease, such as
CC   cancer, diabetes, central nervous system (CNS) disorder, asthma,
CC   metabolic disease or COPD. The human elongase HSELO1-like protein is
CC   useful in preventing, treating or ameliorating the diseases cited above,
CC   including Parkinson's disease, dementia, multiple sclerosis, stroke, HIV,
CC   Alzheimer's disease, Huntington's disease, Creutzfeldt-Jakob disease,
CC   schizophrenia, psychosis, attention deficit disorders, pain associated
CC   with CNS disorders, with cancer, or headache pain, e.g. migraine. It can
CC   also be useful in identifying test compounds that may act as activators
CC   or inhibitors at the enzyme's active site, or in raising specific
```

```
CC   antibodies that can block and effectively reduce its activity
XX
SQ   Sequence 813 BP; 196 A; 231 C; 182 G; 204 T; 0 U; 0 Other;

  Query Match             3.1%;  Score 35.6;  DB 6;  Length 813;
  Best Local Similarity   48.1%;  Pred. No. 13;
  Matches  101;  Conservative    0;  Mismatches  109;  Indels    0;  Gaps    0;

Qy         60 CAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACT 119
              ||   | || | |   | ||     |||| |      | |||  | |    |  |
Db        480 CAAGAACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCAT 539

Qy        120 CCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCAT 179
              |  ||  ||  || ||   ||| |  | |      ||   | ||     | | || ||||
Db        540 CATGTACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCAT 599

Qy        180 GCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTC 239
              || | |  |   ||| ||  | || | | | | | || ||| || ||  ||| |  |
Db        600 GCTCATCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCAC 659

Qy        240 GTGCATGGCACACCAGTCGCAGGAGTGGCA 269
              || |||       |||   ||||  || ||
Db        660 GTACATCTGGAGGCAGGATCAGGGATGCCA 689


RESULT 13
ABN86918
ID   ABN86918 standard; cDNA; 815 BP.
XX
AC   ABN86918;
XX
DT   29-JUL-2002  (first entry)
XX
DE   Human NOV6a encoding cDNA sequence SEQ ID NO:17.
XX
KW   Human; NOVX; cytostatic; antiarteriosclerotic; cardiovascular; lymphoma;
KW   antidiabetic; immunosuppressive; neuroprotective; gene therapy; cancer;
KW   cardiomyopathy; atherosclerosis; cell signal processing; diabetes; AIDS;
KW   metabolic pathway modulation; neoplastic; neurological disorder; asthma;
KW   adenocarcinoma; prostate cancer; uterus cancer; immune response;
KW   Crohn's disease; multiple sclerosis; Graft versus host disease;
KW   chromosome 10; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .813
FT                   /*tag=  a
FT                   /product= "NOV6a"
FT                   /note= "Cold inducible glycoprotein 30-like protein"
XX
PN   WO200230974-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US031922.
XX
PR   12-OCT-2000; 2000US-0240113P.
PR   16-OCT-2000; 2000US-0240625P.
PR   16-OCT-2000; 2000US-0240637P.
PR   16-OCT-2000; 2000US-0240648P.
PR   16-OCT-2000; 2000US-0240662P.
PR   16-OCT-2000; 2000US-0240669P.
PR   16-OCT-2000; 2000US-0240703P.
PR   16-OCT-2000; 2000US-0240732P.
PR   16-OCT-2000; 2000US-0241190P.
PR   18-JAN-2001; 2001US-0262455P.
XX
PA   (CURA-) CURAGEN CORP.
PA   (MILL/) MILLET I.
XX
PI   Grosse WM,  Alsobrook JP,  Lepley DM,  Burgess CE,  Mishra V;
PI   Kekuda R,  Li L,  Padigaru M,  Shimkets RA,  Zerhusen BD,  Spytek KA;
PI   Edinger S,  Gerlach V,  Macdougall J,  Stone D,  Gunther E,  Ellerman K;
XX
DR   WPI; 2002-444172/47.
DR   P-PSDB; ABB78812.
XX
PT   New NOVX polypeptides and polynucleotides, useful for treating or
PT   preventing a NOVX-associated disorder or a pathological state in a
PT   subject, particularly a human, e.g. cardiomyopathy, atherosclerosis,
PT   cancer or diabetes.
XX
PS   Claim 9; Page 51; 227pp; English.
XX
CC   The present invention describes novel human proteins designated NOVX
CC   (where X is 1, 2a, 2b, 2c, 2d, 3, 4, 5, 6a, 6b, 7, 8, or 9). NOV1 is a
CC   tyrosine-protein kinase 6-like protein; NOV2a-d are keratin 4-like
CC   proteins; NOV3 is a collagen-like protein; NOV4 is a cystatin B-like
CC   protein; NOV5 is a serotonin receptor-like protein; NOV6a and NOV65v are
CC   cold inducible glycoprotein 30-like proteins; NOV7 is a matrilin-2-like
CC   protein; NOV8 is a leukocyte surface antigen (CD53)-like protein; and
CC   NOV9 is a tyrosine kinase-like protein. NOVX sequences have cytostatic,
CC   antiarteriosclerotic, cardiovascular, antidiabetic, immunosuppressive and
CC   neuroprotective activities, and can be used in gene therapy. The NOVX
CC   sequences can be used in therapeutics, particularly for treating,
CC   preventing or alleviating a NOVX-associated disorder or a pathological
CC   state in a subject, particularly a human. These disorders include
CC   cardiomyopathy, atherosclerosis, a disorder related to cell signal
CC   processing and metabolic pathway modulation or diabetes. The NOVX
CC   sequences are also useful for determining the presence of or
CC   predisposition to a disease associated with altered levels of NOVX
CC   polypeptide or nucleic acid, particularly cancer. The NOVX sequences are
CC   especially useful in therapeutic or prophylactic applications for
CC   neoplastic or neurological disorders, and in the treatment of
CC   adenocarcinoma, lymphoma, prostate cancer, uterus cancer, immune
CC   response, AIDS, asthma, Crohn's disease, multiple sclerosis or Graft
CC   versus host disease. The present sequence encodes the human NOV6a protein
CC   from the present invention. NOV6a is located to chromosome 10
XX
SQ   Sequence 815 BP; 196 A; 231 C; 183 G; 205 T; 0 U; 0 Other;

  Query Match             3.1%;  Score 35.6;  DB 6;  Length 815;
  Best Local Similarity   48.1%;  Pred. No. 13;
  Matches  101;  Conservative    0;  Mismatches  109;  Indels    0;  Gaps    0;

Qy         60 CAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACT 119
              ||   | || | |   | ||     |||| |      | |||  | |    |  |
Db        480 CAAGAACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCAT 539

Qy        120 CCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCAT 179
              |  ||  ||  || ||   ||| |  | |      ||   | ||     | | || ||||
Db        540 CATGTACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCAT 599

Qy        180 GCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTC 239
              || | |  |   ||| ||  | || | | | | | || ||| || ||  ||| |  |
Db        600 GCTCATCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCAC 659

Qy        240 GTGCATGGCACACCAGTCGCAGGAGTGGCA 269
              || |||       |||   ||||  || ||
Db        660 GTACATCTGGAGGCAGGATCAGGGATGCCA 689


RESULT 14
ABN86919
ID   ABN86919 standard; cDNA; 815 BP.
XX
AC   ABN86919;
XX
DT   29-JUL-2002  (first entry)
XX
DE   Human NOV6b encoding cDNA sequence SEQ ID NO:19.
XX
KW   Human; NOVX; cytostatic; antiarteriosclerotic; cardiovascular; lymphoma;
KW   antidiabetic; immunosuppressive; neuroprotective; gene therapy; cancer;
KW   cardiomyopathy; atherosclerosis; cell signal processing; diabetes; AIDS;
```

```
KW   metabolic pathway modulation; neoplastic; neurological disorder; asthma;
KW   adenocarcinoma; prostate cancer; uterus cancer; immune response;
KW   Crohn's disease; multiple sclerosis; Graft versus host disease;
KW   chromosome 10; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .813
FT                   /*tag=  a
FT                   /product= "NOV6b"
FT                   /note= "Cold inducible glycoprotein 30-like protein"
XX
PN   WO200230974-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US031922.
XX
PR   12-OCT-2000; 2000US-0240113P.
PR   16-OCT-2000; 2000US-0240625P.
PR   16-OCT-2000; 2000US-0240637P.
PR   16-OCT-2000; 2000US-0240648P.
PR   16-OCT-2000; 2000US-0240662P.
PR   16-OCT-2000; 2000US-0240669P.
PR   16-OCT-2000; 2000US-0240703P.
PR   16-OCT-2000; 2000US-0240732P.
PR   16-OCT-2000; 2000US-0241190P.
PR   18-JAN-2001; 2001US-0262455P.
XX
PA   (CURA-) CURAGEN CORP.
PA   (MILL/) MILLET I.
XX
PI   Grosse WM,  Alsobrook JP,  Lepley DM,  Burgess CE,  Mishra V;
PI   Kekuda R,  Li L,  Padigaru M,  Shimkets RA,  Zerhusen BD,  Spytek KA;
PI   Edinger S,  Gerlach V,  Macdougall J,  Stone D,  Gunther E,  Ellerman K;
XX
DR   WPI; 2002-444172/47.
DR   P-PSDB; ABB78813.
XX
PT   New NOVX polypeptides and polynucleotides, useful for treating or
PT   preventing a NOVX-associated disorder or a pathological state in a
PT   subject, particularly a human, e.g. cardiomyopathy, atherosclerosis,
PT   cancer or diabetes.
XX
PS   Claim 9; Page 53; 227pp; English.
XX
CC   The present invention describes novel human proteins designated NOVX
CC   (where X is 1, 2a, 2b, 2c, 2d, 3, 4, 5, 6a, 6b, 7, 8, or 9). NOV1 is a
CC   tyrosine-protein kinase 6-like protein; NOV2a-d are keratin 4-like
CC   proteins; NOV3 is a collagen-like protein; NOV4 is a cystatin B-like
CC   protein; NOV5 is a serotonin receptor-like protein; NOV6a and NOV65v are
CC   cold inducible glycoprotein 30-like proteins; NOV7 is a matrilin-2-like
CC   protein; NOV8 is a leukocyte surface antigen (CD53)-like protein; and
CC   NOV9 is a tyrosine kinase-like protein. NOVX sequences have cytostatic,
CC   antiarteriosclerotic, cardiovascular, antidiabetic, immunosuppressive and
CC   neuroprotective activities, and can be used in gene therapy. The NOVX
CC   sequences can be used in therapeutics, particularly for treating,
CC   preventing or alleviating a NOVX-associated disorder or a pathological
CC   state in a subject, particularly a human. These disorders include
CC   cardiomyopathy, atherosclerosis, a disorder related to cell signal
CC   processing and metabolic pathway modulation or diabetes. The NOVX
CC   sequences are also useful for determining the presence of or
CC   predisposition to a disease associated with altered levels of NOVX
CC   polypeptide or nucleic acid, particularly cancer. The NOVX sequences are
CC   especially useful in therapeutic or prophylactic applications for
CC   neoplastic or neurological disorders, and in the treatment of
CC   adenocarcinoma, lymphoma, prostate cancer, uterus cancer, immune
CC   response, AIDS, asthma, Crohn's disease, multiple sclerosis or Graft
CC   versus host disease. The present sequence encodes the human NOV6b protein
CC   from the present invention. NOV6b is located to chromosome 10
XX
SQ   Sequence 815 BP; 196 A; 231 C; 183 G; 205 T; 0 U; 0 Other;
```

```
  Query Match             3.1%;  Score 35.6;  DB 6;  Length 815;
  Best Local Similarity   48.1%;  Pred. No. 13;
  Matches  101;  Conservative    0;  Mismatches  109;  Indels    0;  Gaps    0;

Qy         60 CAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACT 119
              ||   | || | |   |  ||     |||| |      | |||   | |     |   |
Db        480 CAAGAACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCAT 539

Qy        120 CCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCAT 179
              |  ||  ||  ||  ||   ||| |  | |       ||   | ||     | | || ||||
Db        540 CATGTACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCAT 599

Qy        180 GCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTC 239
              || | |  |   ||| ||  | || | | | | | | || ||| || ||  |||  |  |
Db        600 GCTCATCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCAC 659

Qy        240 GTGCATGGCACACCAGTCGCAGGAGTGGCA 269
              || |||       |||   ||||  || ||
Db        660 GTACATCTGGAGGCAGGATCAGGGATGCCA 689
```

```
RESULT 15
ABZ24216
ID   ABZ24216 standard; DNA; 818 BP.
XX
AC   ABZ24216;
XX
DT   14-APR-2003  (first entry)
XX
DE   Human LCE gene related DNA (sequence Id No. 2).
XX
KW   LCE; long chain fatty acyl elongase; p53; cytostatic; gene therapy;
KW   cancer; human; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200299068-A2.
XX
PD   12-DEC-2002.
XX
PF   03-JUN-2002; 2002WO-US017739.
XX
PR   05-JUN-2001; 2001US-0296076P.
PR   10-OCT-2001; 2001US-0328605P.
PR   15-FEB-2002; 2002US-0357253P.
PR   01-MAR-2002; 2002US-0361196P.
XX
PA   (EXEL-) EXELIXIS INC.
XX
PI   Friedman L,  Plowman GD,  Belvin M,  Francis-Lang H,  Li D,  Funke RP;
PI   Karim FD,  Keyes LN,  Koblizek TI;
XX
DR   WPI; 2003-167338/16.
XX
PT   Identifying a candidate p53 pathway modulating agent for
PT   diagnosing/treating cancer comprises detecting a test agent-biased
PT   activity of an assay system comprising a purified long chain fatty acyl
PT   elongase (LCE) polypeptide or nucleic acid.
XX
PS   Disclosure; Page 50; 69pp; English.
XX
CC   The invention relates to identifying a candidate p53 pathway modulating
CC   agent that involves assaying a purified LCE (long chain fatty acyl
CC   elongase) polypeptide or nucleic acid or its functionally active fragment
CC   or derivative, with a test agent. The methods are useful for identifying
CC   a candidate p53 pathway modulating agent, modulating a p53 pathway of a
CC   cell, or a mammalian cell, diagnosing a disease in a patient, identifying
CC   a candidate branching morphogenesis modulating agent, and modulating
CC   branching morphogenesis in a mammalian cell. The diseases that can be
CC   diagnosed are breast, colon, lung or ovary cancer having greater than 25%
CC   expression level. The method is useful for manufacturing a medicament for
CC   diagnosing or treating breast, colon, lung or ovary cancer. Sequences
```

```
CC   ABZ24215-222 represent DNA sequences related to human LCE gene
XX
SQ   Sequence 818 BP; 198 A; 232 C; 183 G; 205 T; 0 U; 0 Other;

  Query Match             3.1%;  Score 35.6;  DB 7;  Length 818;
  Best Local Similarity   48.1%;  Pred. No. 13;
  Matches  101;  Conservative    0;  Mismatches  109;  Indels    0;  Gaps    0;

Qy          60 CAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACT 119
               ||   | || | |   |  ||     ||||| |      | |||   | |     |   |
Db         484 CAAGAACAAAGTGCCTGCAGGAGGCTGGTTCGTCACCATGAACTTTGGTGTTCATGCCAT 543

Qy         120 CCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCAT 179
               |  ||  ||  || ||   ||| |  | |       ||   | ||     | | || ||||
Db         544 CATGTACACCTACTACACTCTGAAGGCTGCCAACGTGAAGCCCCCCAAGATGCTGCCCAT 603

Qy         180 GCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTC 239
               || | |  |   ||| ||  | || | | | | | | || ||| || ||  |||  |  |
Db         604 GCTCATCACCAGCCTGCAGATCTTGCAGATGTTTGTAGGAGCCATCGTCAGCATCCTCAC 663

Qy         240 GTGCATGGCACACCAGTCGCAGGAGTGGCA 269
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Db         664 GTACATCTGGAGGCAGGATCAGGGATGCCA 693


Search completed: May  8, 2004, 19:18:29
Job time : 334.5 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:36 ; Search time 59.25 Seconds
(without alignments)
10630.705 Million cell updates/sec

Title: US-10-679-999-17
Perfect score: 1135
Sequence: 1 GTATACCTGTTTTGAGTGTG.....AGGCCCAACAATTACCTAGG 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1245136

Minimum DB seq length: 0
Maximum DB seq length: 1135

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	43	3.8	468	1	US-08-236-311-12	Sequence 12, Appl
	2	43	3.8	468	3	US-08-457-918-12	Sequence 12, Appl
c	3	39	3.4	688	3	US-08-998-416-915	Sequence 915, App
c	4	38.4	3.4	533	6	5482709-5	Patent No. 5482709
c	5	38.4	3.4	543	6	5273901-6	Patent No. 5273901
	6	36.4	3.2	1125	4	US-09-252-991A-16469	Sequence 16469, A
c	7	36.2	3.2	615	4	US-09-252-991A-242	Sequence 242, App
	8	36.2	3.2	1041	4	US-09-252-991A-296	Sequence 296, App
c	9	36	3.2	909	4	US-09-252-991A-7481	Sequence 7481, Ap
	10	35.2	3.1	675	4	US-09-252-991A-7278	Sequence 7278, Ap
	11	35	3.1	630	4	US-09-252-991A-953	Sequence 953, App
c	12	35	3.1	777	4	US-09-252-991A-1127	Sequence 1127, Ap
	13	34.6	3.0	505	4	US-09-621-976-15639	Sequence 15639, A
c	14	34.4	3.0	431	4	US-09-433-241A-1	Sequence 1, Appli
	15	34.4	3.0	1011	4	US-09-252-991A-3833	Sequence 3833, Ap
	16	34	3.0	627	4	US-09-252-991A-3035	Sequence 3035, Ap
	17	34	3.0	720	4	US-09-252-991A-3133	Sequence 3133, Ap
c	18	33.6	3.0	839	3	US-08-998-416-519	Sequence 519, App
	19	33.2	2.9	939	4	US-09-489-039A-6098	Sequence 6098, Ap
	20	33.2	2.9	1053	4	US-09-252-991A-15787	Sequence 15787, A
	21	33.2	2.9	1134	4	US-09-252-991A-15842	Sequence 15842, A
c	22	33	2.9	684	4	US-09-252-991A-230	Sequence 230, App
c	23	32.8	2.9	753	4	US-09-252-991A-10372	Sequence 10372, A
	24	32.8	2.9	819	4	US-09-252-991A-10784	Sequence 10784, A
	25	32.8	2.9	861	4	US-09-252-991A-14249	Sequence 14249, A
	26	32.8	2.9	1089	4	US-09-252-991A-13807	Sequence 13807, A
c	27	32.8	2.9	1092	4	US-09-252-991A-14250	Sequence 14250, A
c	28	32.8	2.9	1125	4	US-09-218-489-1	Sequence 1, Appli
	29	32.6	2.9	846	4	US-09-252-991A-6073	Sequence 6073, Ap
c	30	32.6	2.9	872	1	US-08-381-280-19	Sequence 19, Appl
c	31	32.6	2.9	872	2	US-08-445-533-19	Sequence 19, Appl
c	32	32.6	2.9	872	3	US-09-052-085-19	Sequence 19, Appl
c	33	32.6	2.9	1080	4	US-09-252-991A-6480	Sequence 6480, Ap
c	34	32.6	2.9	1116	3	US-09-104-308-2	Sequence 2, Appli
c	35	32.6	2.9	1116	3	US-09-321-981-2	Sequence 2, Appli
c	36	32.6	2.9	1116	4	US-09-739-861A-2	Sequence 2, Appli
c	37	32.6	2.9	1116	4	US-09-795-583-2	Sequence 2, Appli
	38	32.2	2.8	872	1	US-08-381-280-5	Sequence 5, Appli
	39	32.2	2.8	872	2	US-08-445-533-5	Sequence 5, Appli
	40	32.2	2.8	872	3	US-09-052-085-5	Sequence 5, Appli
c	41	32.2	2.8	1026	4	US-09-252-991A-10756	Sequence 10756, A
	42	32	2.8	296	4	US-09-313-294A-5207	Sequence 5207, Ap
c	43	32	2.8	374	4	US-09-536-977-43	Sequence 43, Appl
c	44	32	2.8	660	4	US-09-252-991A-4268	Sequence 4268, Ap
c	45	32	2.8	756	3	US-09-248-335-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-08-236-311-12
; Sequence 12, Application US/08236311
; Patent No. 5565335
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,311
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 444P1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 bases
; TYPE: nucleic acid
; STRANDEDNESS: single

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;      TOPOLOGY:  linear
US-08-236-311-12

  Query Match             3.8%;  Score 43;  DB 1;  Length 468;
  Best Local Similarity   49.5%;  Pred. No. 0.019;
  Matches  143;  Conservative    0;  Mismatches  140;  Indels    6;  Gaps    1;

Qy        379 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 438
              | ||||   || | || | | || |||||    ||  || |||            | |
Db        127 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 186

Qy        439 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 492
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Db        187 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 246

Qy        493 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 552
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Db        247 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 306

Qy        553 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 612
              |||  |  ||||  |||||  || ||  ||  |||        |   || |    || |||
Db        307 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 366

Qy        613 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 661
              | | | |||   || |  ||| |||  |||  |   | |  |||  |||
Db        367 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 415


RESULT 2
US-08-457-918-12
; Sequence 12, Application US/08457918
; Patent No. 6117655
;  GENERAL INFORMATION:
;    APPLICANT:  Capon, Daniel J.
;    APPLICANT:  Gregory, Timothy J.
;    TITLE OF INVENTION:  Adheson Variants
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/457,918
;      FILING DATE:  1-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/236311
;      FILING DATE:  02-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/936190
;      FILING DATE:  26-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/842777
;      FILING DATE:  18-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/250785
;      FILING DATE:  28-SEP-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/104329
;      FILING DATE:  02-OCT-1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kubinec, Jeffrey S.
;      REGISTRATION NUMBER:  36,575
;      REFERENCE/DOCKET NUMBER:  P0444P1C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-8228
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  468 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-457-918-12

  Query Match             3.8%;  Score 43;  DB 3;  Length 468;
  Best Local Similarity   49.5%;  Pred. No. 0.019;
  Matches  143;  Conservative    0;  Mismatches  140;  Indels    6;  Gaps    1;

Qy        379 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 438
              | ||||   || | || | | || |||||    ||  || |||            | |
Db        127 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 186

Qy        439 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 492
              |     |||||| | ||   |||||||||||| ||   |   ||  ||||      |||
Db        187 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 246

Qy        493 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 552
              | |       ||  |||  |||  | |  |||      |     |     |   ||| ||
Db        247 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 306

Qy        553 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 612
              |||  |  ||||  |||||  || ||  ||  |||        |   || |    || |||
Db        307 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 366

Qy        613 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 661
              | | | |||   || |  ||| |||  |||  |   | |  |||  |||
Db        367 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 415


RESULT 3
US-08-998-416-915/c
; Sequence 915, Application US/08998416
; Patent No. 6239264
;  GENERAL INFORMATION:
;    APPLICANT:  Philippsen, Peter
;    APPLICANT:  Pohlmann, Rainer
;    APPLICANT:  Steiner, Sabine
;    APPLICANT:  Mohr, Christine
;    APPLICANT:  Wendland, Jurgen
;    APPLICANT:  Knechtle, Philipp
;    APPLICANT:  Rebischung, Corinne
;    TITLE OF INVENTION:  GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
;    TITLE OF INVENTION:  AND USES THEREOF
;    NUMBER OF SEQUENCES:  1152
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6239264artis Corporation
;      STREET:  3054 Cornwallis Road
;      CITY:  Research Triangle Park
;      STATE:  No. 6239264th Carolina
;      COUNTRY:  USA
;      ZIP:  27709
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/998,416
;      FILING DATE:  24-DEC-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  CH 0016/97
;      FILING DATE:  31-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meigs, J. Timothy
;      REGISTRATION NUMBER:  38,241
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;       REFERENCE/DOCKET NUMBER:  PF/5-30306/A/CGC1976
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  919-541-8587
;       TELEFAX:  919-541-8689
;   INFORMATION FOR SEQ ID NO:  915:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  688 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     ORIGINAL SOURCE:
;       ORGANISM:  PAG1570RP
US-08-998-416-915

  Query Match             3.4%;  Score 39;  DB 3;  Length 688;
  Best Local Similarity   46.0%;  Pred. No. 0.29;
  Matches  132;  Conservative    0;  Mismatches  155;  Indels    0;  Gaps    0;

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Db         526 GTGGTTGCTGTGATTGTGGTTTCAATTGTGGTTGTGGTTGGTGTTGTGTCTGCTGCTGTG 467

Qy         138 CCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCA 197
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Db         466 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCGTCTGCTGCTGCGTCT 407

Qy         198 CGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTC 257
               |  | ||||| || ||      ||| | | |       || |||  ||       | ||
Db         406 GCTGCTGCGGTTGTGGTTGTTGCGCCTGCGCCTGCGCCAGTTGTGGCTGATGAGGCTGTA 347

Qy         258 GCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGTACGCGCCAGAG 317
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Db         346 AACCAAGCTGTTGTTGTTGTTGTAGTTGCGGTTGAGGTTGGGGCTGCTGCTGCTGTTGTG 287

Qy         318 GTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGT 364
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RESULT 4
5482709-5/c
;Patent No. 5482709
;     APPLICANT: JACOBSON, JAMES W.;STRAUSBERG, ROBERT L.;WILSON,
;SUSAN D.;POPE, SHARON H.;STRAUSBERG, SUSAN L.;RUFF, MICHAEL D.;
; AUGUSTINE, PATRICIA C.;DANFORTH, HARRY D.
;     TITLE OF INVENTION: EIMERIA ANTIGENIC COMPOSITION WHICH
;ELICITS ANTIBODIES AGAINST AVIAN COCCIDIOSIS
;     NUMBER OF SEQUENCES: 10
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/148,432
;       FILING DATE: 08-NOV-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 581,693
;       FILING DATE: 12-SEP-1990
;       APPLICATION NUMBER: 215,162
;       FILING DATE: 05-JUL-1989
;       APPLICATION NUMBER: 746,520
;       FILING DATE: 19-JUN-1985
;       APPLICATION NUMBER: 627,811
;       FILING DATE: 05-JUL-1984
;SEQ ID NO:5:
;       LENGTH: 533
5482709-5

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  Best Local Similarity   46.9%;  Pred. No. 0.38;
  Matches  120;  Conservative    0;  Mismatches  136;  Indels    0;  Gaps    0;

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Db         440 TCCCCCAGGCTTACCTGCTGCTGATGCTGCTGCTGCTCTTGCTGCAGCTGCTGTTGTTGC 381

Qy         149 TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT 208
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Db         380 TGCTGTTGCTGCTTGTGTTTTCGCTTTCTCTGCTTCTGCTGCTGCTCCTGCTGCTCCTTC 321

Qy         209 TCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGC 268
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Db         320 GGTTTCTGTTCGTGCTTCCGCTGCCTTTGCTGCTCCTGCTGCTCCTGCTGCGGCTGTCGC 261

Qy         269 AGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGTACGCGCCAGAGGTTGTTTCGGG 328
               | |  |||| |||    |  | | ||| |   ||    ||  |||  | || | | |
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Qy         329 AGGGTCGGGGGTAGCT 344
               ||     |  | ||||
Db         200 AGCTGGTGCTGCAGCT 185


RESULT 5
5273901-6/c
;Patent No. 5273901
;     APPLICANT: JACOBSON, JAMES W.;STRAUSBERG, ROBERT L.;WILSON,
;SUSAN D.;POPE, SHARON H.;STRAUSBERG, SUSAN L.;RUFF,MICHAEL D.;
;AUGUSTINE, PATRICIA C.;DANFORTH, HARRY D.
;     TITLE OF INVENTION: GENETICALLY ENGINEERED COCCIDIOSIS
;SPOROZOITE 21.5 KB ANTIGEN, AC-6B
;     NUMBER OF SEQUENCES: 11
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/581,693
;       FILING DATE: 12-SEP-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 215,162
;       FILING DATE: 05-JUL-1988
;       APPLICATION NUMBER: 746,520
;       FILING DATE: 19-JUN-1985
;       APPLICATION NUMBER: 627,811
;       FILING DATE: 05-JUL-1984
;SEQ ID NO:6:
;       LENGTH:543
5273901-6

  Query Match             3.4%;  Score 38.4;  DB 6;  Length 543;
  Best Local Similarity   46.9%;  Pred. No. 0.38;
  Matches  120;  Conservative    0;  Mismatches  136;  Indels    0;  Gaps    0;

Qy          89 TCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGG 148
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Db         450 TCCCCCAGGCTTACCTGCTGCTGATGCTGCTGCTGCTCTTGCTGCAGCTGCTGTTGTTGC 391

Qy         149 TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT 208
               ||||  ||   ||  |||   | |  |  |||  |||| ||  ||||   |  | |
Db         390 TGCTGTTGCTGCTTGTGTTTTCGCTTTCTCTGCTTCTGCTGCTGCTCCTGCTGCTCCTTC 331

Qy         209 TCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGC 268
               | | |   ||  || |   |  |||  |  | ||   | || |  || |  || || ||
Db         330 GGTTTCTGTTCGTGCTTCCGCTGCCTTTGCTGCTCCTGCTGCTCCTGCTGCGGCTGTCGC 271

Qy         269 AGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGTACGCGCCAGAGGTTGTTTCGGG 328
               | |  |||| |||    |  | | ||| |   ||    ||  |||  | || | | |
Db         270 TGCAGCTGGTGCTGCTGCAGCTCCTGTTGCTGCTGCTGCTGCTGCAGCTGGTGCTGCTGC 211

Qy         329 AGGGTCGGGGGTAGCT 344
               ||     |  | ||||
Db         210 AGCTGGTGCTGCAGCT 195


RESULT 6
US-09-252-991A-16469
; Sequence 16469, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 16469
;   LENGTH: 1125
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16469

  Query Match             3.2%;  Score 36.4;  DB 4;  Length 1125;
  Best Local Similarity   49.5%;  Pred. No. 1.8;
  Matches   94;  Conservative    0;  Mismatches   96;  Indels    0;  Gaps    0;

Qy        412 CTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCG 471
              || || | | |     | || |  || |  ||  || | | |    ||| |  |||
Db        791 CTGCTGGCCGGCAAGGAAGGCCCGCTGGGCAAGAACTACAACATGCGCTGGATCGCCTCG 850

Qy        472 CTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGA 531
              ||        || ||  || |    | ||   |||  | | || |||| |  | |||
Db        851 ATGGTCGCCGACGTCCACCGCATCCTGACCCGTGGCGGCGTCTTCATGTACCCGCGCGAC 910

Qy        532 GGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCG 591
              | | ||| | |   | ||| | |||  |    ||  || |||      ||| | | |||
Db        911 GCCCGCGAGCCGGAGAAGCCCGGCAAGCTGCGCCTGATGTACGAAGCCAACCCGATGTCG 970

Qy        592 TCCACCGTCG 601
              | ||| | |||
Db        971 TTCATCATCG 980


RESULT 7
US-09-252-991A-242/c
; Sequence 242, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 242
;   LENGTH: 615
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-242

  Query Match             3.2%;  Score 36.2;  DB 4;  Length 615;
  Best Local Similarity   49.2%;  Pred. No. 1.6;
  Matches   95;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy        418 GACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAG 477
              |||  |  |   | ||  |  ||   ||| |||| | |   ||  ||  | | | |||  |
Db        359 GACATGCGCCGCGCCCTGGCGCTATGGCCGGAACTGGCGCCTTGGAGCGAGGCCCTGCTG 300

Qy        478 CGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCAC 537
              | ||   |    |  |   || | |  ||       ||  |||| | ||||| ||  |
Db        299 GGCCAGTACCTTGCCGTGCACCCGGGCTTCCAGCGCCTGGCGTTCGCGGGCGGAAGGGTC 240

Qy        538 GACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACC 597
              | |||||  |||| |  |     | |  |||  || |  |  ||| ||   | ||      |
Db        239 GGCCTGACCCTGCTGCTGGGCGATGCCATGGAGTGCCTGCCGCAGCTCGACGCGCGGGTC 180

Qy        598 GTCGTCCCCTTGC 610
              | ||| |   || |
Db        179 GACGCCTGGTTCC 167


RESULT 8
US-09-252-991A-296
; Sequence 296, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 296
;   LENGTH: 1041
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-296

  Query Match             3.2%;  Score 36.2;  DB 4;  Length 1041;
  Best Local Similarity   49.2%;  Pred. No. 2;
  Matches   95;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy        418 GACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAG 477
              |||  |  |   | ||  |  ||   ||| |||| | |   ||  ||  | | | |||  |
Db        338 GACATGCGCCGCGCCCTGGCGCTATGGCCGGAACTGGCGCCTTGGAGCGAGGCCCTGCTG 397

Qy        478 CGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCAC 537
              | ||   |    |  |   || | |  ||       ||  |||| | ||||| ||  |
Db        398 GGCCAGTACCTTGCCGTGCACCCGGGCTTCCAGCGCCTGGCGTTCGCGGGCGGAAGGGTC 457

Qy        538 GACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACC 597
              | |||||  |||| |  |     | |  |||  || |  |  ||| ||   | ||      |
Db        458 GGCCTGACCCTGCTGCTGGGCGATGCCATGGAGTGCCTGCCGCAGCTCGACGCGCGGGTC 517

Qy        598 GTCGTCCCCTTGC 610
              | ||| |   || |
Db        518 GACGCCTGGTTCC 530


RESULT 9
US-09-252-991A-7481/c
; Sequence 7481, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7481
;   LENGTH: 909
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7481

  Query Match             3.2%;  Score 36;  DB 4;  Length 909;
  Best Local Similarity   45.4%;  Pred. No. 2.1;
  Matches  129;  Conservative    0;  Mismatches  155;  Indels    0;  Gaps    0;
```

```
Qy        794 AATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGG 853
Db        350 AAACACTGGCCAGGGAAAACGCCTTGATCTTGCACGAGGGCCCCGCCACCCTTGGCCGGG 291

Qy        854 TCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCT 913
Db        290 TCGGCAACGGACAGAGGTGGGACATGCGTTTGCGCAGAAGGACGACGTTGCTGCTGGTAT 231

Qy        914 AGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGA 973
Db        230 TTGCAGTGCTGTTGCTGCTGGCGTTCGGCTACGGCTGGCATGCCTGGCGCAGCCTGTTGC 171

Qy        974 CGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTC 1033
Db        170 GCGAGCAGGGTGTCGAGCGCCTGGAGTGGCAAGGCCTGGGCCTGTCCGCCGAAGGCATCG 111

Qy       1034 GTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTC 1077
Db        110 GGCTGCGACGGCTGGCGCTGGAGCGGCGCGGCGCGGATGGCGCC 67
```

RESULT 10
US-09-252-991A-7278
; Sequence 7278, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7278
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7278

Query Match 3.1%; Score 35.2; DB 4; Length 675;
Best Local Similarity 46.1%; Pred. No. 3.1;
Matches 118; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

```
Qy        822 CGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAA 881
Db          2 CTTGCACGAGGGCCCCGCCACCCTTGGCCGGGTCGGCAACGGACAGAGGTGGGACATGCG 61

Qy        882 TTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCT 941
Db         62 TTTGCGCAGAAGGACGACGTTGCTGCTGGTATTTGCAGTGCTGTTGCTGCTGGCGTTCGG 121

Qy        942 GGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACT 1001
Db        122 CTACGGCTGGCATGCCTGGCGCAGCCTGTTGCGCGAGCAGGGTGTCGAGCGCCTGGAGTG 181

Qy       1002 CTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACG 1061
Db        182 GCAAGGCCTGGGCCTGTCCGCCGAAGGCATCGGGCTGCGACGGCTGGCGCTGGAGCGGCG 241

Qy       1062 AGACAGGGCAGACGTC 1077
Db        242 CGGCGCGGATGGCGCC 257
```

RESULT 11
US-09-252-991A-953
; Sequence 953, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 953
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-953

Query Match 3.1%; Score 35; DB 4; Length 630;
Best Local Similarity 49.7%; Pred. No. 3.5;
Matches 89; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

```
Qy        470 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 529
Db         59 CCCTGATCCTGGTCAGCGCCATCCTGGTCAACAACTTTGTCCTGGTGCAGTTCCTCGGCC 118

Qy        530 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 589
Db        119 TGTGCCCGTTCATGGGCGTGTCGCGGAAGATCGAGACGGCCATCGGCCTGTCCCTCGCCA 178

Qy        590 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG 648
Db        179 CCACCTTCGTCCTGACCCTGGCGGCGATGTGCAGCCATATCCTGCAACGCTACGTGCTG 237
```

RESULT 12
US-09-252-991A-1127/c
; Sequence 1127, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1127
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1127

Query Match 3.1%; Score 35; DB 4; Length 777;
Best Local Similarity 49.7%; Pred. No. 3.8;
Matches 89; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

```
Qy        470 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 529
Db        686 CCCTGATCCTGGTCAGCGCCATCCTGGTCAACAACTTTGTCCTGGTGCAGTTCCTCGGCC 627

Qy        530 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 589
Db        626 TGTGCCCGTTCATGGGCGTGTCGCGGAAGATCGAGACGGCCATCGGCCTGTCCCTCGCCA 567

Qy        590 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG 648
Db        566 CCACCTTCGTCCTGACCCTGGCGGCGATGTGCAGCCATATCCTGCAACGCTACGTGCTG 508
```

```
RESULT 13
US-09-621-976-15639
; Sequence 15639, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 15639
;   LENGTH: 505
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-15639

  Query Match             3.0%;  Score 34.6;  DB 4;  Length 505;
  Best Local Similarity   14.6%;  Pred. No. 4.1;
  Matches   31;  Conservative   94;  Mismatches   88;  Indels    0;  Gaps    0;

Qy         33 GGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCT 92
              :|::    || |  ::|    : : :: :::|: :: :::     :|: || :  :::  :|
Db         38 RGKYGTSGGRCGGSRGWMCSKWGYRYSYWGYKWKSWSKKMKKYSGKMGTSKSTRKYRTYT 97

Qy         93 GTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCT 152
              :: ::    :   :: :    ::: ::::: : : | : :: : :| :   :| | :||:
Db         98 SKCRKTTCKYRGWWSWKWRMWKRRKMYYYRMKCYSCASYSYSYRRCRKYTGMTRGWYGCK 157

Qy        153 TCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTG 212
              :   ::   :: ::|  :: ||||:  : ::|:|: :  :    ::   :|:| :::  :
Db        158 KRMCKSSTRYMTRYTRYWKMTGACYGSKGMSCKGSRSKYYGSWKWYYGKYTMCTSKYKSS 217

Qy        213 TTTCGGCGCCCTCCTCGTCATGTTGTCGTGCAT 245
              :  ::::::|:|:: | :  :  | |::::: |
Db        218 KMSYKKSSMCYTYMMCYYTYWWCTCTYKKSYYT 250


RESULT 14
US-09-433-241A-1/c
; Sequence 1, Application US/09433241A
; Patent No. 6525244
; GENERAL INFORMATION:
;  APPLICANT: Allen, Steve
;  APPLICANT:  Falco, Carl
;  APPLICANT:  Ralfalski, Antoni
;  TITLE OF INVENTION: Plant Histidinol-Phosphate Aminotransferase Homologs
;  FILE REFERENCE: BB1256 US NA
;  CURRENT APPLICATION NUMBER: US/09/433,241A
;  CURRENT FILING DATE:  1999-11-04
;  PRIOR APPLICATION NUMBER: 60/107,273
;  PRIOR FILING DATE: 1998-11-05
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
;   LENGTH: 431
;   TYPE: DNA
;   ORGANISM: Zea mays
US-09-433-241A-1

  Query Match             3.0%;  Score 34.4;  DB 4;  Length 431;
  Best Local Similarity   60.9%;  Pred. No. 4.4;
  Matches   56;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

Qy        516 GATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGA 575
              ||||  ||| | ||| | |   | |||||||  ||   ||| |||||||    || ||
Db        232 GATGGGCTGATACGGGGCGAGGGTCCTGAGGTGGCGCCGGATGAAGGAGTCACCGGTCAG 173

Qy        576 GTGGCACCTGTTCTCGTCCACCGTCGTCCCCT 607
                | | | |   |||| || ||| ||||  ||
Db        172 CCGCCCCTTCGCCTCGGCCGCCGCCGTCGGCT 141


RESULT 15
US-09-252-991A-3833
; Sequence 3833, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 3833
;   LENGTH: 1011
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3833

  Query Match             3.0%;  Score 34.4;  DB 4;  Length 1011;
  Best Local Similarity   45.5%;  Pred. No. 6.1;
  Matches  122;  Conservative    0;  Mismatches  146;  Indels    0;  Gaps    0;

Qy        364 TTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGG 423
              || |  | || ||| || || | |  |||     | |          ||    | |  ||
Db        388 TTCCAGGGCGTGGCGCTGGGCGCCTTCATCGAAGGCATCCCGGTGGAGAACCGCAGCTTC 447

Qy        424 TTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC 483
              |    |    | |||||||  |  | ||| |||  | |  |   |||   | |  |
Db        448 GCCGGCGGTTCGCTGGACTGGATCGCGCCGTTCCCGCTGTTCTGCGGCCTGGCCCTGATC 507

Qy        484 CTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTG 543
              || ||  | |  | | || | ||  || | |||| |   |  || ||| | |   | |
Db        508 GTCGCCTACACCCTGCTCGGCTGCACCTGGCTGATCATGAAGACCGAAGGCCGCCTGCAG 567

Qy        544 AGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC 603
              ||    |    |  || |    || | | | || |   ||| |  ||  || ||  ||
Db        568 GAGCGCATGCACGACCTGGCGCGCCCGCTGGCGTTGGTGCTGCTGGCGATCATCGGGGTG 627

Qy        604 CCCTTGCAGAAGAGTACGAGGCACTACG 631
              |  | | ||  ||  |  | | |
Db        628 GTCAGCCTGTGGACGCCGCTGGCCCATG 655


Search completed: May  9, 2004, 22:17:17
Job time : 60.25 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2004, 16:13:07 ; Search time 473.75 Seconds
(without alignments)
10852.855 Million cell updates/sec

Title: US-10-679-999-17
Perfect score: 1135
Sequence: 1 GTATACCTGTTTTGAGTGTG.....AGGCCCAACAATTACCTAGG 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 4861726

Minimum DB seq length: 0
Maximum DB seq length: 1135

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1135	100.0	1135	13	US-10-679-999-17	Sequence 17, Appl
	2	1109.4	97.7	1135	13	US-10-679-999-14	Sequence 14, Appl
	3	440.8	38.8	454	9	US-09-366-133-5	Sequence 5, Appli
	4	440.8	38.8	454	13	US-10-679-999-5	Sequence 5, Appli
	5	440.8	38.8	454	15	US-10-214-037-5	Sequence 5, Appli
	6	378.4	33.3	491	9	US-09-366-133-2	Sequence 2, Appli
	7	378.4	33.3	491	13	US-10-679-999-2	Sequence 2, Appli
	8	378.4	33.3	491	15	US-10-214-037-2	Sequence 2, Appli
	9	43	3.8	468	15	US-10-097-044A-12	Sequence 12, Appl
c	10	42.4	3.7	1116	15	US-10-156-761-6640	Sequence 6640, Ap
	11	41.2	3.6	1049	13	US-10-142-426-358	Sequence 358, App
	12	41.2	3.6	1049	15	US-10-123-155-358	Sequence 358, App
	13	41.2	3.6	1049	15	US-10-146-731-358	Sequence 358, App
	14	41.2	3.6	1049	15	US-10-140-472-358	Sequence 358, App
	15	41.2	3.6	1049	15	US-10-141-761-358	Sequence 358, App
	16	41.2	3.6	1049	15	US-10-142-885-358	Sequence 358, App
	17	41.2	3.6	1049	15	US-10-158-790-358	Sequence 358, App
	18	41.2	3.6	1049	16	US-10-137-871-358	Sequence 358, App
	19	41.2	3.6	1049	16	US-10-140-923-358	Sequence 358, App
	20	41.2	3.6	1049	16	US-10-141-756-358	Sequence 358, App
	21	41.2	3.6	1049	16	US-10-141-759-358	Sequence 358, App
	22	41.2	3.6	1049	16	US-10-140-805-358	Sequence 358, App
	23	41.2	3.6	1049	16	US-10-140-864-358	Sequence 358, App
	24	40.6	3.6	754	9	US-09-229-200A-13	Sequence 13, Appl
	25	39.4	3.5	675	15	US-10-156-761-2371	Sequence 2371, Ap
c	26	38.6	3.4	711	15	US-10-156-761-2558	Sequence 2558, Ap
c	27	37.6	3.3	717	15	US-10-133-973-2	Sequence 2, Appli
	28	37.4	3.3	653	15	US-10-184-644-402	Sequence 402, App
	29	37.4	3.3	653	15	US-10-184-634-402	Sequence 402, App
	30	37.4	3.3	945	16	US-10-369-493-42967	Sequence 42967, A
c	31	37	3.3	915	15	US-10-156-761-5089	Sequence 5089, Ap
	32	36.6	3.2	957	15	US-10-156-761-867	Sequence 867, App
	33	36.2	3.2	816	15	US-10-156-761-5917	Sequence 5917, Ap
c	34	36	3.2	608	13	US-10-027-632-87464	Sequence 87464, A
c	35	36	3.2	608	13	US-10-027-632-87465	Sequence 87465, A
c	36	36	3.2	608	16	US-10-027-632-87464	Sequence 87464, A
c	37	36	3.2	608	16	US-10-027-632-87465	Sequence 87465, A
	38	35.8	3.2	866	13	US-10-425-114-18793	Sequence 18793, A
	39	35.8	3.2	962	15	US-10-259-165-591	Sequence 591, App
	40	35.8	3.2	996	13	US-10-425-114-992	Sequence 992, App
c	41	35.6	3.1	459	15	US-10-029-386-26484	Sequence 26484, A
c	42	35.6	3.1	486	13	US-10-465-217-13	Sequence 13, Appl
c	43	35.6	3.1	542	15	US-10-029-386-12784	Sequence 12784, A
	44	35.6	3.1	815	10	US-09-976-782-17	Sequence 17, Appl
	45	35.6	3.1	815	10	US-09-976-782-19	Sequence 19, Appl

ALIGNMENTS

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RESULT 1
US-10-679-999-17
; Sequence 17, Application US/10679999
; Publication No. US20040067520A1
;  GENERAL INFORMATION:
;       APPLICANT: Mann, Michael B.
;                  Hecht, Randy I.
;       TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                           METHODS
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Amgen Inc.
;            STREET: 1840 DeHavilland Drive
;            CITY: Thousand Oaks
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 91320-1789
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/679,999
;            FILING DATE: 06-Oct-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/568,528
;            FILING DATE: 09-May-2000
;            APPLICATION NUMBER: 09/267,517
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Knight, Matthew W.
;            REGISTRATION NUMBER: 36,846
;            REFERENCE/DOCKET NUMBER: A-416
;  INFORMATION FOR SEQ ID NO: 17:
;       SEQUENCE CHARACTERISTICS:
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;           LENGTH: 1135 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: double
;           TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-679-999-17

  Query Match            100.0%;  Score 1135;  DB 13;  Length 1135;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1135;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATACCTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGC 60
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Db          1 GTATACCTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGC 60

Qy         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120

Qy        121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180

Qy        181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240

Qy        241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGA 300

Qy        301 ATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360

Qy        361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420

Qy        421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480

Qy        481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540

Qy        541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600

Qy        601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660

Qy        661 TTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTT 720

Qy        721 TGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCG 780

Qy        781 AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC 840

Qy        841 AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA 900

Qy        901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT 960

Qy        961 AAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCG 1020

Qy       1021 CCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCA 1080

Qy       1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135


RESULT 2
US-10-679-999-14
; Sequence 14, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;       APPLICANT: Mann, Michael B.
;                  Hecht, Randy I.
;       TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                           METHODS
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Amgen Inc.
;            STREET: 1840 DeHavilland Drive
;            CITY: Thousand Oaks
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 91320-1789
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/679,999
;            FILING DATE: 06-Oct-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/568,528
;            FILING DATE: 09-May-2000
;            APPLICATION NUMBER: 09/267,517
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Knight, Matthew W.
;            REGISTRATION NUMBER: 36,846
;            REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 14:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1135 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-679-999-14

  Query Match            97.7%;  Score 1109.4;  DB 13;  Length 1135;
  Best Local Similarity  98.6%;  Pred. No. 0;
  Matches 1119;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 GTATACCTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGC 60
              |||||||||||||||||||||| ||||| || ||||||||||||||   || |||||
Db          1 GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGA 60

Qy         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120
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Qy        121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180

Qy        181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240

Qy        241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC 300

Qy        301 ATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360

Qy        361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420

Qy        421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480

Qy        481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540
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Db        481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540

Qy        541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600

Qy        601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660

Qy        661 TTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTT 720

Qy        721 TGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCG 780

Qy        781 AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC 840

Qy        841 AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA 900
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Db        841 AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA 900

Qy        901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT 960
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Db        901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT 960

Qy        961 AAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCG 1020
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Db        961 AAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCG 1020

Qy       1021 CCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCA 1080
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Db       1021 CCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCA 1080

Qy       1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
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Db       1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
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RESULT 3
US-09-366-133-5
; Sequence 5, Application US/09366133
; Patent No. US20020009798A1

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;  GENERAL INFORMATION:
;    APPLICANT:  Pelleymounter, Mary Ann
;    APPLICANT:  Hecht, Randy I
;    APPLICANT:  Mann, Michael B
;    TITLE OF INVENTION:  OB PROTEIN COMPOSITIONS AND METHODS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  91230-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/366,133
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/920,608
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pessin, Karol M.
;      REFERENCE/DOCKET NUMBER:  A-345
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  454 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-366-133-5

  Query Match             38.8%;  Score 440.8;  DB 9;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 2e-130;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
               ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy         744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
               ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||
Db          63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy         804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
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Db         123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy         864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
               |||||||||||||||||||||||||||||||||||||||| | ||||||||||||||||
Db         183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy         924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy         984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy        1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy        1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
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Db         423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454
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RESULT 4
US-10-679-999-5
; Sequence 5, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 454 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-679-999-5

  Query Match             38.8%;  Score 440.8;  DB 13;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 2e-130;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              |||||||||||||||||||||||||||||||||||||||||| | ||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              ||||||||||||||||||||||||||||||
Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 5
US-10-214-037-5
; Sequence 5, Application US/10214037
; Publication No. US20030054997A1
;   GENERAL INFORMATION:
;        APPLICANT: Pelleymounter, Mary Ann
;                   Hecht, Randy I
;                   Mann, Michael B
;        TITLE OF INVENTION: OB PROTEIN COMPOSITIONS AND METHODS
;        NUMBER OF SEQUENCES: 6
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 Dehavilland Drive
;             CITY: Thousand Oaks
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 91230-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/214,037
;             FILING DATE: 05-Aug-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/920,608
;             FILING DATE: 07-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Pessin, Karol M.
;             REFERENCE/DOCKET NUMBER: A-345
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 454 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-214-037-5

  Query Match             38.8%;  Score 440.8;  DB 15;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 2e-130;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              |||||||||||||||||||||||||||||||||||||||||| | ||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
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                |||||||
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Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||||  | ||||||||   ||||| || ||
Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              |||||||||||| | |||||||||  |||||| | |||||| |||||||
Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||  ||||||
Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
                | | |||||||| |||  | ||| || |||| ||||||||||||||||||   ||
Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||| |||
Db        400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              ||||||| | ||||||| ||||||||||||||
Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491
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RESULT 8
US-10-214-037-2
; Sequence 2, Application US/10214037
; Publication No. US20030054997A1
;   GENERAL INFORMATION:
;        APPLICANT: Pelleymounter, Mary Ann
;                   Hecht, Randy I
;                   Mann, Michael B
;        TITLE OF INVENTION: OB PROTEIN COMPOSITIONS AND METHODS
;        NUMBER OF SEQUENCES: 6
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 Dehavilland Drive
;             CITY: Thousand Oaks
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 91230-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/214,037
;             FILING DATE: 05-Aug-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/920,608
;             FILING DATE: 07-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Pessin, Karol M.
;             REFERENCE/DOCKET NUMBER: A-345
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 491 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-214-037-2

  Query Match             33.3%;  Score 378.4;  DB 15;  Length 491;
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  Best Local Similarity   89.8%;  Pred. No. 2e-110;
  Matches  406;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||||  | ||||||||   ||||| || ||
Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              |||||||||||| | |||||||||  |||||| | |||||| |||||||
Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||  ||||||
Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
                | | |||||||| |||  | ||| || |||| ||||||||||||||||||   ||
Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||| |||
Db        400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              ||||||| | ||||||| ||||||||||||||
Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491
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RESULT 9
US-10-097-044A-12
; Sequence 12, Application US/10097044A
; Publication No. US20030143220A1
;   GENERAL INFORMATION:
;        APPLICANT: Capon, Daniel J.
;                   Gregory, Timothy J.
;        TITLE OF INVENTION: Adheson Variants
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 460 Point San Bruno Blvd
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: patin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/097,044A
;             FILING DATE: 28-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/457,918
;             FILING DATE: 1-JUN-1995
;             APPLICATION NUMBER: 08/236311
;             FILING DATE: 02-MAY-1994
;             APPLICATION NUMBER: 07/936190
;             FILING DATE: 26-AUG-1992
;             APPLICATION NUMBER: 07/842777
;             FILING DATE: 18-FEB-1992
;             APPLICATION NUMBER: 07/250785
;             FILING DATE: 28-SEP-1988
;             APPLICATION NUMBER: 07/104329
```

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;            FILING DATE: 02-OCT-1987
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Kubinec, Jeffrey S.
;            REGISTRATION NUMBER: 36,575
;            REFERENCE/DOCKET NUMBER: P0444P1C3
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415/225-8228
;            TELEFAX: 415/952-9881
;            TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 12:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 468 bases
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-097-044A-12

  Query Match             3.8%;  Score 43;  DB 15;  Length 468;
  Best Local Similarity   49.5%;  Pred. No. 0.0053;
  Matches  143;  Conservative    0;  Mismatches  140;  Indels    6;  Gaps    1;

Qy        379 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 438
              | ||||    || | || | | || |||||     ||  || |||            | |
Db        127 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 186

Qy        439 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 492
              |     |||||| | ||   ||||||||||||| ||    |    ||  ||||      |||
Db        187 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 246

Qy        493 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 552
              | |       ||  |||  |||  | |  |||       |       |    ||| ||
Db        247 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 306

Qy        553 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 612
              |||  |  ||||  |||||  ||  ||  ||  |||        |   || |    || |||
Db        307 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 366

Qy        613 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 661
              | | | |||   || |  ||| |||  |||  |    | |  |||  |||
Db        367 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 415


RESULT 10
US-10-156-761-6640/c
; Sequence 6640, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
;  APPLICANT: OMURA, SATOSHI
;  APPLICANT:  IKEDA, HARUO
;  APPLICANT:  ISHIKAWA, JUN
;  APPLICANT:  HORIKAWA, HIROSHI
;  APPLICANT:  SHIBA, TADAYOSHI
;  APPLICANT:  SAKAKI, YOSHIYUKI
;  APPLICANT:  HATTORI, MASAHIRA
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-262
;  CURRENT APPLICATION NUMBER: US/10/156,761
;  CURRENT FILING DATE:  2002-05-29
;  PRIOR APPLICATION NUMBER: JP 2001-204089
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-272697
;  PRIOR FILING DATE: 2001-08-02
;  NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 6640
;   LENGTH: 1116
;   TYPE: DNA
;   ORGANISM: Streptomyces avermitilis
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1116)
US-10-156-761-6640

  Query Match             3.7%;  Score 42.4;  DB 15;  Length 1116;
  Best Local Similarity   51.0%;  Pred. No. 0.012;
  Matches  100;  Conservative    0;  Mismatches   96;  Indels    0;  Gaps    0;

Qy        434 AGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCT 493
              ||  | |||  |  |     ||   | || ||  ||| ||| || |||     | ||||
Db        706 AGGAGAACTCGGGGTCGAAGACCCGGACGACCGGGGCGCCGTCGCGCTCGCCCACCATGA 647

Qy        494 CGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGA 553
              || | |||||  |    |   |  | | ||  | | | || || | |||  |  |  |
Db        646 CGCTGCCCGTGTGGAGGTCACCGTGGAGCGGGGCCTGCGCGCTCGTCATGAAGACGTGGC 587

Qy        554 GGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGA 613
              ||| |  || ||  ||| |     ||| |  ||   ||    | ||  | | ||  |  |
Db        586 GGAGGTCGGCGACCTCGGTGCGCAGGCGCGGGTCGGCGCGGAACGCGGCCGCCAGGTCGT 527

Qy        614 AGAGTACGAGGCACTA 629
              |||| || ||  | |
Db        526 CGAGTCCGGGGTGCCA 511


RESULT 11
US-10-142-426-358
; Sequence 358, Application US/10142426
; Publication No. US20040048333A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C224
;  CURRENT APPLICATION NUMBER: US/10/142,426
;  CURRENT FILING DATE:  2002-05-09
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 358
;   LENGTH: 1049
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-142-426-358

  Query Match             3.6%;  Score 41.2;  DB 13;  Length 1049;
  Best Local Similarity   4.7%;  Pred. No. 0.028;
  Matches   33;  Conservative  204;  Mismatches  466;  Indels    0;  Gaps    0;

Qy        155 TGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTT 214
              :  |:  :  :  :  :        ::  ::  :   :  : :     |       :
Db        328 KEIGDAKFLHFLPSLIQLDLLSFNFELQVYRASMNLSQAFSSLKSLKILRIRGYVFKELKS 387

Qy        215 TCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACG 274
                :  :      : :  |   :    :: :   :  : : :  :   : |::: :|  :
Db        388 FNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKISPSGDSSEVGFCSN 447

Qy        275 TGGTCCTGACCGACTTACCGTTTCGAATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTC 334
              :  :      :   :: ::::: :  : :    : :::  : ::   | : :  :
Db        448 ARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQTLDLSKNSIFF 507

Qy        335 GGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGT 394
```

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Db        508 VKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLHSTAFEELHK 567

Qy        395 GGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGT 454

Db        568 LEVLDISSNSHYFQSEGITHMLNFTKNLKVLQKLMMNDNDISSSTSRTMESESLRTLEFR 627

Qy        455 TTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGT 514

Db        628 GNHLDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNLSLAKNGL 687

Qy        515 TGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCG 574

Db        688 KSFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQDAF 747

Qy        575 AGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTAC 634

Db        748 QLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDAVWFVWWVNHTEVTIPY 807

Qy        635 TCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCT 694

Db        808 LATDVTCVGPGAHKGQSVISLDDLYTCELDLTNLILFSLSISVSLFLMVMMTASHLYFWDV 867

Qy        695 AGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGC 754

Db        868 WYIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPAVTEWVLAELVAKLEDPREKHFNLC 927

Qy        755 TGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGG 814

Db        928 LEERDWLPGQPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVII 987

Qy        815 GCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTG 857

Db        988 LIFLEKPFQKSKFLQLRKRLCGSSVLEWPTNPQAHPYFWQCLK 1030
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RESULT 12
US-10-123-155-358
; Sequence 358, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C30
; CURRENT APPLICATION NUMBER: US/10/123,155
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 358
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-155-358

Query Match 3.6%; Score 41.2; DB 15; Length 1049;
Best Local Similarity 4.7%; Pred. No. 0.028;

Matches 33; Conservative 204; Mismatches 466; Indels 0; Gaps 0;

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Qy        155 TGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTT 214

Db        328 KEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLKSLKILRIRGYVFKELKS 387

Qy        215 TCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACG 274

Db        388 FNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQPKRLKVIDLSVNKISPSGDSSEVGFCSN 447

Qy        275 TGGTCCTGACCGACTTACCGTTTCGAATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTC 334

Db        448 ARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQTLDLSKNSIFF 507

Qy        335 GGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGT 394

Db        508 VKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLHSTAFEELHK 567

Qy        395 GGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGT 454

Db        568 LEVLDISSNSHYFQSEGITHMLNFTKNLKVLQKLMMNDNDISSSTSRTMESESLRTLEFR 627

Qy        455 TTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGT 514

Db        628 GNHLDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNLSLAKNGL 687

Qy        515 TGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCG 574

Db        688 KSFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQDAF 747

Qy        575 AGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTAC 634

Db        748 QLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDAVWFVWWVNHTEVTIPY 807

Qy        635 TCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCT 694

Db        808 LATDVTCVGPGAHKGQSVISLDDLYTCELDLTNLILFSLSISVSLFLMVMMTASHLYFWDV 867

Qy        695 AGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGC 754

Db        868 WYIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPAVTEWVLAELVAKLEDPREKHFNLC 927

Qy        755 TGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGG 814

Db        928 LEERDWLPGQPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVII 987

Qy        815 GCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTG 857

Db        988 LIFLEKPFQKSKFLQLRKRLCGSSVLEWPTNPQAHPYFWQCLK 1030
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RESULT 13
US-10-146-731-358
; Sequence 358, Application US/10146731
; Publication No. US20030129692A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin

```
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C323
;  CURRENT APPLICATION NUMBER: US/10/146,731
;  CURRENT FILING DATE:  2002-05-15
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 358
;   LENGTH: 1049
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-146-731-358

  Query Match             3.6%;  Score 41.2;  DB 15;  Length 1049;
  Best Local Similarity   4.7%;  Pred. No. 0.028;
  Matches   33;  Conservative  204;  Mismatches  466;  Indels    0;  Gaps    0;

Qy        155 TGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTT 214
              :  |: :  :   :    :          :: :: :    :  : :      |      :
Db        328 KEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLKSLKILRIRGYVFKELKS 387

Qy        215 TCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACG 274
              :  :      : :  |   :    :: :   :  : : :   :  |::: :|  :
Db        388 FNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKISPSGDSSEVGFCSN 447

Qy        275 TGGTCCTGACCGACTTACCGTTTCGAATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTC 334
              :  :      :    :: ::::: :  : :    : :::  : ::   | : :  :
Db        448 ARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQTLDLSKNSIFF 507

Qy        335 GGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGT 394
              :::::      :        : |  |:          : :    :          :
Db        508 VKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLHSTAFEELHK 567

Qy        395 GGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGT 454
              :  :: ::   :   |::      :   :      :  ::   |     : :
Db        568 LEVLDISSNSHYFQSEGITHMLNFTKNLKVLQKLMMNDNDISSSTSRTMESESLRTLEFR 627

Qy        455 TTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGT 514
              : ::  :  : ::    :              : :   :|  : :    :  : : |
Db        628 GNHLDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNLSLAKNGL 687

Qy        515 TGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCG 574
              ::   ::    :  : ::    :  : : : :          :   :: |::   :
Db        688 KSFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQDAF 747

Qy        575 AGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTAC 634
              ::  : :  :|:    :    :  :  :  :  : :  :  :  :|  :   :
Db        748 QLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDAVWFVWWVNHTEVTIPY 807

Qy        635 TCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCT 694
              ::  :| | ::|  :: : :  ||          : : :::   ::::|  : :
Db        808 LATDVTCVGPGAHKGQSVISLDLYTCELDLTNLILFSLSISVSLFLMVMMTASHLYFWDV 867

Qy        695 AGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGC 754
              :  ::  :   :      :  ::   : :|::   |  : |  :|:  : :      |
Db        868 WYIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPAVTEWVLAELVAKLEDPREKHFNLC 927

Qy        755 TGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGG 814
              :::  |      :  :  ::  : : |::: :|      :  :    :  :::
Db        928 LEERDWLPGQPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVII 987

Qy        815 GCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTG 857
              :   :::    :::  |: :    |   |: :   | :
Db        988 LIFLEKPFQKSKFLQLRKRLCGSSVLEWPTNPQAHPYFWQCLK 1030


RESULT 14
US-10-140-472-358
; Sequence 358, Application US/10140472
; Publication No. US20030138888A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C168
;  CURRENT APPLICATION NUMBER: US/10/140,472
;  CURRENT FILING DATE:  2002-05-06
;  Prior Apploication removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 358
;   LENGTH: 1049
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-140-472-358

  Query Match             3.6%;  Score 41.2;  DB 15;  Length 1049;
  Best Local Similarity   4.7%;  Pred. No. 0.028;
  Matches   33;  Conservative  204;  Mismatches  466;  Indels    0;  Gaps    0;

Qy        155 TGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTT 214
              :  |: :  :   :    :          :: :: :    :  : :      |      :
Db        328 KEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLKSLKILRIRGYVFKELKS 387

Qy        215 TCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACG 274
              :  :      : :  |   :    :: :   :  : : :   :  |::: :|  :
Db        388 FNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKISPSGDSSEVGFCSN 447

Qy        275 TGGTCCTGACCGACTTACCGTTTCGAATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTC 334
              :  :      :    :: ::::: :  : :    : :::  : ::   | : :  :
Db        448 ARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQTLDLSKNSIFF 507

Qy        335 GGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGT 394
              :::::      :        : |  |:          : :    :          :
Db        508 VKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLHSTAFEELHK 567

Qy        395 GGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGT 454
              :  :: ::   :   |::      :   :      :  ::   |     : :
Db        568 LEVLDISSNSHYFQSEGITHMLNFTKNLKVLQKLMMNDNDISSSTSRTMESESLRTLEFR 627

Qy        455 TTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGT 514
              : ::  :  : ::    :              : :   :|  : :    :  : : |
Db        628 GNHLDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNLSLAKNGL 687

Qy        515 TGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCG 574
              ::   ::    :  : ::    :  : : : :          :   :: |::   :
Db        688 KSFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQDAF 747

Qy        575 AGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTAC 634
              ::  : :  :|:    :    :  :  :  :  : :  :  :  :|  :   :
Db        748 QLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDAVWFVWWVNHTEVTIPY 807

Qy        635 TCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCT 694
              ::  :| | ::|  :: : :  ||          : : :::   ::::|  : :
Db        808 LATDVTCVGPGAHKGQSVISLDLYTCELDLTNLILFSLSISVSLFLMVMMTASHLYFWDV 867

Qy        695 AGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGC 754
              :  ::  :   :      :  ::   : :|::   |  : |  :|:  : :      |
Db        868 WYIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPAVTEWVLAELVAKLEDPREKHFNLC 927

Qy        755 TGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGG 814
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Db        928 LEERDWLPGQPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVII 987

Qy        815 GCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTG 857
Db        988 LIFLEKPFQKSKFLQLRKRLCGSSVLEWPTNPQAHPYFWQCLK 1030


RESULT 15
US-10-141-761-358
; Sequence 358, Application US/10141761
; Publication No. US20030148432A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C198
;  CURRENT APPLICATION NUMBER: US/10/141,761
;  CURRENT FILING DATE:  2002-05-08
;  Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 358
;   LENGTH: 1049
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-141-761-358

  Query Match             3.6%;  Score 41.2;  DB 15;  Length 1049;
  Best Local Similarity   4.7%;  Pred. No. 0.028;
  Matches   33;  Conservative  204;  Mismatches  466;  Indels    0;  Gaps    0;

Qy        155 TGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTT 214
Db        328 KEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLKSLKILRIRGYVFKELKS 387

Qy        215 TCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACG 274
Db        388 FNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKISPSGDSSEVGFCSN 447

Qy        275 TGGTCCTGACCGACTTACCGTTTCGAATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTC 334
Db        448 ARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQTLDLSKNSIFF 507

Qy        335 GGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGT 394
Db        508 VKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLHSTAFEELHK 567

Qy        395 GGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGT 454
Db        568 LEVLDISSNSHYFQSEGITHMLNFTKNLKVLQKLMMNDNDISSSTSRTMESESLRTLEFR 627

Qy        455 TTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGT 514
Db        628 GNHLDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNLSLAKNGL 687

Qy        515 TGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCG 574
Db        688 KSFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQDAF 747

Qy        575 AGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTAC 634
Db        748 QLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDAVWFVWWVNHTEVTIPY 807

Qy        635 TCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCT 694
Db        808 LATDVTCVGPGAHKGQSVISLDLYTCELDLTNLILFSLSISVSLFLMVMMTASHLYFWDV 867

Qy        695 AGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGC 754
Db        868 WYIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPAVTEWVLAELVAKLEDPREKHFNLC 927

Qy        755 TGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGG 814
Db        928 LEERDWLPGQPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVII 987

Qy        815 GCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTG 857
Db        988 LIFLEKPFQKSKFLQLRKRLCGSSVLEWPTNPQAHPYFWQCLK 1030


Search completed: May 11, 2004, 09:06:46
Job time : 475.75 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 18:55:54 ; Search time 2223.5 Seconds
(without alignments)
15243.344 Million cell updates/sec

Title: US-10-679-999-17
Perfect score: 1135
Sequence: 1 GTATACCTGTTTTGAGTGTG.....AGGCCCAACAATTACCTAGG 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 54259654

Minimum DB seq length: 0
Maximum DB seq length: 1135

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	3	43.2	3.8	910	29	CNS006ON	AL065629 Drosophil
c	4	42.8	3.8	509	10	BF593096	BF593096 7o56e02.x
c	5	42.8	3.8	552	14	CA686322	CA686322 wlm96.pk0
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	12	41.6	3.7	340	9	AA302570	AA302570 EST15740
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c	23	41.6	3.7	455	10	AW590575	AW590575 hg46c10.x
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c	27	41.6	3.7	467	9	AI752976	AI752976 cr03b09.x
c	28	41.6	3.7	467	9	AI879509	AI879509 au53d05.x
c	29	41.6	3.7	469	9	AI088760	AI088760 qa16h11.x
c	30	41.6	3.7	472	14	CA448944	CA448944 UI-H-EI1-
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	32	41.6	3.7	480	10	BE873734	BE873734 601483878
c	33	41.6	3.7	481	9	AI347031	AI347031 qp54h02.x
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c	36	41.6	3.7	492	10	AW402830	AW402830 UI-HF-BK0
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c	38	41.6	3.7	500	9	AI149427	AI149427 qc72f02.x
c	39	41.6	3.7	506	14	CA661058	CA661058 wlm1.pk00
c	40	41.6	3.7	511	14	CA679280	CA679280 wlm4.pk00
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ALIGNMENTS

RESULT 1
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DEFINITION SCJLLR2006A05.g LR2 Saccharum officinarum cDNA clone SCJLLR2006A05 5', mRNA sequence.
ACCESSION CA128348
VERSION CA128348.1 GI:35009126
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE 1 (bases 1 to 1039)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br

Plate: 006 row: A column: 05
Seq primer: T7 Promoter Primer.

FEATURES Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCJLLR2006A05"
/lab_host="DH10B"
/clone_lib="LR2"
/note="Organ: Leaf roll from field grown adult plants (small insert library); Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [Leaf roll from field grown adult plants (small insert library)]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"

ORIGIN

Query Match 3.8%; Score 43.6; DB 13; Length 1039;
Best Local Similarity 45.6%; Pred. No. 27;
Matches 154; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

```
Qy        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
              | |||  || || ||  ||   ||   ||   | | |   | | || | | | || ||
Db        303 TCGGTGGAGACGTACAAGATCTACATCTTCAAGGTGCTGAAGCAGGTGCACCCGGACATC 362

Qy        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546
                | ||||||     | |     | |  |||  ||||    |   |    |  ||  ||
Db        363 TGCATCTCGTCCAAGGCCATGTCCATCATGAACTTCTTCATCAACGACATCTTCCATAAG 422

Qy        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
              ||| ||  | ||  ||  |    |      |   ||  |    |  |||  |      || |
Db        423 CTGGCGGCGGAGGCGGCCAAACTGGCGCGCTACAACAAGAAGCCCACCATCACGTGCCGC 482

Qy        607 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 666
                |    ||| |      | |  ||| |||| | || | | |  | |  || |||||
Db        483 GAGATCCAGACTTTCGTCCGCCTCGTCCTCCCCGGCGAGCTCGCCAAGCACGCCTTCTTC 542

Qy        667 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 726
              |||  | ||  |||||  |  || |    |    | | |  |  ||  |||     |  |
Db        543 GAGGTGCACCAAGGCCGTTACCAAGTTCACCAGCTCCTATGCGAGCGATGGGACCTGCCT 602

Qy        727 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGT 764
              || ||| | |    | | |      || ||| ||  ||
Db        603 TAGTTTCGTTCATGAAGTACTAGTGTGTTGTCGTGTGT 640
```

RESULT 2
AI869699/c
LOCUS AI869699 486 bp mRNA linear EST 07-MAR-2000
DEFINITION wm02f07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2433253 3' similar to gb:J05016 PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AI869699
VERSION AI869699.1 GI:5543667
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 486)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 751 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 282.

FEATURES Location/Qualifiers
source 1. .486
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2433253"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Brn25"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATAGGTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 3.8%; Score 43.2; DB 9; Length 486;
Best Local Similarity 54.4%; Pred. No. 24;
Matches 87; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

```
Qy        914 AGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGA 973
              | |||   |||||||  |||    | |    || |  || | |   ||   |   ||||
Db        430 ACAGAGATCTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGA 371

Qy        974 CGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTC 1033
              |   ||| |      |||| || ||  |||| ||   | | ||   | |  | | ||| |
Db        370 CCAAGGAAGAGCTTTGAAGGCCTGAGGTCTGCGAAAGGTGGGAGGAGGCAGACGCCCTGC 311

Qy       1034 GTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1073
              || | |||  |||| ||| || ||  |||| | ||  | ||
Db        310 GTGGCCCATGGTCGGGGCGTCCACGCCGAGGCCGGCAACA 271
```

RESULT 3
CNS006ON
LOCUS CNS006ON 910 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14J21 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL065629
VERSION AL065629.1 GI:4944698
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 910)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information

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            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES              Location/Qualifiers
     source           1. .910
                      /organism="Drosophila melanogaster"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:7227"
                      /clone="BACR14J21"
                      /clone_lib="RPCI-98"
                      /note="end : T7"
ORIGIN

  Query Match             3.8%;  Score 43.2;  DB 29;  Length 910;
  Best Local Similarity   19.2%;  Pred. No. 31;
  Matches   81;  Conservative  159;  Mismatches  180;  Indels    2;  Gaps    1;

Qy        315 GAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG 374
              | ||: |  : ||| ||| :||||| | | |:|: |  : ||    |:   :::: |
Db        468 GGGGKGGGGKGGGGGGGGGHGGGGGSGGGTDTKTWTGGKSTGGGGGGGSSGGSSSKGGGC 527

Qy        375 GGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCA 434
              |:  :  || |:      : ||| :::| :  :::::: :  : ::| : :   | |:
Db        528 GSGSYGGGGGGYGGTGSGSGGGGSSSSGCSSSSSSSSSSSSCGSSSBGCBSSCGCGSCSY 587

Qy        435 GTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTC 494
              : ::  :||:   | :: :  ::     | :::|:|| : ::: :| : : : :|
Db        588 SSSSTGSTGSCGCGSSSSSSSSSCSSTSTSSSSTSGCGYSSSGSBSSSCSSTBTSSSTT 647

Qy        495 GTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAG 554
              :|:  : :|:: ::|:|  ||: |:|::: ::|::: : :: ::  : : ::: :::  :
Db        648 BTBTKBTSTYSTSYTST--TTSTTSTBSBTSYGSBBKSTSSTSSSTSSSTSSSSSSSTSS 705

Qy        555 GAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAA 614
                : : :::::||:   |: : ::|  |:: ::   : :   : : :| : :
Db        706 CTSTKBYSTSTBSYSBTTBTBTTSTSTBBTTSTBYTBBTTBYTKSTTSMTSTYTTBBSTS 765

Qy        615 GAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGA 674
              : :|  : :::  |  :| :|  : :: : |:    |: ::::: :|: :   : :
Db        766 KBSTBTSTBKSTGTKTBTSBTTSCTSSSSSBSTSYSYSTSCBSSBSBSSTSYSBCTSTST 825

Qy        675 CAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTG 734
              : : :::::    :   ::| ::|:||    :| |: :||:::: |  :  ||  || |
Db        826 STSSBBSSBSSSSSCGTSBTSSSTSTTSTCTSTTCKTSTGBSSYGTGTSTYTTBTTTATT 885

Qy        735 CT 736
              :|
Db        886 ST 887


RESULT 4
BF593096/c
LOCUS       BF593096                509 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  7o56e02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578187 3'
            similar to TR:Q29305 Q29305 DISULFIDE ISOMERASE-RELATED PROTEIN ;,
            mRNA sequence.
ACCESSION   BF593096
VERSION     BF593096.1  GI:11685420
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 509)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 405.
FEATURES              Location/Qualifiers
     source           1. .509
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:3578187"
                      /lab_host="DH10B"
                      /clone_lib="NCI_CGAP_Kid11"
                      /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                      a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                      Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
                      prepared, and ss circles were made in vitro. Following HAP
                      purification, this DNA was used as tracer in a subtractive
                      hybridization reaction. The driver was PCR-amplified cDNAs
                      from a pool of 5,000 clones made from the same library
                      (cloneIDs 1322376-1323911, 1456007-1456775, and
                      1500552-1502855). Subtraction by Bento Soares and M.
                      Fatima Bonaldo.  "
ORIGIN

  Query Match             3.8%;  Score 42.8;  DB 10;  Length 509;
  Best Local Similarity   54.4%;  Pred. No. 30;
  Matches   86;  Conservative    0;  Mismatches   72;  Indels    0;  Gaps    0;

Qy        916 AGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACG 975
              |||   |||||||  |||     | |    || |  || | |   ||   |  |||||
Db        425 AGAAATCTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGACC 366

Qy        976 GTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGT 1035
                |||  |      |||| || ||  |||| |    | | ||   | |  | | ||| |||
Db        365 AAGGAAGAGCTTTGAAGGCCTGAGGTCTGCGGAAGGTGGGAGGAGGCAGACGCCCTGCGT 306

Qy       1036 AGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1073
               | |||  |||| ||| || ||| |||| | ||  | |
Db        305 GGCCCATGGTCGGGGCGTCCACACCGAGGCCGGCAACA 268


RESULT 5
CA686322/c
LOCUS       CA686322                552 bp    mRNA    linear   EST 25-NOV-2002
DEFINITION  wlm96.pk032.g24 wlm96 Triticum aestivum cDNA clone wlm96.pk032.g24
            5' end, mRNA sequence.
ACCESSION   CA686322
VERSION     CA686322.1  GI:25275677
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 552)
  AUTHORS   Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
            Miao,G., Caraher,N. and Hanafey,M.K.
  TITLE     DuPont Wheat cDNA Sequence
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Scott V. Tingey
            Crop Genetics
            E. I. DuPont de Nemours and Company
```

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          1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
          Tel: 302-631-2602
          Fax: 302-631-2607
          Email: Scott.V.Tingey@USA.dupont.com
          Seq primer: M13.
FEATURES             Location/Qualifiers
     source          1. .552
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /cultivar="Stephens"
                     /db_xref="taxon:4565"
                     /clone="wlm96.pk032.g24"
                     /tissue_type="leaf"
                     /clone_lib="wlm96"
                     /note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
                     XhoI; Wheat (Triticum aestivum L.) seedlings 96 hr after
                     inoculation w/ E. graminis"
ORIGIN

  Query Match             3.8%;  Score 42.8;  DB 14;  Length 552;
  Best Local Similarity   48.0%;  Pred. No. 31;
  Matches  119;  Conservative    0;  Mismatches  129;  Indels    0;  Gaps    0;

Qy        402 GGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAA 461
              |||||| | | ||| |||          || ||||  || | || | |  ||||  ||| |
Db        347 GGGTAGAGGCGTACGCGATGACCGAGAGGCCCAGCGGGGCGGGCCTGTTCAGTGGCCGCA 288

Qy        462 GATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTT 521
              | |  || | || ||  ||| ||  | |      || | | |      ||  |  |
Db        287 GGTGCAGTTGGTGCAGGTGCAGCTGGCGCCGCACTTGCACTTGCCGTCGTTCTCCGCGGC 228

Qy        522 CTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCA 581
              ||  |||     | |    ||      |  |  ||  | |  |||| |||    || ||
Db        227 CTCCTGCACCTCGAAGTGNCTCTTNTCGGTGTCGACCATGACGATGCCGTAGCCGTCGCC 168

Qy        582 CCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGA 641
              | | ||| ||  |   ||| |  |   ||||  |      | |||||    |  |   |
Db        167 CTTCTTCACGCACTGGGTCTTGTCGGCGCAGTCGCAGTTGCCGCACTTGTCAGCCATGGC 108

Qy        642 CGTGTTGG 649
              || ||||
Db        107 GGTCTTGG 100


RESULT 6
CNS012I3
LOCUS       CNS012I3                 645 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC
            BACN08C07 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL101589
VERSION     AL101589.1  GI:5613200
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 645)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .645
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACN08C07"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : T7"
ORIGIN

  Query Match             3.7%;  Score 42.4;  DB 29;  Length 645;
  Best Local Similarity   14.0%;  Pred. No. 41;
  Matches   73;  Conservative  117;  Mismatches  330;  Indels    2;  Gaps    1;

Qy         14 GAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAGAAGGAGA 73
              | |          |||           |  :      |          |||        :: |
Db         73 GNGNNNNNNNTGGTNNTNNTNNNGGTCKKGCGNNGNNNNNNNGGGCCNNNTNGGKKKGG 132

Qy         74 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 133
              |||    |  |||    | ||| |      |      |      |        :|
Db        133 NGGGNNNGTNGTGGTNGNNGGGGGGGGNNNNNGGNNNTTNNTNGGTTTNNNGGNNNNNSC 192

Qy        134 ACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACC 193
              |: |        | :  : : :        :  :        ::  : :
Db        193 CCSNCTNCNNNNTNTTNSSSSSSNSNNNTNNNNNSNNSNNNSNNNNSSGSSSNNNNSGG 252

Qy        194 TCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACC 253
              ::  :    :|:  :    |::   :  | :    :     :| :  :  :::
Db        253 SSNNNSNSNNGSGSSSSSNSNTSSNNNSNNTNSNNNSSNNNNSSTNSNNSNNSSSSTSTT 312

Qy        254 AGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGTACGCGCC 313
                :  :  :  |: :: :: ||| : | ::: :  ::      |   ::|  : :
Db        313 NTSNSTSSNNSATGSSSSNSSSGGTTBSGSSSSSSSSNSSSNNNNNNASNNSBT--SNSNN 370

Qy        314 AGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCG 373
                  | :|  ::|: ::: :::: :   :|: |  ::    ::|| :::|| : :  ::
Db        371 SNSATTSSTNGSSGSSSSSSSSSSTSSNTSTSSTSNSSNSNTSSTTSSSSTTNSTSTSSS 430

Qy        374 GGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCC 433
              :: :|   ::| |   :| :   :    | :  :    :|  | :  |        : |
Db        431 SSNSTGSSSSTTTTNSSASSNNNSNNNNGNSSSSNAANSTSTTNSSNTTTSSNNSNSSCN 490

Qy        434 AGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCT 493
                  :       |      |:::     :   :   :  |:| :   |: ::|| |
Db        491 TTSANNTSSTNTTNTAGNNNNATSSSNSNNNSSNNNSNNNSNSGSGTSSGNTSSSSCTGT 550

Qy        494 CGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGC 535
              ::   : ::   :|  :  : ||  :  :   ||::: : ::
Db        551 BSSGNSNSSNNNSCNGSNNSCTGNSSNSSSTTTGSSSSSNSS 592


RESULT 7
CNS017SY/c
LOCUS       CNS017SY                 1101 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN37L08 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL108460
VERSION     AL108460.1  GI:5628764
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
```

http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.

```
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACN37L08"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : SP6"
ORIGIN

  Query Match             3.7%;  Score 42.4;  DB 29;  Length 1101;
  Best Local Similarity   18.2%;  Pred. No. 53;
  Matches   48;  Conservative  112;  Mismatches  104;  Indels    0;  Gaps    0;

Qy         16 GTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAGAAGGAGAAG 75
Db        968 SKSBTSBSSBSTSSSASBSSSSSSSBSSTSTTBSTSBBBSTSSSSSGSSSSSBBSTBSBS 909

Qy         76 GGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCAC 135
Db        908 SBTBTTTTTBTKSTSSTSSSSTSBTTTSBBSSSSSSSBSSSBSTTTSBSSTBSSYGSSSB 849

Qy        136 CACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTC 195
Db        848 TCTSKCSTBTSGSTBTSTBMSKBSSTSSTSBTSGSSBCGGSCGSTSGSSCSSBCGKSTSS 789

Qy        196 CACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAG 255
Db        788 GSTSSGTTCGBCSSTGGCSCCCYCSCCCTCSTCGTSTCCSCSCSGTGSSBKCCYSTSSSA 729

Qy        256 TCGCAGGAGTGGCAGGACGTGGTC 279
Db        728 STGSSCSSSTSSSSGGTKMTGGCC 705
```

```
RESULT 8
AI289506/c
LOCUS       AI289506                512 bp    mRNA    linear   EST 21-DEC-1998
DEFINITION  qw28e11.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:1992428 3'
            similar to gb:J05016 PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN
            PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   AI289506
VERSION     AI289506.1  GI:3932686
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 512)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 2198   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 307.
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FEATURES             Location/Qualifiers
     source          1. .512
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1992428"
                     /tissue_type="serous papillary carcinoma, high grade, 2
                     pooled tumors"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Ut4"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.48 kb. Life Technologies catalog #:
                     11542-016"
ORIGIN

  Query Match             3.7%;  Score 42.2;  DB 9;  Length 512;
  Best Local Similarity   53.8%;  Pred. No. 41;
  Matches   86;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy        914 AGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGA 973
Db        435 ACAGAGATCTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGA 376

Qy        974 CGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTC 1033
Db        375 CCAAGGAAGAGCTTTGAAGGCCTGAGGTCTGCGGAAGGTGGGAGGAGGCANACGCCCTGC 316

Qy       1034 GTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1073
Db        315 GTGGCCCATGGTCGGGGCGTCCACGCCGAGGCCGGCAACA 276
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RESULT 9
AI687271/c
LOCUS       AI687271                586 bp    mRNA    linear   EST 14-DEC-1999
DEFINITION  tp94e04.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2206974 3'
            similar to gb:J05016 PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN
            PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   AI687271
VERSION     AI687271.1  GI:4898565
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 586)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 2159   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 399.
FEATURES             Location/Qualifiers
     source          1. .586
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2206974"
                     /tissue_type="poorly-differentiated endometrial
                     adenocarcinoma, 2 pooled tumors"
                     /lab_host="DH10B"
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                     /clone_lib="NCI_CGAP_Ut3"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.45 kb. Life Technologies catalog #:
                     11541-018"
ORIGIN

  Query Match             3.7%;  Score 42.2;  DB 9;  Length 586;
  Best Local Similarity   53.8%;  Pred. No. 44;
  Matches   86;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy        914 AGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGA 973
              | |||   |||||| |||    | |    || |  || | |   ||   |   ||||
Db        423 ACAGAGATCTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGA 364

Qy        974 CGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTC 1033
              |   ||| |      |||| || ||  |||| |    | | ||   | |  | | ||| |
Db        363 CCAAGGAAGAGCTTTGAAGGCCTGAGGTCTGCGGAAGGTGGGAGGAGGCANACGCCCTGC 304

Qy       1034 GTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1073
              || | |||  |||| ||| || ||  |||| | ||  | |
Db        303 GTGGCCCATGGTCGGGGCGTCCACGCCGAGGCCGGCAACA 264


RESULT 10
AA330793
LOCUS       AA330793                343 bp    mRNA    linear   EST 21-APR-1997
DEFINITION  EST34531 Embryo, 6 week I Homo sapiens cDNA 5' end similar to
            protein disulfide isomerase related protein, mRNA sequence.
ACCESSION   AA330793
VERSION     AA330793.1  GI:1983035
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 343)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   96026280
   PUBMED   7566098
COMMENT     Other_ESTs: THC189915
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .343
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="ATCC (inhost):132414"
                     /db_xref="taxon:9606"
                     /dev_stage="embryo, 6 wks"
                     /clone_lib="Embryo, 6 week I"
                     /note="Organ: embryo; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI"
ORIGIN

  Query Match             3.7%;  Score 41.8;  DB 9;  Length 343;
  Best Local Similarity   53.1%;  Pred. No. 43;
  Matches   85;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy        914 AGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGA 973
              | |||   |||||| |||    | |    || |  || | |   ||   |   ||||
Db        161 ACAGAGATCTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGA 220

Qy        974 CGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTC 1033
              |   ||| |      |||| || ||  |||| |    | | ||   | |  | | ||| |
Db        221 CCAAGGAAGAGCTTTGAAGGCCTGAGGTCTGCGGAAGGTGGGAGGAGGCAGACGNCCTGC 280

Qy       1034 GTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1073
              || | |||  |||| ||| |  ||  |||| | ||  | |
Db        281 GTGGCCCATGGTCGGGGCGTNCACGNCGAGGCCGGCAACA 320


RESULT 11
CB047414
LOCUS       CB047414                337 bp    mRNA    linear   EST 17-JAN-2003
DEFINITION  NISC_gg02g05.y1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
            IMAGE:3253425 5', mRNA sequence.
ACCESSION   CB047414
VERSION     CB047414.1  GI:27785701
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 337)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation:
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
             DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC)
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            info@image.llnl.gov
            Plate: LLAM7961  row: M  column: 10
            Seq primer: M13RP1 reverse primer (ABI).
FEATURES             Location/Qualifiers
     source          1. .337
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3253425"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Kid11"
                     /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
                     prepared, and ss circles were made in vitro. Following HAP
                     purification, this DNA was used as tracer in a subtractive
                     hybridization reaction. The driver was PCR-amplified cDNAs
                     from a pool of 5,000 clones made from the same library
                     (cloneIDs 1322376-1323911, 1456007-1456775, and
                     1500552-1502855). Subtraction by Bento Soares and M.
                     Fatima Bonaldo.  "
```

```
ORIGIN

  Query Match             3.7%;  Score 41.6;  DB 14;  Length 337;
  Best Local Similarity   53.8%;  Pred. No. 47;
  Matches   86;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy        914 AGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGA 973
              | |||   |||||||  |||     | |     || |  || | |   ||   |   ||||
Db         16 ACAGAGATCTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGA 75

Qy        974 CGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTC 1033
              |  ||| |      ||||  || ||  |||| |   | | ||   | |  | | ||| |
Db         76 CCAAGGAAGAGCTTTGAAGGCCTGAGGTCTGCGGAAGGTGGGAGGAGGCAGACGCCCTGC 135

Qy       1034 GTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1073
              || | |||  |||| ||| || ||  |||| | ||  | |
Db        136 GTGGCCCATGGTCGGGGCGTCCACGCCGAGGCCGGCAACA 175


RESULT 12
AA302570
LOCUS       AA302570                340 bp    mRNA    linear   EST 18-APR-1997
DEFINITION  EST15740 Aorta endothelial cells Homo sapiens cDNA 5' end similar
            to protein disulfide isomerase related protein, mRNA sequence.
ACCESSION   AA302570
VERSION     AA302570.1  GI:1954902
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   96026280
   PUBMED   7566098
COMMENT     Other_ESTs: THC189915
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .340
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="ATCC (inhost):114748"
                     /db_xref="taxon:9606"
                     /cell_type="endothelial cell"
                     /dev_stage="adult"
                     /clone_lib="Aorta endothelial cells"
                     /note="Organ: aorta; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI"
ORIGIN

  Query Match             3.7%;  Score 41.6;  DB 9;  Length 340;
  Best Local Similarity   53.8%;  Pred. No. 47;
  Matches   86;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy        914 AGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGA 973
              | |||   |||||||  |||     | |     || |  || | |   ||   |   ||||
Db         61 ACAGAGATCTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGA 120

Qy        974 CGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTC 1033
              |  ||| |      ||||  || ||  |||| |   | | ||   | |  | | ||| |
Db        121 CCAAGGAAGAGCTTTGAAGGCCTGAGGTCTGCGGAAGGTGGGAGGAGGCAGACGCCCTGC 180

Qy       1034 GTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1073
              || | |||  |||| ||| || ||  |||| | ||  | |
Db        181 GTGGCCCATGGTCGGGGCGTCCACGCCGAGGCCGGCAACA 220


RESULT 13
CA720412/c
LOCUS       CA720412                408 bp    mRNA    linear   EST 26-NOV-2002
DEFINITION  wkm2n.pk007.a4 wkm2n Triticum aestivum cDNA clone wkm2n.pk007.a4 5'
            end, mRNA sequence.
ACCESSION   CA720412
VERSION     CA720412.1  GI:25442205
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 408)
  AUTHORS   Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
            Miao,G., Caraher,N. and Hanafey,M.K.
  TITLE     DuPont Wheat cDNA Sequence
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Scott V. Tingey
            Crop Genetics
            E. I. DuPont de Nemours and Company
            1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
            Tel: 302-631-2602
            Fax: 302-631-2607
            Email: Scott.V.Tingey@USA.dupont.com
            Seq primer: M13.
FEATURES             Location/Qualifiers
     source          1. .408
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /cultivar="Spring wheat"
                     /db_xref="taxon:4565"
                     /clone="wkm2n.pk007.a4"
                     /tissue_type="kernel"
                     /lab_host="DH10B"
                     /clone_lib="wkm2n"
                     /note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
                     XhoI; Wheat (Triticum aestivum L.) kernel malted 175 hours
                     at 4 C, normalized"
ORIGIN

  Query Match             3.7%;  Score 41.6;  DB 14;  Length 408;
  Best Local Similarity   48.0%;  Pred. No. 51;
  Matches  119;  Conservative    0;  Mismatches  129;  Indels    0;  Gaps    0;

Qy        402 GGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAA 461
              ||||||  | | |||  |||          || ||||  ||  | ||  | |  ||||  ||| |
Db        302 GGGTAGAGGCGTACGCGATGACCGAGAGGCCCAGCGGGGCGGGCCTGTTCAGTGGCCGCA 243

Qy        462 GATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTT 521
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Db        242 GGTGCAGTTGGTGCAGGTGCAGCTGGCGCCGCACTTGCACTTGCCGTCGTTCTCCGCGGC 183

Qy        522 CTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCA 581

Db        182 CTCCTGCACCTCGAAGTGGCTCTTCTCGGTGTCGACCATGACGATGCCGTAGCCGTCGCC 123

Qy        582 CCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGA 641

Db        122 CTTCTTCACGCACTGGGTCTTGTCGGCGCAGTCGCAGTTGCCGCACTTGTCAGCCATGGC 63

Qy        642 CGTGTTGG 649

Db         62 GGTCTTGG 55


RESULT 14
BJ248630/c
LOCUS       BJ248630                414 bp    mRNA    linear   EST 05-APR-2002
DEFINITION  BJ248630 Y. Ogihara unpublished cDNA library, Wh_f Triticum
            aestivum cDNA clone whf7e08 5', mRNA sequence.
ACCESSION   BJ248630
VERSION     BJ248630.1  GI:20059367
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 414)
  AUTHORS   Ogihara,Y. and Murai,K.
  TITLE     Expressed genes in Triticum aestivum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .414
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="whf7e08"
                     /tissue_type="spike at flowering date"
                     /dev_stage="Feekes' scale 10.5.1"
                     /clone_lib="Y. Ogihara unpublished cDNA library, Wh_f"
ORIGIN

  Query Match             3.7%;  Score 41.6;  DB 12;  Length 414;
  Best Local Similarity   48.0%;  Pred. No. 52;
  Matches  119;  Conservative    0;  Mismatches  129;  Indels    0;  Gaps    0;

Qy        402 GGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAA 461

Db        278 GGGTAGAGGCGTACGCGATGACCGAGAGGCCCAGCGGGGCGGGCCTGTTCAGTGGCCGCA 219

Qy        462 GATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTT 521

Db        218 GGTGCAGTTGGTGCAGGTGCAGCTGGCGCCGCACTTGCACTTGCCGTCGTTCTCCGCGGC 159

Qy        522 CTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCA 581

Db        158 CTCCTGCACCTCGAAGTGGCTCTTCTCGGTGTCGACCATGACGATGCCGTAGCCGTCGCC 99

Qy        582 CCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGA 641

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Db         38 GGTCTTGG 31


RESULT 15
BE488609/c
LOCUS       BE488609                439 bp    mRNA    linear   EST 31-JUL-2000
DEFINITION  WHE1051_G06_M11ZS Wheat unstressed seedling shoot normalized cDNA
            library Triticum aestivum cDNA clone WHE1051_G06_M11, mRNA
            sequence.
ACCESSION   BE488609
VERSION     BE488609.1  GI:9608142
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 439)
  AUTHORS   Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D.,
            Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
            Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Normalized shoot cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES             Location/Qualifiers
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                     /organism="Triticum aestivum"
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                     /cultivar="Chinese Spring"
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                     /dev_stage="Five day old seedling"
                     /lab_host="E. coli DH10B"
                     /clone_lib="Wheat unstressed seedling shoot normalized
                     cDNA library"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid
                     pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
                     surface-sterilized, germinated and grown aseptically in
                     the  dark at room temperature on filter paper with water,
                     nystatin and  cefotaxime in covered crystallization
                     dishes. Roots were harvested.  The tissue, total RNA, and
                     poly(A) RNA were prepared, a cDNA library  was made in the
                     TJ Close lab (Choi, Close, Fenton) at the University  of
                     California, Riverside.  The cDNA clones were in vivo
                     excised to  give pBluescript phagemids before
                     normalization was carried out.   The mass excision of
                     phagemid library and normalization were done in  HT Nguyen
                     lab by D. Zhang at Texas Tech Univeristy.  Normalization
                     protocol used was that of Soares'.  Plasmid DNA
                     preparations and DNA  sequencing were performed in the OD
                     Anderson lab (all other authors)."
ORIGIN

  Query Match             3.7%;  Score 41.6;  DB 10;  Length 439;
  Best Local Similarity   48.0%;  Pred. No. 53;
  Matches  119;  Conservative    0;  Mismatches  129;  Indels    0;  Gaps    0;

Qy        402 GGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAA 461

Db        292 GGGTAGAGGCGTACGCGATGACCGAGAGGCCCAGCGGGGCGGGCCTGTTCAGTGGCCGCA 233
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Qy        462 GATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTT 521
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Db        232 GGTGCAGTTGGTGCAGGTGCAGCTGGCGCCGCACTTGCACTTGCCGTCGTTCTCCGCGGC 173

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